



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 189458

TO: Bao-Qun Li
Location: REM-3D24/3C18
Art Unit: 1648
Wednesday, May 17, 2006
Case Serial Number: 10/764985

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: (571)272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2523

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg. 7



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GenCore version 5.1.8
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OM protein¹ protein search, using sw model

Run on: May 17, 2006, 06:11:57 ; Search time 232 Seconds
(without alignments)
17.737 Million cell updates/sec

Title: US-10-764-985-2

Perfect score: 9

Sequence: 1 KVDDTRYV 9

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2520123

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_8.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*
- 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 9 | 100.0 | 9 | ADRI2417 | Adri2417 Vaccinia |
| 2 | 9 | 100.0 | 150 | ADJ66069 | Adj66069 MVA CTL e |
| 3 | 8 | 88.9 | 9 | ADRI2435 | Adri2435 Vaccinia |
| 4 | 8 | 88.9 | 9 | ADRI2433 | Adri2433 Vaccinia |
| 5 | 8 | 88.9 | 9 | ADRI2434 | Adri2434 Vaccinia |
| 6 | 6 | 66.7 | 9 | ADRI2442 | Adri2442 Vaccinia |
| 7 | 6 | 66.7 | 9 | ADRI2437 | Adri2437 Vaccinia |
| 8 | 6 | 66.7 | 9 | ADRI2438 | Adri2438 Vaccinia |
| 9 | 6 | 66.7 | 9 | ADRI2444 | Adri2444 Vaccinia |
| 10 | 6 | 66.7 | 9 | ADRI2436 | Adri2436 Vaccinia |
| 11 | 6 | 66.7 | 9 | ADRI2443 | Adri2443 Vaccinia |
| 12 | 6 | 66.7 | 231 | AAO29584 | Aao29584 Ricordea |
| 13 | 6 | 66.7 | 267 | ADT56958 | Adt56958 Plant pol |
| 14 | 6 | 66.7 | 326 | 3 AAG42271 | Aag42271 Arabidops |
| 15 | 6 | 66.7 | 329 | 3 AAG04698 | Aag04698 Arabidops |
| 16 | 6 | 66.7 | 331 | 6 ABU28452 | Abu28452 Protein e |
| 17 | 6 | 66.7 | 331 | 6 ABU31900 | Abu31900 Protein e |
| 18 | 6 | 66.7 | 382 | 7 AB064234 | Ab064234 Klebsiell |
| 19 | 6 | 66.7 | 399 | 6 ABU33347 | Abu33347 Protein e |
| 20 | 6 | 66.7 | 399 | 9 AEB33625 | Aeb33625 L. pneumo |
| 21 | 6 | 66.7 | 400 | 6 ABP78086 | Abp78086 N. gonorr |
| 22 | 6 | 66.7 | 400 | 6 ABU37336 | Abu37336 Protein e |
| 23 | 6 | 66.7 | 400 | 6 ABU37892 | Abu37892 Protein e |

| | | | | | | |
|----|---|------|------|---|-----------|---------------------|
| 24 | 6 | 66.7 | 405 | 9 | AE836203 | Aeb36203 L. pneumo |
| 25 | 6 | 66.7 | 409 | 6 | ABU41410 | Abu41410 Protein e |
| 26 | 6 | 66.7 | 479 | 8 | ADY24554 | Ady24554 Plant ful |
| 27 | 6 | 66.7 | 485 | 3 | AAG04697 | Aag04697 Arabidops |
| 28 | 6 | 66.7 | 485 | 8 | ADN72665 | Adn72665 Thale cre |
| 29 | 6 | 66.7 | 496 | 3 | AAG04696 | Aag04696 Arabidops |
| 30 | 6 | 66.7 | 500 | 3 | AAG42270 | Aag42270 Arabidops |
| 31 | 6 | 66.7 | 510 | 3 | AB923358 | Ab923358 Herbigida |
| 32 | 6 | 66.7 | 510 | 3 | AAG42269 | Aag42269 Arabidops |
| 33 | 6 | 66.7 | 510 | 8 | ADMA48028 | Adm48028 Polypepti |
| 34 | 6 | 66.7 | 800 | 4 | ABBS59871 | Abbs59871 Drosophil |
| 35 | 6 | 66.7 | 900 | 4 | ABBB71398 | Abbb71398 Drosophil |
| 36 | 6 | 66.7 | 1136 | 8 | ADN21456 | Adn21456 Bacterial |
| 37 | 5 | 55.6 | 21 | 5 | AAU89238 | Aau89238 Insulin i |
| 38 | 5 | 55.6 | 21 | 6 | ADA04060 | Ada04060 Insulin r |
| 39 | 5 | 55.6 | 21 | 7 | ADH95273 | Adh95273 Insulin r |
| 40 | 5 | 55.6 | 21 | 8 | ADL67964 | Adl67964 IGF-1R/IR |
| 41 | 5 | 55.6 | 21 | 8 | ADM37809 | Adm37809 Anti-IR f |
| 42 | 5 | 55.6 | 27 | 6 | ADA04794 | Ada04794 IGF-1R bi |
| 43 | 5 | 55.6 | 27 | 7 | ADH96007 | Adh96007 Insulin g |
| 44 | 5 | 55.6 | 27 | 8 | ADL68698 | Adl68698 IGF-1R/IR |
| 45 | 5 | 55.6 | 27 | 8 | ADM38543 | Adm38543 Insulin a |
| 46 | 5 | 55.6 | 59 | 8 | ABO57827 | Abos7827 Human gen |
| 47 | 5 | 55.6 | 62 | 4 | AAU44424 | Aau44424 Propionib |
| 48 | 5 | 55.6 | 62 | 6 | ABM40943 | Abm40943 Propionib |
| 49 | 5 | 55.6 | 74 | 8 | ADM97962 | Adm97962 Vetispira |
| 50 | 5 | 55.6 | 74 | 8 | ADM97960 | Adm97960 5-epi-Axi |
| 51 | 5 | 55.6 | 74 | 8 | ADM97963 | Adm97963 Vetispira |
| 52 | 5 | 55.6 | 74 | 9 | AEAS1017 | Aeas1017 Tobacco 5 |
| 53 | 5 | 55.6 | 74 | 9 | AEAS1019 | Aeas1019 Potato ve |
| 54 | 5 | 55.6 | 74 | 9 | AEAS1020 | Aeas1020 Hyoscyamu |
| 55 | 5 | 55.6 | 78 | 9 | ADC88085 | Adc88085 Ribosomal |
| 56 | 5 | 55.6 | 80 | 7 | ADC88093 | Adc88093 Ribosomal |
| 57 | 5 | 55.6 | 109 | 8 | ABG28513 | Abg28513 Novel hum |
| 58 | 5 | 55.6 | 110 | 8 | ADX92114 | Adx92114 Plant ful |
| 59 | 5 | 55.6 | 118 | 7 | ADM05832 | Adm05832 Human pro |
| 60 | 5 | 55.6 | 118 | 9 | AEC88762 | Aec88762 Human cdn |
| 61 | 5 | 55.6 | 119 | 2 | AAW13923 | Aaw13923 Heavy cha |
| 62 | 5 | 55.6 | 126 | 2 | AAW11635 | Aaw11635 Human ant |
| 63 | 5 | 55.6 | 127 | 6 | ABU07100 | Abu07100 Maize Sta |
| 64 | 5 | 55.6 | 128 | 9 | AEA24151 | Aea24151 Anti-HAAR |
| 65 | 5 | 55.6 | 134 | 5 | ABG94245 | Abg94245 Apis cera |
| 66 | 5 | 55.6 | 134 | 5 | ABG80557 | Abg80557 Bee phosp |
| 67 | 5 | 55.6 | 138 | 7 | ADSE62328 | Adse62328 Rat Prote |
| 68 | 5 | 55.6 | 146 | 4 | AAU19377 | Aau19377 Human G p |
| 69 | 5 | 55.6 | 152 | 3 | AA53696 | Aa53696 Human col |
| 70 | 5 | 55.6 | 157 | 7 | AAE39932 | Aae39932 Corn phos |
| 71 | 5 | 55.6 | 157 | 7 | ADJ26813 | Adj26813 Corn phos |
| 72 | 5 | 55.6 | 159 | 4 | ABB70518 | Abb70518 Drosophil |
| 73 | 5 | 55.6 | 166 | 2 | AAW31742 | Aaw31742 Canine ob |
| 74 | 5 | 55.6 | 170 | 4 | ABB70366 | Abb70366 Drosophil |
| 75 | 5 | 55.6 | 173 | 8 | ADY05039 | Ady05039 Plant ful |
| 76 | 5 | 55.6 | 177 | 4 | ADG82719 | Adg82719 S. epider |
| 77 | 5 | 55.6 | 182 | 8 | ADY11020 | Ady11020 Plant ful |
| 78 | 5 | 55.6 | 182 | 8 | ADY11256 | Ady11256 Plant ful |
| 79 | 5 | 55.6 | 189 | 6 | ABU30050 | Abu30050 Protein e |
| 80 | 5 | 55.6 | 189 | 8 | ADY10671 | Ady10671 Plant ful |
| 81 | 5 | 55.6 | 201 | 4 | ABG21277 | Abg21277 Novel hum |
| 82 | 5 | 55.6 | 202 | 7 | ADC94805 | Adc94805 E. faeciu |
| 83 | 5 | 55.6 | 211 | 4 | AA96683 | Aab96683 Putative |
| 84 | 5 | 55.6 | 230 | 2 | AAAY29015 | Aay29015 T. gondii |
| 85 | 5 | 55.6 | 230 | 7 | ADG17081 | Adg17081 T. gondii |
| 86 | 5 | 55.6 | 235 | 3 | AB25468 | Aab25468 Pinus rad |
| 87 | 5 | 55.6 | 235 | 8 | ADQ66091 | Adq66091 Novel hum |
| 88 | 5 | 55.6 | 238 | 9 | ADY64614 | Ady64614 S. mansoni |
| 89 | 5 | 55.6 | 240 | 8 | ADX70680 | Adx70680 Plant ful |
| 90 | 5 | 55.6 | 244 | 3 | AAAG28321 | Aag28321 Arabidops |
| 91 | 5 | 55.6 | 245 | 8 | ADM22321 | Adm22321 Bacterial |
| 92 | 5 | 55.6 | 254 | 4 | ADM20093 | Adm20093 Protein e |
| 93 | 5 | 55.6 | 254 | 6 | AAE37328 | Aae37328 Human VLC |
| 94 | 5 | 55.6 | 254 | 6 | ADX74695 | Adx74695 Plant ful |
| 95 | 5 | 55.6 | 259 | 9 | AEA24176 | Aea24176 Anti-HAAR |

| | | | | | | | | | | | | | |
|-----|---|------|-----|---|-----------|---------------------|-----|---|------|-----|----|----------|--------------------|
| 97 | 5 | 55.6 | 266 | 7 | ADJ11794 | Adj11794 Rice prot | 170 | 5 | 55.6 | 451 | 4 | AAG89796 | Aag89796 C glutami |
| 98 | 5 | 55.6 | 267 | 7 | ADJ11440 | Adj11440 Rice prot | 171 | 5 | 55.6 | 451 | 9 | AEb15157 | Aeb15157 C glutami |
| 99 | 5 | 55.6 | 268 | 7 | ABM88716 | Abm88716 Rice abio | 172 | 5 | 55.6 | 452 | 3 | AAy74388 | Aay74388 Neisseria |
| 100 | 5 | 55.6 | 280 | 6 | ABU43599 | Abu43599 Protein e | 173 | 5 | 55.6 | 452 | 3 | AAy74386 | Aay74386 Neisseria |
| 101 | 5 | 55.6 | 285 | 7 | ABO82245 | AbO82245 Pseudomon | 174 | 5 | 55.6 | 452 | 3 | AAy90302 | Aay90302 1-2-rhamn |
| 102 | 5 | 55.6 | 297 | 8 | ADR46377 | Adr46377 Human End | 175 | 5 | 55.6 | 452 | 6 | ABU38141 | Abu38141 Protein e |
| 103 | 5 | 55.6 | 297 | 8 | ABM81069 | Abm81069 Tumour-as | 176 | 5 | 55.6 | 453 | 8 | ADT56183 | Adt56183 Plant pol |
| 104 | 5 | 55.6 | 299 | 7 | ADb70043 | Adb70043 C. neofor | 177 | 5 | 55.6 | 455 | 3 | AAy74387 | Aay74387 Neisseria |
| 105 | 5 | 55.6 | 300 | 8 | ADT58018 | Adt58018 Plant pol | 178 | 5 | 55.6 | 465 | 3 | ABU44153 | Abu44153 Protein e |
| 106 | 5 | 55.6 | 301 | 6 | ADA35398 | Ada35398 Acinetoba | 179 | 5 | 55.6 | 468 | 8 | ADN22809 | Adn22809 Bacterial |
| 107 | 5 | 55.6 | 302 | 3 | AAG20740 | Aag20740 Arabidops | 180 | 5 | 55.6 | 470 | 7 | ABM87867 | Abm87867 Rice abio |
| 108 | 5 | 55.6 | 306 | 8 | ADN21573 | Adn21573 Bacterial | 181 | 5 | 55.6 | 475 | 2 | AAW11641 | Aaw11641 Human ant |
| 109 | 5 | 55.6 | 307 | 3 | AAG51074 | Aag51074 Arabidops | 182 | 5 | 55.6 | 475 | 5 | ABB92034 | Abb92034 Herbicida |
| 110 | 5 | 55.6 | 307 | 3 | AAG14587 | Aag14587 Arabidops | 183 | 5 | 55.6 | 476 | 7 | ABM87991 | Abm87991 Rice abio |
| 111 | 5 | 55.6 | 308 | 9 | AEA20222 | Aea20222 Novel hum | 184 | 5 | 55.6 | 479 | 5 | ABP39590 | Abp39590 Scaphyloc |
| 112 | 5 | 55.6 | 311 | 3 | AAG20739 | Aag20739 Arabidops | 185 | 5 | 55.6 | 479 | 8 | ADSO5581 | Adso5581 Staphyloc |
| 113 | 5 | 55.6 | 311 | 8 | ADT55972 | Adt55972 Plant pol | 186 | 5 | 55.6 | 483 | 2 | AAO7445 | Aao7445 Represibl |
| 114 | 5 | 55.6 | 313 | 5 | ABB49170 | Abb49170 Listeria | 187 | 5 | 55.6 | 483 | 3 | AAG53799 | Aag53799 Arabidops |
| 115 | 5 | 55.6 | 313 | 8 | ADN99771 | Adn99771 Novel hum | 188 | 5 | 55.6 | 483 | 7 | ADM26386 | Adm26386 Hyperther |
| 116 | 5 | 55.6 | 316 | 3 | AAG14586 | Aag14586 Arabidops | 189 | 5 | 55.6 | 483 | 8 | ADT56350 | Adt56350 Plant pol |
| 117 | 5 | 55.6 | 316 | 3 | AAG51073 | Aag51073 Arabidops | 190 | 5 | 55.6 | 483 | 8 | ADT55750 | Adt55750 Plant pol |
| 118 | 5 | 55.6 | 316 | 4 | ADM19847 | Adm19847 Protein e | 191 | 5 | 55.6 | 484 | 7 | ADJ69412 | Adj69412 Human hea |
| 119 | 5 | 55.6 | 317 | 4 | ABM68103 | Abm68103 Drosophil | 192 | 5 | 55.6 | 484 | 8 | ADS44836 | Ads44836 Bacterial |
| 120 | 5 | 55.6 | 322 | 4 | ABM60330 | Abm60330 Drosophil | 193 | 5 | 55.6 | 486 | 6 | AAO26537 | Aao26537 Soybean h |
| 121 | 5 | 55.6 | 323 | 8 | ADY25260 | Ady25260 plant ful | 194 | 5 | 55.6 | 486 | 10 | AEF16012 | Aef16012 Glycine m |
| 122 | 5 | 55.6 | 326 | 3 | AAG20738 | Aag20738 Arabidops | 195 | 5 | 55.6 | 487 | 3 | AAG53798 | Aag53798 Arabidops |
| 123 | 5 | 55.6 | 328 | 6 | ABM57463 | Abm57463 AC fami | 196 | 5 | 55.6 | 497 | 5 | ABP29237 | Abp29237 Streptoco |
| 124 | 5 | 55.6 | 329 | 3 | AAG51072 | Aag51072 Arabidops | 197 | 5 | 55.6 | 497 | 6 | AAO26536 | Aao26536 Rice high |
| 125 | 5 | 55.6 | 329 | 6 | ABM52858 | Abm52858 Protein s | 198 | 5 | 55.6 | 497 | 8 | ADR83912 | Adr83912 S. pyogen |
| 126 | 5 | 55.6 | 329 | 7 | ADK62318 | Adk62318 Disease t | 199 | 5 | 55.6 | 497 | 10 | AEF16010 | Aef16010 Oryza sat |
| 127 | 5 | 55.6 | 329 | 8 | ADK343699 | Adk343699 Bacterial | 200 | 5 | 55.6 | 504 | 8 | ADJ49082 | Adj49082 Oil-assoc |
| 128 | 5 | 55.6 | 329 | 8 | ADT87145 | Adt87145 Yeast Str | 201 | 5 | 55.6 | 508 | 9 | ABE26749 | Abe26749 Consensus |
| 129 | 5 | 55.6 | 330 | 6 | ABU44842 | Abu44842 Protein e | 202 | 5 | 55.6 | 518 | 8 | ADN25097 | Adn25097 Bacterial |
| 130 | 5 | 55.6 | 330 | 6 | ABU50533 | Abu50533 Protein e | 203 | 5 | 55.6 | 523 | 3 | ABE27210 | Abe27210 Pinus rad |
| 131 | 5 | 55.6 | 331 | 3 | AAG14585 | Aag14585 Arabidops | 204 | 5 | 55.6 | 526 | 4 | AAW93809 | Aaw93809 Human pol |
| 132 | 5 | 55.6 | 331 | 6 | ABU47384 | Abu47384 Protein e | 205 | 5 | 55.6 | 526 | 8 | ADL31820 | Adl31820 Human pro |
| 133 | 5 | 55.6 | 331 | 6 | ABU15092 | Abu15092 Protein e | 206 | 5 | 55.6 | 528 | 8 | ADN23692 | Adn23692 Bacterial |
| 134 | 5 | 55.6 | 337 | 6 | ABU21270 | Abu21270 Protein e | 207 | 5 | 55.6 | 535 | 6 | ABU21542 | Abu21542 Protein e |
| 135 | 5 | 55.6 | 347 | 3 | AAG53800 | Aag53800 Arabidops | 208 | 5 | 55.6 | 545 | 9 | ABE26744 | Abe26744 Tomato sh |
| 136 | 5 | 55.6 | 348 | 8 | ADN00790 | Adn00790 Mycobacte | 209 | 5 | 55.6 | 547 | 7 | ABO68617 | AbO68617 Pseudomon |
| 137 | 5 | 55.6 | 368 | 3 | AAG28320 | Aag28320 Arabidops | 210 | 5 | 55.6 | 548 | 3 | AAy90836 | Aay90836 Tobacco s |
| 138 | 5 | 55.6 | 370 | 3 | AAG28319 | Aag28319 Arabidops | 211 | 5 | 55.6 | 548 | 3 | AAy90831 | Aay90831 Tobacco s |
| 139 | 5 | 55.6 | 370 | 7 | ADH87165 | Adh87165 Enterococ | 212 | 5 | 55.6 | 548 | 3 | AAy90833 | Aay90833 Tobacco s |
| 140 | 5 | 55.6 | 373 | 3 | ABO8467 | AbO8467 Amino aci | 213 | 5 | 55.6 | 548 | 3 | AAy90832 | Aay90832 Tobacco s |
| 141 | 5 | 55.6 | 378 | 7 | ADD02198 | Add02198 B2L viral | 214 | 5 | 55.6 | 548 | 3 | AAy90834 | Aay90834 Tobacco s |
| 142 | 5 | 55.6 | 378 | 7 | ADD02200 | Add02200 B2L viral | 215 | 5 | 55.6 | 550 | 2 | AAW01637 | Aaw01637 Tobacco e |
| 143 | 5 | 55.6 | 378 | 7 | ADJ63965 | Adj63965 Parapox v | 216 | 5 | 55.6 | 550 | 2 | AAW01637 | Aaw01637 Tobacco e |
| 144 | 5 | 55.6 | 378 | 7 | ADJ63963 | Adj63963 Parapox v | 217 | 5 | 55.6 | 550 | 5 | AAW50095 | Aaw50095 Armopha-4 |
| 145 | 5 | 55.6 | 378 | 8 | ADG46065 | Adg46065 Parapoxvi | 218 | 5 | 55.6 | 551 | 8 | ADP21177 | Adp21177 Potato ve |
| 146 | 5 | 55.6 | 378 | 8 | ADG46067 | Adg46067 Parapoxvi | 219 | 5 | 55.6 | 555 | 3 | AAW48733 | Aaw48733 Tobacco D |
| 147 | 5 | 55.6 | 378 | 8 | ADK01348 | Adk01348 D1701 B2L | 220 | 5 | 55.6 | 556 | 3 | AAy90843 | Aay90843 Potato ve |
| 148 | 5 | 55.6 | 378 | 8 | ADK01346 | Adk01346 Envelope | 221 | 5 | 55.6 | 566 | 6 | ADA54977 | Ada54977 Human pro |
| 149 | 5 | 55.6 | 378 | 8 | ADT99512 | Adt99512 Parapox o | 222 | 5 | 55.6 | 567 | 9 | ABM92568 | Abm92568 M. xanthu |
| 150 | 5 | 55.6 | 378 | 8 | ADT99514 | Adt99514 Parapox o | 223 | 5 | 55.6 | 569 | 9 | ABE26745 | Abe26745 Tobacco s |
| 151 | 5 | 55.6 | 387 | 3 | AAy99482 | Aay99482 Jojoba ac | 224 | 5 | 55.6 | 575 | 6 | AAO23887 | Aao23887 Phi-29 DN |
| 152 | 5 | 55.6 | 389 | 6 | ABM67123 | Abm67123 Phototrab | 225 | 5 | 55.6 | 575 | 6 | AAO23894 | Aao23894 Phi-29 DN |
| 153 | 5 | 55.6 | 400 | 8 | ADS43420 | Ads43420 Bacterial | 226 | 5 | 55.6 | 575 | 6 | AAO23878 | Aao23878 Phi-29 DN |
| 154 | 5 | 55.6 | 408 | 3 | AAy95855 | Aay95855 Autoantig | 227 | 5 | 55.6 | 575 | 6 | AAO23889 | Aao23889 Phi-29 DN |
| 155 | 5 | 55.6 | 413 | 6 | ABG74936 | Abg74936 A. gossyp | 228 | 5 | 55.6 | 575 | 6 | AAO23911 | Aao23911 Phi-29 DN |
| 156 | 5 | 55.6 | 426 | 6 | ABU26778 | Abu26778 Protein e | 229 | 5 | 55.6 | 575 | 6 | AAO23881 | Aao23881 Phi-29 DN |
| 157 | 5 | 55.6 | 428 | 2 | AAy35302 | Aay35302 Amino aci | 230 | 5 | 55.6 | 575 | 6 | AAO23881 | Aao23881 Phi-29 DN |
| 158 | 5 | 55.6 | 428 | 5 | ABP74064 | Abp74064 Candida a | 231 | 5 | 55.6 | 575 | 6 | AAO23885 | Aao23885 Phi-29 DN |
| 159 | 5 | 55.6 | 431 | 9 | AEb41690 | Aeb41690 L. pneumo | 232 | 5 | 55.6 | 575 | 6 | AAO23898 | Aao23898 Phi-29 DN |
| 160 | 5 | 55.6 | 431 | 8 | ADS27786 | Ads27786 Bacterial | 233 | 5 | 55.6 | 575 | 6 | AAO23899 | Aao23899 Phi-29 DN |
| 161 | 5 | 55.6 | 436 | 9 | ABE38420 | Abe38420 L. pneumo | 234 | 5 | 55.6 | 575 | 6 | AAO23900 | Aao23900 Phi-29 DN |
| 162 | 5 | 55.6 | 436 | 6 | ABP80582 | Abp80582 N. gonorr | 235 | 5 | 55.6 | 575 | 6 | AAO23910 | Aao23910 Phi-29 DN |
| 163 | 5 | 55.6 | 436 | 6 | ABU37208 | Abu37208 Protein e | 236 | 5 | 55.6 | 575 | 6 | AAO23877 | Aao23877 Native ph |
| 164 | 5 | 55.6 | 438 | 8 | ADX90021 | Adx90021 Plant ful | 237 | 5 | 55.6 | 575 | 6 | AAO23883 | Aao23883 Phi-29 DN |
| 165 | 5 | 55.6 | 440 | 2 | AAE11515 | Aae11515 Soybean c | 238 | 5 | 55.6 | 575 | 6 | AAO23891 | Aao23891 Phi-29 DN |
| 166 | 5 | 55.6 | 441 | 8 | ADY58797 | Ady58797 Tobacco e | 239 | 5 | 55.6 | 575 | 6 | AAO23893 | Aao23893 Phi-29 DN |
| 167 | 5 | 55.6 | 447 | 8 | ADN00792 | Adn00792 Mycobacte | 240 | 5 | 55.6 | 575 | 6 | AAO23896 | Aao23896 Phi-29 DN |
| 168 | 5 | 55.6 | 449 | 9 | AEA49233 | Aea49233 L. rhamno | 241 | 5 | 55.6 | 575 | 6 | AAO23907 | Aao23907 Phi-29 DN |
| 169 | 5 | 55.6 | 449 | 9 | AED03641 | Aed03641 L. rhamno | 242 | 5 | 55.6 | 575 | 6 | AAO23909 | Aao23909 Phi-29 DN |

| | | | | | | | | | |
|-----|---|------|-----|---|------|------|---|----------|--------------------|
| 243 | 5 | 55.6 | 316 | 5 | 55.6 | 1308 | 3 | AAB18167 | Aab18167 Plasmodiu |
| 244 | 5 | 55.6 | 317 | 5 | 55.6 | 1361 | 6 | ABR53440 | AbR53440 Protein s |
| 245 | 5 | 55.6 | 318 | 5 | 55.6 | 1361 | 7 | ADK64644 | ADK64644 Disease t |
| 246 | 5 | 55.6 | 319 | 5 | 55.6 | 1499 | 9 | ADV16756 | E faecal |
| 247 | 5 | 55.6 | 320 | 5 | 55.6 | 1679 | 8 | ADs43650 | Bacterial |
| 248 | 5 | 55.6 | 321 | 5 | 55.6 | 1788 | 4 | AU000016 | Human Ple |
| 249 | 5 | 55.6 | 322 | 5 | 55.6 | 1903 | 9 | ADW23580 | Lactobaci |
| 250 | 5 | 55.6 | 323 | 5 | 55.6 | 1903 | 9 | ADW23577 | Lactobaci |
| 251 | 5 | 55.6 | 324 | 5 | 55.6 | 1903 | 9 | ADW23578 | Lactobaci |
| 252 | 5 | 55.6 | 325 | 5 | 55.6 | 1903 | 9 | ADW23579 | Lactobaci |
| 253 | 5 | 55.6 | 326 | 5 | 55.6 | 1903 | 9 | ADW23480 | Lactobaci |
| 254 | 5 | 55.6 | 327 | 5 | 55.6 | 1903 | 9 | ADW23581 | Lactobaci |
| 255 | 5 | 55.6 | 328 | 5 | 55.6 | 1915 | 4 | ABBS2635 | Escherich |
| 256 | 5 | 55.6 | 329 | 5 | 55.6 | 3871 | 8 | ADN23885 | Bacterial |
| 257 | 5 | 55.6 | 330 | 5 | 55.6 | 3871 | 8 | ADN23886 | Bacterial |
| 258 | 5 | 55.6 | 331 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 259 | 5 | 55.6 | 332 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 260 | 5 | 55.6 | 333 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 261 | 5 | 55.6 | 334 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 262 | 5 | 55.6 | 335 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 263 | 5 | 55.6 | 336 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 264 | 5 | 55.6 | 337 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 265 | 5 | 55.6 | 338 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 266 | 5 | 55.6 | 339 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 267 | 5 | 55.6 | 340 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 268 | 5 | 55.6 | 341 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 269 | 5 | 55.6 | 342 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 270 | 5 | 55.6 | 343 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 271 | 5 | 55.6 | 344 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 272 | 5 | 55.6 | 345 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 273 | 5 | 55.6 | 346 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 274 | 5 | 55.6 | 347 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 275 | 5 | 55.6 | 348 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 276 | 5 | 55.6 | 349 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 277 | 5 | 55.6 | 350 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 278 | 5 | 55.6 | 351 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 279 | 5 | 55.6 | 352 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 280 | 5 | 55.6 | 353 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 281 | 5 | 55.6 | 354 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 282 | 5 | 55.6 | 355 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 283 | 5 | 55.6 | 356 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 284 | 5 | 55.6 | 357 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
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| 288 | 5 | 55.6 | 361 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 289 | 5 | 55.6 | 362 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 290 | 5 | 55.6 | 363 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 291 | 5 | 55.6 | 364 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 292 | 5 | 55.6 | 365 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 293 | 5 | 55.6 | 366 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 294 | 5 | 55.6 | 367 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 295 | 5 | 55.6 | 368 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 296 | 5 | 55.6 | 369 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 297 | 5 | 55.6 | 370 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 298 | 5 | 55.6 | 371 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 299 | 5 | 55.6 | 372 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 300 | 5 | 55.6 | 373 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 301 | 5 | 55.6 | 374 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 302 | 5 | 55.6 | 375 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 303 | 5 | 55.6 | 376 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 304 | 5 | 55.6 | 377 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 305 | 5 | 55.6 | 378 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 306 | 5 | 55.6 | 379 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 307 | 5 | 55.6 | 380 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 308 | 5 | 55.6 | 381 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 309 | 5 | 55.6 | 382 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 310 | 5 | 55.6 | 383 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 311 | 5 | 55.6 | 384 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 312 | 5 | 55.6 | 385 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 313 | 5 | 55.6 | 386 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 314 | 5 | 55.6 | 387 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |
| 315 | 5 | 55.6 | 388 | 5 | 55.6 | 4313 | 7 | ADJ95084 | Novel NOV |

| | | | | | | | | | | | | | |
|-----|---|------|----|----|-----------|---------------------|-----|---|------|----|----|-----------|---------------------|
| 389 | 4 | 44.4 | 9 | 8 | ADRI2440 | Adri2440 Vaccinia | 462 | 4 | 44.4 | 15 | 9 | AED21559 | Aed21559 Mycobacte |
| 390 | 4 | 44.4 | 9 | 8 | ADRI2441 | Adri2441 Vaccinia | 463 | 4 | 44.4 | 15 | 9 | AED21560 | Aed21560 Mycobacte |
| 391 | 4 | 44.4 | 9 | 8 | ADRI2439 | Adri2439 Vaccinia | 464 | 4 | 44.4 | 15 | 9 | AED21558 | Aed21558 Mycobacte |
| 392 | 4 | 44.4 | 9 | 8 | ADRI2445 | Adri2445 Vaccinia | 465 | 4 | 44.4 | 16 | 2 | AAR49461 | Aar49461 HLA-A30 p |
| 393 | 4 | 44.4 | 9 | 9 | AD237248 | Ad237248 Human CKI | 466 | 4 | 44.4 | 16 | 8 | ADK69565 | Adk69565 Epitope 1 |
| 394 | 4 | 44.4 | 9 | 10 | AEE25636 | Aee25636 RANKL pre | 467 | 4 | 44.4 | 16 | 8 | ADU80761 | Adu80761 Staphyloc |
| 395 | 4 | 44.4 | 9 | 10 | AEF95893 | Aef95893 Soluble M | 468 | 4 | 44.4 | 16 | 10 | AEF32533 | Aef32533 Human cor |
| 396 | 4 | 44.4 | 9 | 10 | AEF96030 | Aef96030 Soluble M | 469 | 4 | 44.4 | 17 | 2 | AAR49398 | Aar49398 HLA-Cw9 p |
| 397 | 4 | 44.4 | 9 | 10 | AEF96536 | Aef96536 SHLA-BL5 | 470 | 4 | 44.4 | 17 | 2 | AAR49387 | Aar49387 HLA-A2 po |
| 398 | 4 | 44.4 | 10 | 2 | AAR79781 | Aar79781 Rabbit te | 471 | 4 | 44.4 | 17 | 2 | AAW39861 | Aaw39861 Heavy cha |
| 399 | 4 | 44.4 | 10 | 2 | AAR79782 | Aar79782 Rabbit te | 472 | 4 | 44.4 | 17 | 3 | AAW39861 | Aaw39861 Heavy cha |
| 400 | 4 | 44.4 | 10 | 2 | AAW42663 | Aaw42663 Antigenic | 473 | 4 | 44.4 | 17 | 3 | AAW39861 | Aaw39861 Heavy cha |
| 401 | 4 | 44.4 | 10 | 2 | AAW42662 | Aaw42662 Antigenic | 474 | 4 | 44.4 | 17 | 4 | AAU16718 | Aau16718 Peptide E |
| 402 | 4 | 44.4 | 10 | 2 | AAW30139 | Aay30139 Peptide t | 475 | 4 | 44.4 | 17 | 5 | ABJ00248 | Abj00248 Human IqE |
| 403 | 4 | 44.4 | 10 | 4 | AGC68237 | Agc68237 Saccharom | 476 | 4 | 44.4 | 17 | 9 | ADY26785 | Ady26785 Human ant |
| 404 | 4 | 44.4 | 10 | 4 | ANM42842 | Anm42842 Mycoplasma | 477 | 4 | 44.4 | 17 | 9 | ADY26791 | Ady26791 Human ant |
| 405 | 4 | 44.4 | 10 | 6 | ABU090819 | Abu090819 Peptide # | 478 | 4 | 44.4 | 17 | 10 | AEF97404 | Aef97404 Phox-spec |
| 406 | 4 | 44.4 | 10 | 8 | ADK03915 | Adk03915 Hepatitis | 479 | 4 | 44.4 | 17 | 10 | AEF32554 | Aef32554 Human cor |
| 407 | 4 | 44.4 | 11 | 4 | AAU25284 | Aau25284 Schizophr | 480 | 4 | 44.4 | 18 | 2 | AAR49396 | Aar49396 HLA-Cw9 p |
| 408 | 4 | 44.4 | 11 | 4 | AAU15628 | Aau15628 Schizophr | 481 | 4 | 44.4 | 18 | 5 | AAO22320 | Aao22320 Anti-CD14 |
| 409 | 4 | 44.4 | 11 | 5 | ABG96938 | Abg96938 Human Ieu | 482 | 4 | 44.4 | 18 | 6 | ABP82344 | Abp82344 G protein |
| 410 | 4 | 44.4 | 11 | 5 | ABG96579 | Abg96579 Human Ieu | 483 | 4 | 44.4 | 18 | 9 | ADV12667 | Adv12667 Human pho |
| 411 | 4 | 44.4 | 11 | 5 | ABG97251 | Abg97251 Human Ieu | 484 | 4 | 44.4 | 18 | 10 | AEF01963 | Aef01963 Ii-key/ H |
| 412 | 4 | 44.4 | 11 | 5 | ABG96723 | Abg96723 Human Ieu | 485 | 4 | 44.4 | 19 | 2 | AAAR49395 | Aaar49395 HLA-C pos |
| 413 | 4 | 44.4 | 11 | 5 | ABR58835 | AbR58835 Alzheimer | 486 | 4 | 44.4 | 19 | 2 | AAAR49384 | Aaar49384 HLA-A2 po |
| 414 | 4 | 44.4 | 11 | 6 | ADL98772 | Adl98772 Human Ieu | 487 | 4 | 44.4 | 19 | 3 | AAAY69298 | Aay69298 Expressed |
| 415 | 4 | 44.4 | 11 | 7 | ADL98421 | Adl98421 Human Ieu | 488 | 4 | 44.4 | 19 | 3 | ADY39840 | Ady39840 Human pla |
| 416 | 4 | 44.4 | 11 | 7 | ADL99087 | Adl99087 Human Ieu | 489 | 4 | 44.4 | 20 | 1 | ADY39840 | Ady39840 Human pla |
| 417 | 4 | 44.4 | 11 | 7 | ADL98540 | Adl98540 Human Ieu | 490 | 4 | 44.4 | 20 | 2 | AAAR49383 | Aaar49383 HLA-A2 po |
| 418 | 4 | 44.4 | 11 | 8 | ADH35803 | Adh35803 Kininogen | 491 | 4 | 44.4 | 20 | 2 | AAAR49394 | Aaar49394 HLA-C pos |
| 419 | 4 | 44.4 | 11 | 8 | ADN32062 | Adn32062 Human Alz | 492 | 4 | 44.4 | 20 | 2 | AAW54559 | Aaw54559 Peptide f |
| 420 | 4 | 44.4 | 11 | 8 | ADW78895 | Adw78895 Schizophr | 493 | 4 | 44.4 | 20 | 2 | AAW82296 | Aaw82296 Dynamin 4 |
| 421 | 4 | 44.4 | 11 | 9 | ADW56518 | Adw56518 Cardiovas | 494 | 4 | 44.4 | 20 | 2 | AAW82295 | Aaw82295 Dynamin 4 |
| 422 | 4 | 44.4 | 11 | 10 | AEF95894 | Aef95894 Soluble M | 495 | 4 | 44.4 | 20 | 3 | AAAY57072 | Aay57072 Neglected |
| 423 | 4 | 44.4 | 11 | 10 | AEF96041 | Aef96041 Soluble M | 496 | 4 | 44.4 | 20 | 7 | ADG15779 | Adg15779 Rv3879c-d |
| 424 | 4 | 44.4 | 12 | 9 | ADW52295 | Adw52295 SP-3b1 he | 497 | 4 | 44.4 | 20 | 7 | ADW33877 | Adw33877 HLA bindi |
| 425 | 4 | 44.4 | 13 | 2 | AAW64576 | Aaw64576 Human Fac | 498 | 4 | 44.4 | 20 | 7 | ADW33877 | Adw33877 HLA bindi |
| 426 | 4 | 44.4 | 13 | 5 | AAE27772 | Aae27772 Human bet | 499 | 4 | 44.4 | 21 | 2 | AAAR49393 | Aaar49393 HLA-C pos |
| 427 | 4 | 44.4 | 13 | 5 | AAE27774 | Aae27774 Human bet | 500 | 4 | 44.4 | 21 | 2 | AAAR49382 | Aaar49382 HLA-A2 po |
| 428 | 4 | 44.4 | 13 | 5 | AAE27773 | Aae27773 Human bet | 501 | 4 | 44.4 | 21 | 7 | ADW35108 | Adw35108 HLA bindi |
| 429 | 4 | 44.4 | 13 | 5 | AAE27771 | Aae27771 Human bet | 502 | 4 | 44.4 | 21 | 7 | ADW33874 | Adw33874 HLA bindi |
| 430 | 4 | 44.4 | 13 | 5 | AAE27775 | Aae27775 Human bet | 503 | 4 | 44.4 | 21 | 7 | ADW33874 | Adw33874 HLA bindi |
| 431 | 4 | 44.4 | 13 | 5 | ADG66069 | Adg66069 Human bet | 504 | 4 | 44.4 | 21 | 7 | ADW33875 | Adw33875 HLA bindi |
| 432 | 4 | 44.4 | 13 | 5 | ADG66237 | Adg66237 Human pro | 505 | 4 | 44.4 | 21 | 7 | ADW33876 | Adw33876 HLA bindi |
| 433 | 4 | 44.4 | 13 | 5 | ADG66071 | Adg66071 Human bet | 506 | 4 | 44.4 | 21 | 7 | ADW35112 | Adw35112 HLA bindi |
| 434 | 4 | 44.4 | 13 | 5 | ADG66236 | Adg66236 Human pro | 507 | 4 | 44.4 | 21 | 7 | ADW33879 | Adw33879 HLA bindi |
| 435 | 4 | 44.4 | 13 | 5 | ADG66238 | Adg66238 Human pro | 508 | 4 | 44.4 | 21 | 7 | ADW35109 | Adw35109 HLA bindi |
| 436 | 4 | 44.4 | 13 | 5 | ADG66070 | Adg66070 Human bet | 509 | 4 | 44.4 | 21 | 9 | ADW56589 | Adw56589 G protein |
| 437 | 4 | 44.4 | 13 | 5 | ADG66068 | Adg66068 Human bet | 510 | 4 | 44.4 | 21 | 9 | ADW57274 | Adw57274 G protein |
| 438 | 4 | 44.4 | 13 | 5 | ADG66072 | Adg66072 Human bet | 511 | 4 | 44.4 | 21 | 9 | ADY38489 | Ady38489 Antigenic |
| 439 | 4 | 44.4 | 13 | 5 | ADG66235 | Adg66235 Human pro | 512 | 4 | 44.4 | 22 | 2 | AAW00599 | Aaw00599 Heparan s |
| 440 | 4 | 44.4 | 13 | 7 | ADM75453 | Adm75453 Potential | 513 | 4 | 44.4 | 22 | 2 | AAW42690 | Aaw42690 Peptide G |
| 441 | 4 | 44.4 | 13 | 7 | ADM75188 | Adm75188 Potential | 514 | 4 | 44.4 | 22 | 8 | ADU07977 | Adu07977 Dentin ma |
| 442 | 4 | 44.4 | 13 | 7 | ADM74924 | Adm74924 Potential | 515 | 4 | 44.4 | 22 | 8 | ADU07977 | Adu07977 Dentin ma |
| 443 | 4 | 44.4 | 13 | 7 | ADM75718 | Adm75718 Potential | 516 | 4 | 44.4 | 23 | 2 | AAAR10791 | Aaar10791 Interphot |
| 444 | 4 | 44.4 | 13 | 7 | ADM74923 | Adm74923 Potential | 517 | 4 | 44.4 | 23 | 2 | AAAR49391 | Aar49391 HLA-C pos |
| 445 | 4 | 44.4 | 13 | 7 | ADM75189 | Adm75189 Potential | 518 | 4 | 44.4 | 23 | 2 | AAAR49485 | Aar49485 HLA-A2 po |
| 446 | 4 | 44.4 | 13 | 9 | ADM03565 | Adm03565 Human RIN | 519 | 4 | 44.4 | 23 | 2 | AAW82310 | Aaw82310 Transport |
| 447 | 4 | 44.4 | 13 | 10 | AEF02153 | Aef02153 Ii-key hy | 520 | 4 | 44.4 | 23 | 3 | AAAB39086 | Aaab39086 Human sec |
| 448 | 4 | 44.4 | 14 | 1 | APB83024 | Apb83024 Shiga tox | 521 | 4 | 44.4 | 23 | 6 | ABO12608 | Abol2608 Human zin |
| 449 | 4 | 44.4 | 14 | 2 | AAV41869 | Aav41869 Rheumatoid | 522 | 4 | 44.4 | 23 | 6 | ABO12608 | Abol2608 Human zin |
| 450 | 4 | 44.4 | 14 | 5 | ABB74800 | Abb74800 Nuclear p | 523 | 4 | 44.4 | 23 | 7 | ADJ94225 | Adj94225 Interphot |
| 451 | 4 | 44.4 | 14 | 5 | ADJ23197 | Adj23197 Breast ca | 524 | 4 | 44.4 | 24 | 4 | AAAB87096 | Aaab87096 Human TAN |
| 452 | 4 | 44.4 | 14 | 7 | ADD23836 | Add23836 Breast ca | 525 | 4 | 44.4 | 24 | 4 | AAAB87096 | Aaab87096 Human TAN |
| 453 | 4 | 44.4 | 14 | 8 | ADR15907 | Adr15907 Transferr | 526 | 4 | 44.4 | 27 | 5 | AAU89414 | Aau89414 Insulin/i |
| 454 | 4 | 44.4 | 14 | 8 | ADR15967 | Adr15967 Transferr | 527 | 4 | 44.4 | 27 | 8 | ABO57756 | Abos7756 Human gen |
| 455 | 4 | 44.4 | 14 | 8 | ADS13243 | Ads13243 Human rhe | 528 | 4 | 44.4 | 28 | 2 | AAW42765 | Aaw42765 Peptide o |
| 456 | 4 | 44.4 | 14 | 9 | ADX17313 | Adx17313 Human ser | 529 | 4 | 44.4 | 29 | 10 | AEF36919 | Aef36919 Human ser |
| 457 | 4 | 44.4 | 14 | 9 | ADX56868 | Adx56868 Cardiovas | 530 | 4 | 44.4 | 30 | 4 | AAAM66739 | Aam66739 Human bon |
| 458 | 4 | 44.4 | 15 | 5 | ADG68279 | Adg68279 Human con | 531 | 4 | 44.4 | 30 | 4 | AAAM54339 | Aam54339 Human bra |
| 459 | 4 | 44.4 | 15 | 8 | ADR97649 | Adr97649 Low molec | 532 | 4 | 44.4 | 31 | 4 | ABG36393 | Abg36393 Human pep |
| 460 | 4 | 44.4 | 15 | 9 | ADW77852 | Adw77852 Human can | 533 | 4 | 44.4 | 31 | 6 | ABU12540 | Abu12540 Novel hum |
| 461 | 4 | 44.4 | 15 | 9 | ADY39841 | Ady39841 Human pla | 534 | 4 | 44.4 | 31 | 8 | ADJ28566 | Adj28566 Human mus |

| | | | | | | | | | | | | |
|-----|------|----|----|----------|--------------------|-----|---|------|----|---|-----------|---------------------|
| 535 | 44.4 | 31 | 9 | ADY30798 | Ady30798 Human epi | 608 | 4 | 44.4 | 45 | 5 | ABB79951 | Abb79951 Human pro |
| 536 | 44.4 | 31 | 9 | ADY30797 | Ady30797 Human epi | 609 | 4 | 44.4 | 45 | 5 | ABB79950 | Abb79950 Human pro |
| 537 | 44.4 | 31 | 10 | AEF32082 | Aef32082 Human cor | 610 | 4 | 44.4 | 45 | 5 | ABB79947 | Abb79947 Human pro |
| 538 | 44.4 | 32 | 10 | ABE38354 | Abe38354 Human ser | 611 | 4 | 44.4 | 45 | 7 | ADB71159 | Adb71159 Human pro |
| 539 | 44.4 | 33 | 5 | ABG99540 | Abg99540 Conus sp | 612 | 4 | 44.4 | 45 | 7 | ADB71155 | Adb71155 Human pro |
| 540 | 44.4 | 33 | 5 | ABG99548 | Abg99548 Conus sp | 613 | 4 | 44.4 | 46 | 2 | AAM60934 | Aaw60934 Streptoco |
| 541 | 44.4 | 33 | 5 | ABG99568 | Abg99568 Conus sp | 614 | 4 | 44.4 | 46 | 2 | AAM65444 | Aaw65444 Lebetin d |
| 542 | 44.4 | 33 | 7 | ABO23567 | Abo23567 Helicobac | 615 | 4 | 44.4 | 46 | 4 | AAM21521 | Aaw21521 Peptide # |
| 543 | 44.4 | 33 | 2 | ABO23567 | Abo23567 Helicobac | 616 | 4 | 44.4 | 46 | 4 | ABB43867 | Abb43867 Peptide # |
| 544 | 44.4 | 34 | 6 | ADY5095 | Aar75095 Rat SIII | 617 | 4 | 44.4 | 46 | 4 | ABM37782 | Abm37782 Peptide # |
| 545 | 44.4 | 34 | 10 | AEF38056 | Aef38056 Human ser | 618 | 4 | 44.4 | 46 | 4 | ABB26792 | Abb26792 Protein # |
| 546 | 44.4 | 35 | 10 | AEF13661 | Aef13661 Human MBL | 619 | 4 | 44.4 | 46 | 4 | AAM77593 | Aam77593 Human bon |
| 547 | 44.4 | 36 | 4 | ABB37297 | Abb37297 Peptide # | 620 | 4 | 44.4 | 46 | 4 | AAM64850 | Aam64850 Human bra |
| 548 | 44.4 | 36 | 4 | AAE08075 | Aam80875 Human imm | 621 | 4 | 44.4 | 46 | 4 | ABG59242 | Abg59242 Human liv |
| 549 | 44.4 | 36 | 4 | AAE03915 | Aae03915 Human gen | 622 | 4 | 44.4 | 46 | 4 | ADSO5557 | Adso5557 Staphyloc |
| 550 | 44.4 | 36 | 4 | ABG28481 | Abg28481 Novel hum | 623 | 4 | 44.4 | 46 | 8 | ADSO5557 | Adso5557 Staphyloc |
| 551 | 44.4 | 36 | 8 | ADK01635 | Adk01635 Hepatitis | 624 | 4 | 44.4 | 47 | 2 | AAM36149 | Aaw36149 Mutant N. |
| 552 | 44.4 | 36 | 8 | ADS93011 | Ads93011 Human alp | 625 | 4 | 44.4 | 47 | 2 | AAM36150 | Aaw36150 Wild type |
| 553 | 44.4 | 37 | 2 | AAW65450 | Aaw65450 Lebetin d | 626 | 4 | 44.4 | 47 | 2 | AAAY11508 | Aay11508 Human 5' |
| 554 | 44.4 | 37 | 3 | AAW45168 | Aaw45168 Human sec | 627 | 4 | 44.4 | 47 | 2 | ADY27478 | Ady27478 Amino aci |
| 555 | 44.4 | 37 | 4 | AAW91020 | Aam91020 Human imm | 628 | 4 | 44.4 | 47 | 9 | ADX83802 | Adx83802 Human cor |
| 556 | 44.4 | 37 | 4 | AAW64430 | Aab64430 Human sec | 629 | 4 | 44.4 | 47 | 9 | ADZ59262 | Adz59262 Bidentate |
| 557 | 44.4 | 37 | 6 | ABM72198 | Abm72198 Staphyloc | 630 | 4 | 44.4 | 48 | 2 | AAW13552 | Aaw13552 Human c-I |
| 558 | 44.4 | 37 | 8 | ABO57148 | Abo57148 Human gen | 631 | 4 | 44.4 | 48 | 2 | AAW13551 | Aaw13551 Human c-I |
| 559 | 44.4 | 38 | 2 | AAW37637 | Aaw37637 Peptide c | 632 | 4 | 44.4 | 48 | 4 | ABB41156 | Abb41156 Peptide # |
| 560 | 44.4 | 38 | 2 | AAW65449 | Aaw65449 Lebetin d | 633 | 4 | 44.4 | 48 | 4 | AAM34934 | Aam34934 Peptide # |
| 561 | 44.4 | 38 | 4 | ABB39710 | Abb39710 Peptide # | 634 | 4 | 44.4 | 48 | 4 | ABW25192 | Abw25192 Protein # |
| 562 | 44.4 | 38 | 4 | AAW33287 | Aam33287 Peptide # | 635 | 4 | 44.4 | 48 | 4 | AAW74818 | Aam74818 Human bon |
| 563 | 44.4 | 38 | 4 | AAW33068 | Aam73068 Human bon | 636 | 4 | 44.4 | 48 | 4 | AAW62016 | Aam62016 Human bra |
| 564 | 44.4 | 38 | 4 | AAW60428 | Aam60428 Human bra | 637 | 4 | 44.4 | 48 | 4 | ABG56599 | Abg56599 Human liv |
| 565 | 44.4 | 38 | 4 | ABG54782 | Abg54782 Human liv | 638 | 4 | 44.4 | 48 | 5 | ABG44605 | Abg44605 Human pep |
| 566 | 44.4 | 38 | 5 | AAU07968 | Aau07968 Human WW | 639 | 4 | 44.4 | 49 | 4 | AAW14643 | Aam14643 Peptide # |
| 567 | 44.4 | 38 | 5 | ABG42912 | Abg42912 Human pep | 640 | 4 | 44.4 | 49 | 4 | ABW40367 | Abw40367 Peptide # |
| 568 | 44.4 | 38 | 5 | ADH32374 | Adh32374 Yeast smc | 641 | 4 | 44.4 | 49 | 4 | ABW33803 | Abw33803 Peptide # |
| 569 | 44.4 | 38 | 7 | ADW49229 | Adw49229 Novel hum | 642 | 4 | 44.4 | 49 | 4 | ABW27062 | Abw27062 Peptide # |
| 570 | 44.4 | 38 | 9 | ABM94521 | Abm94521 M. xanthu | 643 | 4 | 44.4 | 49 | 4 | ABW28422 | Abw28422 Peptide # |
| 571 | 44.4 | 38 | 10 | AEF43788 | Aef43788 Lebetin 2 | 644 | 4 | 44.4 | 49 | 4 | ABB19058 | Abb19058 Protein # |
| 572 | 44.4 | 39 | 8 | ABO55221 | Abo55221 Human gen | 645 | 4 | 44.4 | 49 | 4 | AAW66777 | Aam66777 Human bon |
| 573 | 44.4 | 39 | 9 | ADV13140 | Adv13140 Human pho | 646 | 4 | 44.4 | 49 | 4 | AAW73891 | Aam73891 Human bon |
| 574 | 44.4 | 41 | 2 | AAW11905 | Aaw11905 Protein C | 647 | 4 | 44.4 | 49 | 4 | AAM54376 | Aam54376 Human bra |
| 575 | 44.4 | 41 | 2 | AAW14037 | Aay14037 Repeat se | 648 | 4 | 44.4 | 49 | 4 | ABG55642 | Abg55642 Human liv |
| 576 | 44.4 | 41 | 3 | AAW05922 | Aag05922 Arabidops | 649 | 4 | 44.4 | 49 | 4 | ABG48445 | Abg48445 Human liv |
| 577 | 44.4 | 41 | 4 | AAW84382 | Aam84382 Human imm | 650 | 4 | 44.4 | 49 | 4 | AAM02368 | Aam02368 Peptide # |
| 578 | 44.4 | 41 | 6 | ABR83861 | Abr83861 Caenorhab | 651 | 4 | 44.4 | 49 | 5 | ABG36432 | Abg36432 Human pep |
| 579 | 44.4 | 42 | 7 | ABR57036 | Abr57036 Regulator | 652 | 4 | 44.4 | 49 | 5 | ABG43779 | Abg43779 Human pep |
| 580 | 44.4 | 42 | 7 | ADP69907 | Adp69907 Acma-type | 653 | 4 | 44.4 | 49 | 9 | AEA30857 | Aea30857 Pertussis |
| 581 | 44.4 | 42 | 8 | ADP79566 | Adp79566 Human MAD | 654 | 4 | 44.4 | 50 | 4 | ABG22352 | Abg22352 Novel hum |
| 582 | 44.4 | 42 | 8 | AAW82294 | Aaw82294 Dynamin 4 | 655 | 4 | 44.4 | 50 | 6 | ABP99632 | Abp99632 Human sec |
| 583 | 44.4 | 43 | 4 | ABG22764 | Abg22764 Novel hum | 656 | 4 | 44.4 | 50 | 6 | ABR01112 | AbR01112 Human gen |
| 584 | 44.4 | 43 | 6 | ADY20643 | Ady20643 PRO polyp | 657 | 4 | 44.4 | 50 | 8 | ADU79164 | Adu79164 Human pro |
| 585 | 44.4 | 43 | 9 | ADY20643 | Ady20643 PRO polyp | 658 | 4 | 44.4 | 50 | 8 | ADU79178 | Adu79178 Human pro |
| 586 | 44.4 | 44 | 2 | AAW18297 | Aay18297 Modified | 659 | 4 | 44.4 | 51 | 2 | AAW19528 | Aay19528 Amino aci |
| 587 | 44.4 | 44 | 2 | AAW18300 | Aay18300 Modified | 660 | 4 | 44.4 | 51 | 3 | AAW45159 | Aab45159 Human sec |
| 588 | 44.4 | 44 | 2 | AAW18307 | Aay18307 Modified | 661 | 4 | 44.4 | 51 | 3 | AAW61663 | Aag61663 Arabidops |
| 589 | 44.4 | 44 | 2 | AAW18299 | Aay18299 Modified | 662 | 4 | 44.4 | 51 | 3 | ABP35025 | Abp35025 Human ORF |
| 590 | 44.4 | 44 | 2 | AAW18301 | Aay18301 Modified | 663 | 4 | 44.4 | 51 | 5 | ADK35859 | Adk35859 Novel hum |
| 591 | 44.4 | 44 | 2 | AAW18309 | Aay18309 Modified | 664 | 4 | 44.4 | 52 | 4 | AAW74895 | Aag74895 Human col |
| 592 | 44.4 | 44 | 2 | AAW18298 | Aay18298 Modified | 665 | 4 | 44.4 | 52 | 4 | AAU65249 | Aau65249 Propionib |
| 593 | 44.4 | 44 | 2 | AAW18303 | Aay18303 Human pro | 666 | 4 | 44.4 | 52 | 5 | ABP07470 | Abp07470 Human ORF |
| 594 | 44.4 | 44 | 4 | AAW36402 | Aab36402 Human pro | 667 | 4 | 44.4 | 52 | 5 | ABP34254 | Abp34254 Human gly |
| 595 | 44.4 | 44 | 7 | ADD50094 | Add50094 Human vit | 668 | 4 | 44.4 | 52 | 6 | ABM61768 | Abm61768 Propionib |
| 596 | 44.4 | 44 | 7 | ADP69958 | Adp69958 Acma-type | 669 | 4 | 44.4 | 53 | 3 | AAW493561 | Aaw493561 M. xanthu |
| 597 | 44.4 | 44 | 8 | ABO57670 | Abo57670 Human gen | 670 | 4 | 44.4 | 53 | 8 | ADM01104 | Adm01104 Legume le |
| 598 | 44.4 | 44 | 8 | ADQ26900 | Adq26900 Human pro | 671 | 4 | 44.4 | 53 | 8 | ADL95705 | Adl95705 Legume le |
| 599 | 44.4 | 44 | 9 | ADZ14055 | Adz14055 Human pro | 672 | 4 | 44.4 | 53 | 8 | ADX80309 | Adx80309 Plant ful |
| 600 | 44.4 | 44 | 9 | ADZ14077 | Adz14076 Human pro | 673 | 4 | 44.4 | 54 | 3 | AAW493561 | Aaw493561 M. xanthu |
| 601 | 44.4 | 44 | 9 | ADZ14077 | Adz14077 Human pro | 674 | 4 | 44.4 | 54 | 3 | AAW493561 | Aaw493561 M. xanthu |
| 602 | 44.4 | 45 | 2 | AAW75710 | Aaw75710 Partial h | 675 | 4 | 44.4 | 54 | 6 | ABP76021 | Abp76021 Human GEN |
| 603 | 44.4 | 45 | 4 | AAW33007 | Aam33007 Peptide # | 676 | 4 | 44.4 | 54 | 6 | ABP76023 | Abp76023 Human GEN |
| 604 | 44.4 | 45 | 4 | AAW87412 | Aam87412 Human imm | 677 | 4 | 44.4 | 54 | 6 | ABP76177 | Abp76177 Human GEN |
| 605 | 44.4 | 45 | 4 | ABG23395 | Abg23395 Novel hum | 678 | 4 | 44.4 | 55 | 4 | ABP76022 | Abp76022 Human GEN |
| 606 | 44.4 | 45 | 5 | ABB79946 | Abb79946 Human pro | 679 | 4 | 44.4 | 55 | 4 | AAU44636 | Aau44636 Propionib |
| 607 | 44.4 | 45 | 5 | ABB79949 | Abb79949 Human pro | 680 | 4 | 44.4 | 55 | 5 | ABP31524 | Abp31524 Human gly |

| | | | | | | | | | | | | | |
|-----|---|------|----|----|-----------|---------------------|-----|---|------|----|---|----------|---------------------|
| 681 | 4 | 44.4 | 55 | 6 | ABW411155 | Abm411155 Propionib | 754 | 4 | 44.4 | 62 | 6 | ABM64244 | Abm64244 Propionib |
| 682 | 4 | 44.4 | 56 | 6 | ABW47442 | Abm47442 Propionib | 755 | 4 | 44.4 | 63 | 3 | AAQ42912 | Aeq42912 Arabidops |
| 683 | 4 | 44.4 | 56 | 2 | AAr11103 | Aar11103 Bovine bo | 756 | 4 | 44.4 | 63 | 3 | AAQ09746 | Aaq09746 Arabidops |
| 684 | 4 | 44.4 | 56 | 2 | AAr11102 | Aar11102 Human bon | 757 | 4 | 44.4 | 63 | 4 | AAU55093 | Aau55093 Propionib |
| 685 | 4 | 44.4 | 56 | 2 | AAr11102 | Aar11102 Human bon | 758 | 4 | 44.4 | 63 | 6 | ABM51612 | Abm51612 Propionib |
| 686 | 4 | 44.4 | 57 | 4 | AAQ00446 | Aaq00446 Human sec | 759 | 4 | 44.4 | 63 | 8 | ADL69531 | Adl69531 Insulin-1 |
| 687 | 4 | 44.4 | 57 | 4 | AAQ17778 | Aaq17778 Peptide # | 760 | 4 | 44.4 | 64 | 3 | AAQ01175 | Aaq01175 Human gen |
| 688 | 4 | 44.4 | 57 | 4 | AAQ30288 | Aaq30288 Peptide # | 761 | 4 | 44.4 | 64 | 4 | AAE03973 | Aae03973 Human gen |
| 689 | 4 | 44.4 | 57 | 4 | AAQ86357 | Aaq86357 Human imm | 762 | 4 | 44.4 | 64 | 5 | ABP10905 | Abp10905 Human ORF |
| 690 | 4 | 44.4 | 57 | 5 | ABG51646 | Abg51646 Human liv | 763 | 4 | 44.4 | 65 | 3 | AAQ32879 | Aaq32879 Zea maye |
| 691 | 4 | 44.4 | 57 | 8 | ADP02961 | Adp02961 Human ORF | 764 | 4 | 44.4 | 65 | 3 | AAU52432 | Aau52432 Propionib |
| 692 | 4 | 44.4 | 58 | 2 | AAQ92199 | Aaq92199 Plant ful | 765 | 4 | 44.4 | 65 | 4 | ABG13119 | Abg13119 Novel hum |
| 693 | 4 | 44.4 | 58 | 2 | AAQ48161 | Aaq48161 BPTI (11D | 766 | 4 | 44.4 | 65 | 5 | ABG04984 | Abg04984 Human ORF |
| 694 | 4 | 44.4 | 58 | 2 | AAQ48170 | Aaq48170 BPTI (11P | 767 | 4 | 44.4 | 65 | 6 | ABM48951 | Abm48951 Propionib |
| 695 | 4 | 44.4 | 58 | 2 | AAQ48177 | Aaq48177 BPTI (11T | 768 | 4 | 44.4 | 65 | 8 | ADU98759 | Adu98759 Borrelia |
| 696 | 4 | 44.4 | 58 | 2 | AAQ48174 | Aaq48174 BPTI (11P | 769 | 4 | 44.4 | 66 | 6 | ABU19955 | Abu19955 Protein e |
| 697 | 4 | 44.4 | 58 | 2 | AAQ48181 | Aaq48181 BPTI (11E | 770 | 4 | 44.4 | 67 | 4 | AAQ21412 | Aaq21412 Peptide # |
| 698 | 4 | 44.4 | 58 | 2 | AAQ48198 | Aaq48198 BPTI (11E | 771 | 4 | 44.4 | 67 | 4 | AAQ74748 | Aaq74748 Human col |
| 699 | 4 | 44.4 | 58 | 2 | AAQ48193 | Aaq48193 BPTI (11L | 772 | 4 | 44.4 | 67 | 4 | ABQ43752 | Abq43752 Peptide # |
| 700 | 4 | 44.4 | 58 | 2 | AAQ48166 | Aaq48166 BPTI (11S | 773 | 4 | 44.4 | 67 | 4 | ABB26695 | Abb26695 Protein # |
| 701 | 4 | 44.4 | 58 | 2 | AAQ48169 | Aaq48169 BPTI (11S | 774 | 4 | 44.4 | 67 | 4 | AAQ64714 | Aaq64714 Human bra |
| 702 | 4 | 44.4 | 58 | 2 | AAQ48175 | Aaq48175 BPTI (11A | 775 | 4 | 44.4 | 67 | 4 | ABG59124 | Abg59124 Human liv |
| 703 | 4 | 44.4 | 58 | 2 | AAQ48180 | Aaq48180 BPTI (11P | 776 | 4 | 44.4 | 67 | 9 | ABE42462 | Abe42462 L. pneumo |
| 704 | 4 | 44.4 | 58 | 2 | AAQ48197 | Aaq48197 BPTI (8S, | 777 | 4 | 44.4 | 68 | 2 | AAU20813 | Aau20813 Human neu |
| 705 | 4 | 44.4 | 58 | 2 | AAW80030 | Aaw80030 Bovine pa | 778 | 4 | 44.4 | 68 | 4 | AAU41313 | Aau41313 Propionib |
| 706 | 4 | 44.4 | 58 | 2 | AAW80033 | Aaw80033 Bovine pa | 779 | 4 | 44.4 | 68 | 4 | ABG02152 | Abg02152 Novel hum |
| 707 | 4 | 44.4 | 58 | 2 | AAW80036 | Aaw80036 Bovine pa | 780 | 4 | 44.4 | 68 | 5 | ABP00072 | Abp00072 Human ORF |
| 708 | 4 | 44.4 | 58 | 2 | AAW80003 | Aaw80003 Bovine pa | 781 | 4 | 44.4 | 68 | 6 | ABM37832 | Abm37832 Propionib |
| 709 | 4 | 44.4 | 58 | 2 | AAW80039 | Aaw80039 Bovine pa | 782 | 4 | 44.4 | 68 | 7 | ADB61816 | Adb61816 Human inh |
| 710 | 4 | 44.4 | 58 | 2 | AAW80068 | Aaw80068 Bovine pa | 783 | 4 | 44.4 | 68 | 7 | ADB61813 | Adb61813 Human inh |
| 711 | 4 | 44.4 | 58 | 2 | AAW80057 | Aaw80057 Bovine pa | 784 | 4 | 44.4 | 68 | 8 | ADK48020 | Adk48020 Streptoco |
| 712 | 4 | 44.4 | 58 | 2 | AAW80001 | Aaw80001 Bovine pa | 785 | 4 | 44.4 | 68 | 8 | ADR94505 | Adr94505 Novel S. |
| 713 | 4 | 44.4 | 58 | 2 | AAW80127 | Aaw80127 Bovine pa | 786 | 4 | 44.4 | 68 | 9 | AEA58375 | Aea58375 Streptoco |
| 714 | 4 | 44.4 | 58 | 2 | AAW80004 | Aaw80004 Bovine pa | 787 | 4 | 44.4 | 69 | 2 | AAQ72540 | Aaq72540 ADP-ribos |
| 715 | 4 | 44.4 | 58 | 2 | AAW80035 | Aaw80035 Bovine pa | 788 | 4 | 44.4 | 69 | 2 | AAQ41811 | Aaq41811 Escherich |
| 716 | 4 | 44.4 | 58 | 2 | AAW80080 | Aaw80080 Bovine pa | 789 | 4 | 44.4 | 69 | 2 | AAQ95221 | Aaq95221 Verotoxin |
| 717 | 4 | 44.4 | 58 | 2 | AAW80085 | Aaw80085 Bovine pa | 790 | 4 | 44.4 | 69 | 2 | AAQ43008 | Aaq43008 Mutant Sh |
| 718 | 4 | 44.4 | 58 | 2 | AAW80013 | Aaw80013 Bovine pa | 791 | 4 | 44.4 | 69 | 2 | AAQ43001 | Aaq43001 Mutant Sh |
| 719 | 4 | 44.4 | 58 | 2 | AAW80056 | Aaw80056 Bovine pa | 792 | 4 | 44.4 | 69 | 2 | AAQ43003 | Aaq43003 Mutant Sh |
| 720 | 4 | 44.4 | 58 | 2 | AAW80075 | Aaw80075 Bovine pa | 793 | 4 | 44.4 | 69 | 2 | AAQ43005 | Aaq43005 Mutant Sh |
| 721 | 4 | 44.4 | 58 | 2 | AAW80126 | Aaw80126 Bovine pa | 794 | 4 | 44.4 | 69 | 2 | AAQ39394 | Aaq39394 Shiga-lik |
| 722 | 4 | 44.4 | 58 | 2 | AAW80078 | Aaw80078 Bovine pa | 795 | 4 | 44.4 | 69 | 2 | AAQ43007 | Aaq43007 Mutant Sh |
| 723 | 4 | 44.4 | 58 | 2 | AAW80090 | Aaw80090 Bovine pa | 796 | 4 | 44.4 | 69 | 2 | AAQ43010 | Aaq43010 Mutant Sh |
| 724 | 4 | 44.4 | 58 | 2 | AAW80123 | Aaw80123 Bovine pa | 797 | 4 | 44.4 | 69 | 2 | AAQ43012 | Aaq43012 Mutant Sh |
| 725 | 4 | 44.4 | 58 | 2 | AAW80070 | Aaw80070 Bovine pa | 798 | 4 | 44.4 | 69 | 2 | AAQ43015 | Aaq43015 Mutant Sh |
| 726 | 4 | 44.4 | 58 | 2 | AAW80071 | Aaw80071 Bovine pa | 799 | 4 | 44.4 | 69 | 3 | AAQ68360 | Aaq68360 Verotoxin |
| 727 | 4 | 44.4 | 58 | 2 | AAW80093 | Aaw80093 Bovine pa | 800 | 4 | 44.4 | 69 | 3 | AAQ22733 | Aaq22733 Zea maye |
| 728 | 4 | 44.4 | 58 | 2 | AAW80095 | Aaw80095 Bovine pa | 801 | 4 | 44.4 | 69 | 4 | AAQ92284 | Aaq92284 Human dig |
| 729 | 4 | 44.4 | 58 | 2 | AAW80040 | Aaw80040 Bovine pa | 802 | 4 | 44.4 | 69 | 4 | ABB14787 | Abb14787 Human ner |
| 730 | 4 | 44.4 | 58 | 2 | AAW80058 | Aaw80058 Bovine pa | 803 | 4 | 44.4 | 69 | 4 | AAQ66234 | Aaq66234 E. coli he |
| 731 | 4 | 44.4 | 58 | 2 | AAW80081 | Aaw80081 Bovine pa | 804 | 4 | 44.4 | 69 | 8 | ADF39753 | Adf39753 E. coli O |
| 732 | 4 | 44.4 | 58 | 2 | AAW80089 | Aaw80089 Bovine pa | 805 | 4 | 44.4 | 69 | 8 | ADX89931 | Adx89931 Plant tox |
| 733 | 4 | 44.4 | 58 | 2 | AAW80128 | Aaw80128 Bovine pa | 806 | 4 | 44.4 | 70 | 9 | ADV34850 | Adv34850 Shiga tox |
| 734 | 4 | 44.4 | 58 | 2 | AAW80055 | Aaw80055 Bovine pa | 807 | 4 | 44.4 | 70 | 6 | ABP78501 | Abp78501 N. gonorr |
| 735 | 4 | 44.4 | 58 | 2 | AAW80094 | Aaw80094 Bovine pa | 808 | 4 | 44.4 | 70 | 7 | ABO77947 | AbO77947 Pseudomon |
| 736 | 4 | 44.4 | 58 | 2 | AAW80094 | Aaw80094 Bovine pa | 809 | 4 | 44.4 | 70 | 8 | ADX95352 | Adx95352 Plant ful |
| 737 | 4 | 44.4 | 58 | 2 | AAW80002 | Aaw80002 Bovine pa | 810 | 4 | 44.4 | 70 | 9 | ABM94713 | Abm94713 M. xanthu |
| 738 | 4 | 44.4 | 58 | 2 | AAW80054 | Aaw80054 Bovine pa | 811 | 4 | 44.4 | 71 | 4 | AAQ50535 | Aaq50535 Rat C-CAM |
| 739 | 4 | 44.4 | 58 | 2 | AAW80084 | Aaw80084 Bovine pa | 812 | 4 | 44.4 | 71 | 5 | ABQ53126 | Abq53126 Human ORF |
| 740 | 4 | 44.4 | 58 | 2 | AAW80122 | Aaw80122 Bovine pa | 813 | 4 | 44.4 | 71 | 7 | ADF07705 | Adf07705 Bacterial |
| 741 | 4 | 44.4 | 58 | 4 | AAW86826 | Aaw86826 Human imm | 814 | 4 | 44.4 | 71 | 8 | ABO56689 | AbO56689 Human gen |
| 742 | 4 | 44.4 | 59 | 5 | ABP00924 | Abp00924 Human ORF | 815 | 4 | 44.4 | 72 | 2 | AAW71701 | Aaw71701 Truncated |
| 743 | 4 | 44.4 | 60 | 2 | AAQ08823 | Aaq08823 Yeast Ynu | 816 | 4 | 44.4 | 72 | 3 | AAQ90847 | Aaq90847 Cotton de |
| 744 | 4 | 44.4 | 60 | 2 | AAQ08795 | Aaq08795 Yeast Nup | 817 | 4 | 44.4 | 72 | 5 | ABR01785 | AbR01785 Human bre |
| 745 | 4 | 44.4 | 60 | 5 | ABP09967 | Abp09967 Human ORF | 818 | 4 | 44.4 | 72 | 9 | ADY51931 | AdY51931 Phage SPO |
| 746 | 4 | 44.4 | 60 | 10 | AAE91657 | Aae91657 HLA-B*400 | 819 | 4 | 44.4 | 73 | 4 | AAU62590 | Aau62590 Propionib |
| 747 | 4 | 44.4 | 60 | 10 | AAE91655 | Aae91655 HLA-B*400 | 820 | 4 | 44.4 | 73 | 4 | AAQ50534 | Aaq50534 Mouse C-C |
| 748 | 4 | 44.4 | 60 | 10 | AAE91656 | Aae91656 HLA-B*400 | 821 | 4 | 44.4 | 73 | 6 | ABM59109 | Abm59109 Propionib |
| 749 | 4 | 44.4 | 61 | 4 | AAW84043 | Aaw84043 Human imm | 822 | 4 | 44.4 | 73 | 7 | ABM74310 | Abm74310 DNA clone |
| 750 | 4 | 44.4 | 62 | 2 | AAW27868 | Aaw27868 Staphyloc | 823 | 4 | 44.4 | 74 | 3 | AAQ42911 | Aaq42911 Arabidops |
| 751 | 4 | 44.4 | 62 | 3 | AAQ38599 | Aaq38599 Human sec | 824 | 4 | 44.4 | 74 | 4 | AAW43511 | Aaw43511 Human pol |
| 752 | 4 | 44.4 | 62 | 4 | AAQ67725 | Aaq67725 Propionib | 825 | 4 | 44.4 | 74 | 8 | ADM24532 | Adm24532 Human PRO |
| 753 | 4 | 44.4 | 62 | 6 | ADA05627 | Ada05627 IGF-1R ag | 826 | 4 | 44.4 | 74 | 8 | ADM97961 | Adm97961 5-epi-Ari |

| | | | | | | | | | | | | | |
|-----|----|------|----|----|-----------|------------|-----|---|------|----|---|-----------|------------|
| 827 | 54 | 44.4 | 74 | 8 | AdM97959 | Sesquiter | 900 | 4 | 44.4 | 85 | 8 | AdK99932 | Streptococ |
| 828 | 4 | 44.4 | 74 | 8 | AdM97956 | Germacren | 901 | 4 | 44.4 | 85 | 8 | AdK99929 | Streptococ |
| 829 | 4 | 44.4 | 74 | 9 | AdY60919 | Abiotic s | 902 | 4 | 44.4 | 85 | 8 | AdK99930 | Streptococ |
| 830 | 4 | 44.4 | 74 | 9 | AEa51016 | Citrus ju | 903 | 4 | 44.4 | 85 | 8 | AdK99927 | Streptococ |
| 831 | 4 | 44.4 | 74 | 9 | AEa51018 | Capicum | 904 | 4 | 44.4 | 85 | 8 | AdK99931 | Streptococ |
| 832 | 4 | 44.4 | 74 | 9 | AEa51013 | Tomato ge | 905 | 4 | 44.4 | 85 | 8 | AdK99933 | Streptococ |
| 833 | 4 | 44.4 | 75 | 3 | AGa09745 | Arabidops | 906 | 4 | 44.4 | 86 | 6 | ABU20346 | Protein e |
| 834 | 4 | 44.4 | 75 | 4 | ANM24190 | Human EST | 907 | 4 | 44.4 | 86 | 8 | AdK99928 | Streptococ |
| 835 | 4 | 44.4 | 75 | 4 | ABBi1010 | Human sec | 908 | 4 | 44.4 | 86 | 8 | AdK99935 | Streptococ |
| 836 | 4 | 44.4 | 75 | 4 | AAO01295 | Human pol | 909 | 4 | 44.4 | 86 | 8 | AdM97964 | delta-Cad |
| 837 | 4 | 44.4 | 75 | 5 | ADK34405 | Novel hum | 910 | 4 | 44.4 | 86 | 9 | AEA51021 | Gosayplum |
| 838 | 4 | 44.4 | 75 | 8 | ADL04493 | M. catarr | 911 | 4 | 44.4 | 87 | 2 | AEa71700 | CxslAT pr |
| 839 | 4 | 44.4 | 76 | 4 | AAu87658 | Human imm | 912 | 4 | 44.4 | 87 | 3 | AGa05143 | Arabidops |
| 840 | 4 | 44.4 | 76 | 4 | AAu44841 | Human imm | 913 | 4 | 44.4 | 88 | 4 | AAu84966 | Human imm |
| 841 | 4 | 44.4 | 76 | 6 | AEa41360 | Propionib | 914 | 4 | 44.4 | 88 | 4 | AAu62383 | Shiga tox |
| 842 | 4 | 44.4 | 77 | 2 | AAW28050 | Staphyloc | 915 | 4 | 44.4 | 88 | 4 | AAU29445 | Human G p |
| 843 | 4 | 44.4 | 77 | 3 | AGa035920 | Arabidops | 916 | 4 | 44.4 | 88 | 5 | ABG60733 | Novel G p |
| 844 | 4 | 44.4 | 77 | 4 | AAO12504 | Human pol | 917 | 4 | 44.4 | 88 | 5 | ABP62867 | Human pol |
| 845 | 4 | 44.4 | 77 | 5 | ABP10618 | Human ORF | 918 | 4 | 44.4 | 88 | 5 | ADK82413 | Phenol hy |
| 846 | 4 | 44.4 | 77 | 6 | AEU43322 | Protein e | 919 | 4 | 44.4 | 88 | 2 | AAW06406 | Verotoxig |
| 847 | 4 | 44.4 | 78 | 3 | ABBi16346 | Bacteriop | 920 | 4 | 44.4 | 89 | 2 | AAW06404 | Shiga tox |
| 848 | 4 | 44.4 | 78 | 5 | AGB99547 | Conus sp | 921 | 4 | 44.4 | 89 | 2 | AAW58830 | Verotoxig |
| 849 | 4 | 44.4 | 78 | 5 | ABP33640 | Human syn | 922 | 4 | 44.4 | 89 | 2 | AAW58828 | Shiga tox |
| 850 | 4 | 44.4 | 78 | 6 | ADA05631 | IGF-IR ag | 923 | 4 | 44.4 | 89 | 3 | AAW56684 | E. coli v |
| 851 | 4 | 44.4 | 78 | 6 | ADMa05611 | IGF-IR ag | 924 | 4 | 44.4 | 89 | 3 | AAW96682 | E. coli v |
| 852 | 4 | 44.4 | 78 | 6 | ADMe4595 | Propionib | 925 | 4 | 44.4 | 89 | 4 | AAU14326 | Peptide # |
| 853 | 4 | 44.4 | 78 | 8 | ADL69535 | Insulin-1 | 926 | 4 | 44.4 | 89 | 4 | AAU22174 | Human car |
| 854 | 4 | 44.4 | 78 | 8 | ADL69515 | Insulin-1 | 927 | 4 | 44.4 | 89 | 4 | ABB33273 | Peptide # |
| 855 | 4 | 44.4 | 78 | 10 | AEe69701 | Human pap | 928 | 4 | 44.4 | 89 | 4 | ABM26736 | Peptide # |
| 856 | 4 | 44.4 | 78 | 10 | AEe69714 | Human pap | 929 | 4 | 44.4 | 89 | 4 | ABM26736 | Peptide # |
| 857 | 4 | 44.4 | 79 | 3 | AGa01174 | Human sec | 930 | 4 | 44.4 | 89 | 4 | ABM18735 | Protein # |
| 858 | 4 | 44.4 | 79 | 4 | AAu18309 | Peptide # | 931 | 4 | 44.4 | 89 | 4 | ABM18735 | Protein # |
| 859 | 4 | 44.4 | 79 | 4 | AAu70472 | Human bon | 932 | 4 | 44.4 | 89 | 4 | AAU02795 | Human pol |
| 860 | 4 | 44.4 | 79 | 4 | AAW05915 | Peptide # | 933 | 4 | 44.4 | 89 | 4 | AAU45183 | Propionib |
| 861 | 4 | 44.4 | 79 | 5 | ABG40111 | Human pep | 934 | 4 | 44.4 | 89 | 4 | AAU54065 | Human bra |
| 862 | 4 | 44.4 | 79 | 5 | ABG99539 | Conus sp | 935 | 4 | 44.4 | 89 | 4 | ABG48122 | Human liv |
| 863 | 4 | 44.4 | 79 | 5 | ABP32367 | Human pho | 936 | 4 | 44.4 | 89 | 4 | ABM02055 | Peptide # |
| 864 | 4 | 44.4 | 79 | 5 | ADK88099 | Ribosomal | 937 | 4 | 44.4 | 89 | 4 | ABG18574 | Novel hum |
| 865 | 4 | 44.4 | 79 | 7 | ADK88092 | Ribosomal | 938 | 4 | 44.4 | 89 | 4 | ABG18598 | Novel hum |
| 866 | 4 | 44.4 | 79 | 7 | ADK88090 | Ribosomal | 939 | 4 | 44.4 | 89 | 5 | ABG36105 | Human pep |
| 867 | 4 | 44.4 | 79 | 7 | ADK88094 | Ribosomal | 940 | 4 | 44.4 | 89 | 5 | ABU77818 | E. coli v |
| 868 | 4 | 44.4 | 80 | 4 | ADJ48869 | Oil-assoc | 941 | 4 | 44.4 | 89 | 5 | AAU77820 | E. coli v |
| 869 | 4 | 44.4 | 80 | 4 | ABB38582 | Peptide # | 942 | 4 | 44.4 | 89 | 6 | ABM41702 | Propionib |
| 870 | 4 | 44.4 | 80 | 4 | AAm32035 | Peptide # | 943 | 4 | 44.4 | 89 | 6 | ABR57176 | B subunit |
| 871 | 4 | 44.4 | 80 | 4 | AAm71743 | Human bon | 944 | 4 | 44.4 | 89 | 6 | ABR57176 | B subunit |
| 872 | 4 | 44.4 | 80 | 4 | AAm59208 | Human bra | 945 | 4 | 44.4 | 89 | 7 | ADK00544 | Enterohae |
| 873 | 4 | 44.4 | 80 | 4 | ABG53428 | Human liv | 946 | 4 | 44.4 | 89 | 7 | ADK00246 | Enterohae |
| 874 | 4 | 44.4 | 80 | 4 | AAU31185 | Novel hum | 947 | 4 | 44.4 | 89 | 8 | ADJ07560 | Human car |
| 875 | 4 | 44.4 | 80 | 5 | ABP09391 | Human ORF | 948 | 4 | 44.4 | 89 | 9 | ADV34851 | Shiga tox |
| 876 | 4 | 44.4 | 80 | 5 | ABP38663 | Staphyloc | 949 | 4 | 44.4 | 90 | 2 | AAy55746 | HLA allele |
| 877 | 4 | 44.4 | 80 | 5 | ABG411557 | Human pep | 950 | 4 | 44.4 | 90 | 2 | AAy55742 | HLA allele |
| 878 | 4 | 44.4 | 81 | 5 | ADU05173 | Staphyloc | 951 | 4 | 44.4 | 90 | 2 | AAy55744 | HLA allele |
| 879 | 4 | 44.4 | 81 | 5 | ABG68278 | Human con | 952 | 4 | 44.4 | 90 | 3 | AAy55744 | HLA allele |
| 880 | 4 | 44.4 | 81 | 6 | ABP81309 | Protein e | 953 | 4 | 44.4 | 90 | 3 | AGa54457 | Zea mays |
| 881 | 4 | 44.4 | 81 | 6 | ABU26465 | Human liv | 954 | 4 | 44.4 | 90 | 4 | AAU50831 | Propionib |
| 882 | 4 | 44.4 | 81 | 7 | ADK54519 | Rat Prote | 955 | 4 | 44.4 | 90 | 4 | AAU61518 | Propionib |
| 883 | 4 | 44.4 | 81 | 7 | ADK54523 | Rat Prote | 956 | 4 | 44.4 | 90 | 5 | ABP02757 | Human ORF |
| 884 | 4 | 44.4 | 81 | 7 | ADK54527 | Rat Prote | 957 | 4 | 44.4 | 90 | 5 | ABP02757 | Human ORF |
| 885 | 4 | 44.4 | 81 | 7 | ADK54531 | Rat Prote | 958 | 4 | 44.4 | 90 | 6 | ABM47350 | Propionib |
| 886 | 4 | 44.4 | 81 | 8 | ADN20308 | Bacterial | 959 | 4 | 44.4 | 90 | 6 | ABM47350 | Propionib |
| 887 | 4 | 44.4 | 82 | 5 | ABP39029 | Staphyloc | 960 | 4 | 44.4 | 90 | 6 | ABM58037 | Propionib |
| 888 | 4 | 44.4 | 82 | 8 | ADK07014 | Staphyloc | 961 | 4 | 44.4 | 90 | 6 | ABM58037 | Propionib |
| 889 | 4 | 44.4 | 83 | 3 | AGB30539 | Arabidops | 962 | 4 | 44.4 | 90 | 6 | ABR57174 | B subunit |
| 890 | 4 | 44.4 | 83 | 6 | ABM73016 | Staphyloc | 963 | 4 | 44.4 | 90 | 6 | ABR57175 | B subunit |
| 891 | 4 | 44.4 | 83 | 8 | ADK99934 | Streptococ | 964 | 4 | 44.4 | 90 | 8 | ADK021856 | Human ves |
| 892 | 4 | 44.4 | 83 | 8 | ABO60637 | Human gen | 965 | 4 | 44.4 | 90 | 8 | ADK68302 | Plant ful |
| 893 | 4 | 44.4 | 84 | 3 | AAK53312 | Arabidops | 966 | 4 | 44.4 | 90 | 9 | ADK285775 | Human leu |
| 894 | 4 | 44.4 | 84 | 5 | ABG99614 | Conus sp | 967 | 4 | 44.4 | 90 | 9 | ADK285785 | Human leu |
| 895 | 4 | 44.4 | 84 | 5 | ABG99853 | Conus sp | 968 | 4 | 44.4 | 90 | 9 | ADK285735 | Human leu |
| 896 | 4 | 44.4 | 84 | 7 | ABO63079 | Klebsiell | 969 | 4 | 44.4 | 90 | 9 | ADK285805 | HLA-E (1- |
| 897 | 4 | 44.4 | 84 | 8 | ADK99926 | Streptococ | 970 | 4 | 44.4 | 90 | 9 | ADK285765 | Human leu |
| 898 | 4 | 44.4 | 85 | 4 | AAu89909 | Human imm | 971 | 4 | 44.4 | 90 | 9 | ADK285755 | Human leu |
| 899 | 4 | 44.4 | 85 | 6 | ADB07132 | Allolococ | 972 | 4 | 44.4 | 90 | 9 | ADK285815 | HLA-E (1- |

973 4 44.4 90 9 AD285745 Human leu
974 4 44.4 91 3 AAG53511 Arabidops
975 4 44.4 91 5 AA017189 Human sec
976 4 44.4 91 5 AA017222 Human sec
977 4 44.4 91 5 ABG64786 Human alb
978 4 44.4 91 5 ABG64788 Human alb
979 4 44.4 91 5 ABP51250 Human MDD
980 4 44.4 91 6 ADL78053 Alloiococ
981 4 44.4 91 8 ADL78053 Albumin f
982 4 44.4 91 8 ADL78055 Albumin f
983 4 44.4 91 10 AEF79706 E. coli a
984 4 44.4 92 4 AAO06285 Human pol
985 4 44.4 92 5 AAU79450 HLA-G alp
986 4 44.4 92 7 ADG15775 Rv3879c 8
987 4 44.4 92 7 ABO65306 Klebsiell
988 4 44.4 93 2 AAW82562 Corn glyc
989 4 44.4 93 3 AAY64754 Human 5,
990 4 44.4 93 4 AA05243 Corn glyc
991 4 44.4 93 4 AAM90556 Human imm
992 4 44.4 93 5 ABP01546 Human ORF
993 4 44.4 93 5 AAU76197 Corn glyc
994 4 44.4 93 6 ABO00505 Novel hum
995 4 44.4 93 7 AAE38777 Corn glyc
996 4 44.4 93 8 ADU72318 Signal pe
997 4 44.4 93 8 ADV89101 Streptoco
998 4 44.4 93 8 ADV80354 Streptoco
999 4 44.4 93 8 ADV82466 Streptoco
1000 4 44.4 93 9 ADZ73309 Human inc

ALIGNMENTS

RESULT 1
ADL12417
ID ADL12417 standard; peptide; 9 AA.
XX AC ADL12417;
XX AC ADL12417;
DT 04-NOV-2004 (first entry)
XX XX
XX Vaccinia virus immunisation peptide 165.
XX virucide; vaccine; immunisation; vaccinia; variola; immune response.
XX Vaccinia virus; strain Ankara.
XX WO2004067032-A2.
XX
XX 12-AUG-2004.
XX
XX 26-JAN-2004; 2004WO-US002141.
XX
XX 24-JAN-2003; 2003US-0442846P.
XX (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX
XX Terajima M, Cruz J, Ennis FA;
XX WPI; 2004-594031/57.
XX
XX Immunizing an individual against infection by vaccinia and/or variola
PT virus comprises inducing an immune response against a polypeptide
PT comprising peptide 74A or 165.
XX
XX Claim 19; SEQ ID NO 2; 32pp; English.
XX
XX The invention relates to a method of immunizing an individual against
CC infection by vaccinia and/or variola virus by inducing an immune response
CC against a polypeptide comprising peptide 74A or 165, or its immunogenic
CC fragments or mutants. The method is useful for immunizing an individual
CC against infection by vaccinia and/or variola virus. This sequence
CC represents a vaccinia virus peptide used in the method of the invention.

XX SQ Sequence 9 AA;
Query Match 100.0%; Score 9; DB 8; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDTFYVV 9
Db 1 KVDDTFYVV 9
RESULT 2
ADJ66069
ID ADJ66069 standard; protein; 150 AA.
XX AC ADJ66069;
XX AC ADJ66069;
DT 06-MAY-2004 (first entry)
XX
DE MVA C7L encoded amino acid sequence, seq id 1.
KW Virucide; vaccine; virus; Vaccinia virus; host range gene; avipoxvirus;
XX avian.
XX Vaccinia virus (strain Ankara).
XX OS Vaccinia virus (strain Ankara).
XX WO2004015118-A1.
XX
XX PD 19-FEB-2004.
XX
XX 29-JUL-2003; 2003WO-EP008359.
XX
XX 07-AUG-2002; 2002DK-00001189.
XX (BAVA-) BAVARIAN NORDIC AS.
XX
XX Howley P, Meisinger C;
XX
XX WPI; 2004-180680/17.
XX N-PSDB; ADJ66068.
XX
XX New avipoxvirus comprising in the viral genome a Vaccinia virus host
PT range gene or a homologue of the host range gene, useful for the
PT preparation of a medicament or as a vaccine for affecting immunological
PT response in human.
XX
XX Disclosure; SEQ ID NO 2; 53pp; English.
XX
XX The invention relates to a new avipoxvirus comprising in the viral
CC genome, a Vaccinia virus host range gene or a homologue of the host range
CC gene, provided that the host range gene is not the E3L gene if the
CC avipoxvirus is a recombinant Canary poxvirus comprising in the viral
CC genome the Vaccinia virus K3L gene as well as expression cassettes for
CC HIV gag-pro, gp120/TM and a Nef/Pol poly-epitope string, respectively.
CC The virus is useful for the preparation of a medicament or as a vaccine.
CC The composition or the vaccine is useful as a drug for affecting,
CC preferably inducing immunological response in a living animal, including
CC a human. The Vaccinia virus host range gene or its homologue, preferably
CC a host range gene is useful to increase the titer of avipoxviruses
CC produced from avian cells after infection of the cells with the
CC avipoxvirus, where the host range gene is expressed in the cells. The
CC current sequence represents the amino acid sequence encoded by the C7L
CC (host range gene) region of modified Vaccinia Ankara.
XX
XX SQ Sequence 150 AA;
Query Match 100.0%; Score 9; DB 8; Length 150;
Best Local Similarity 100.0%; Pred.No. 0.0048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDTFYVV 9
|||||||


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Db          74 KVDDTFYV 82

RESULT 3
ADRI2435
ID ADR12435 standard; peptide; 9 AA.
XX AC ADR12435;
XX DT 04-NOV-2004 (first entry)
XX DE Vaccinia virus immunisation peptide 165 variant #3.
XX KW virucide; vaccine; immunisation; vaccinia; variola; immune response.
XX OS Vaccinia virus; strain Ankara.
XX PN WO2004067032-A2.
XX PD 12-AUG-2004.
XX PF 26-JAN-2004; 2004WO-US002141.
XX PR 24-JAN-2003; 2003US-0442846P.
XX PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX PI Terajima M, Cruz J, Ennis FA;
XX DR WPI; 2004-594031/57.
XX PT Immunizing an individual against infection by vaccinia and/or variola
XX PT virus comprises inducing an immune response against a polypeptide
XX PT comprising peptide 74A or 165.
XX PS Disclosure; SEQ ID NO 21; 32pp; English.
XX CC The invention relates to a method of immunizing an individual against
XX CC infection by vaccinia and/or variola virus by inducing an immune response
XX CC against a polypeptide comprising peptide 74A or 165, or its immunogenic
XX CC fragments or mutants. The method is useful for immunizing an individual
XX CC against infection by vaccinia and/or variola virus. This sequence
XX CC represents a vaccinia virus peptide used in the method of the invention.
XX SQ Sequence 9 AA;

Query Match      88.9%; Score 8; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 VDDTFYV 9
Db          |||||
           2 VDDTFYV 9

RESULT 4
ADRI2433
ID ADR12433 standard; peptide; 9 AA.
XX AC ADR12433;
XX DT 04-NOV-2004 (first entry)
XX DE Vaccinia virus immunisation peptide 165 variant #1.
XX KW virucide; vaccine; immunisation; vaccinia; variola; immune response.
XX OS Vaccinia virus; strain Ankara.
XX PN WO2004067032-A2.
XX PD 12-AUG-2004.

Query Match      88.9%; Score 8; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 VDDTFYV 9
Db          |||||
           2 VDDTFYV 9

RESULT 5
ADRI2434
ID ADR12434 standard; peptide; 9 AA.
XX AC ADR12434;
XX DT 04-NOV-2004 (first entry)
XX DE Vaccinia virus immunisation peptide 165 variant #2.
XX KW virucide; vaccine; immunisation; vaccinia; variola; immune response.
XX OS Vaccinia virus; strain Ankara.
XX PN WO2004067032-A2.
XX PD 12-AUG-2004.
XX PF 26-JAN-2004; 2004WO-US002141.
XX PR 24-JAN-2003; 2003US-0442846P.
XX PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX PI Terajima M, Cruz J, Ennis FA;
XX DR WPI; 2004-594031/57.
XX PT Immunizing an individual against infection by vaccinia and/or variola
XX PT virus comprises inducing an immune response against a polypeptide
XX PT comprising peptide 74A or 165.
XX PS Disclosure; SEQ ID NO 20; 32pp; English.
XX CC The invention relates to a method of immunizing an individual against
XX CC infection by vaccinia and/or variola virus by inducing an immune response
XX CC against a polypeptide comprising peptide 74A or 165, or its immunogenic
XX CC fragments or mutants. The method is useful for immunizing an individual
XX CC against infection by vaccinia and/or variola virus. This sequence
XX CC represents a vaccinia virus peptide used in the method of the invention.
XX SQ Sequence 9 AA;

Query Match      88.9%; Score 8; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 VDDTFYV 9
Db          |||||
           2 VDDTFYV 9

```

CC represents a vaccinia virus peptide used in the method of the invention.
XX Sequence 9 AA;
SQ

Query Match 88.9%; Score 8; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFYV 9
Db 2 VDDTFYV 9

RESULT 6
ADRI2442
ID ADRI2442 standard; peptide; 9 AA.
XX AC
XX ADR12442;
XX DT 04-NOV-2004 (first entry)
XX DE Vaccinia virus immunisation peptide 165 variant #10.
XX KW virucide; vaccine; immunisation; vaccinia; variola; immune response.
XX OS Vaccinia virus; strain Ankara.
XX PN WO2004067032-A2.
XX PD 12-AUG-2004.
XX PF 26-JAN-2004; 2004WO-US002141.
XX PR 24-JAN-2003; 2003US-0442846P.
XX PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX PI Terajima M, Cruz J, Ennis FA;
XX PI WPI; 2004-594031/57.
XX PS Immunizing an individual against infection by vaccinia and/or variola virus comprises inducing an immune response against a polypeptide comprising peptide 74A or 165.
XX PT
XX SQ Sequence 9 AA;
XX Query Match 66.7%; Score 6; DB 8; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTF 6
Db 1 KVDDTF 6

RESULT 7
ADRI2437
ID ADRI2437 standard; peptide; 9 AA.
XX AC
XX ADR12437;
XX DT 04-NOV-2004 (first entry)
XX

DE Vaccinia virus immunisation peptide 165 variant #5.
XX virucide; vaccine; immunisation; vaccinia; variola; immune response.
XX OS Vaccinia virus; strain Ankara.
XX PN WO2004067032-A2.
XX PD 12-AUG-2004.
XX PF 26-JAN-2004; 2004WO-US002141.
XX PR 24-JAN-2003; 2003US-0442846P.
XX PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX PI Terajima M, Cruz J, Ennis FA;
XX PI WPI; 2004-594031/57.
XX PS Immunizing an individual against infection by vaccinia and/or variola virus comprises inducing an immune response against a polypeptide comprising peptide 74A or 165.
XX PT
XX SQ Sequence 9 AA;
XX Query Match 66.7%; Score 6; DB 8; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
Db 4 DTFYV 9

RESULT 8
ADRI2438
ID ADRI2438 standard; peptide; 9 AA.
XX AC
XX ADR12438;
XX DT 04-NOV-2004 (first entry)
XX DE Vaccinia virus immunisation peptide 165 variant #6.
XX KW virucide; vaccine; immunisation; vaccinia; immune response.
XX OS Vaccinia virus; strain Ankara.
XX PN WO2004067032-A2.
XX PD 12-AUG-2004.
XX PF 26-JAN-2004; 2004WO-US002141.
XX PR 24-JAN-2003; 2003US-0442846P.
XX PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX PI Terajima M, Cruz J, Ennis FA;
XX PI WPI; 2004-594031/57.
XX PT Immunizing an individual against infection by vaccinia and/or variola

PT virus comprises inducing an immune response against a polypeptide
 PT comprising peptide 74A or 165.

FS Disclosure; SEQ ID NO 24; 32pp; English.

XX The invention relates to a method of immunizing an individual against
 CC infection by vaccinia and/or variola virus by inducing an immune response
 CC against a polypeptide comprising peptide 74A or 165, or its immunogenic
 CC fragments or mutants. The method is useful for immunizing an individual
 CC against infection by vaccinia and/or variola virus. This sequence
 CC represents a vaccinia virus peptide used in the method of the invention.

XX Sequence 9 AA;

Query Match 66.7%; Score 6; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
 |||||
 Db 4 DTFYV 9

RESULT 9

ID ADR12444 standard; peptide; 9 AA.
 AC ADR12444;

XX 04-NOV-2004 (first entry)

XX Vaccinia virus immunisation peptide 165 variant #12.

XX virucide; vaccine; immunisation; vaccinia; variola; immune response.

OS Vaccinia virus; strain Ankara.

PN WO2004067032-A2.

XX 12-AUG-2004.

XX 26-JAN-2004; 2004WO-US002141.

XX 24-JAN-2003; 2003US-0442846P.

XX (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.

XX Terajima M, Cruz J, Ennis FA;

XX WPI; 2004-594031/57.

XX Immunizing an individual against infection by vaccinia and/or variola
 PT virus comprises inducing an immune response against a polypeptide
 PT comprising peptide 74A or 165.

PS Disclosure; SEQ ID NO 30; 32pp; English.

XX The invention relates to a method of immunizing an individual against
 CC infection by vaccinia and/or variola virus by inducing an immune response
 CC against a polypeptide comprising peptide 74A or 165, or its immunogenic
 CC fragments or mutants. The method is useful for immunizing an individual
 CC against infection by vaccinia and/or variola virus. This sequence
 CC represents a vaccinia virus peptide used in the method of the invention.

XX Sequence 9 AA;

Query Match 66.7%; Score 6; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
 |||||
 Db 4 DTFYV 9

RESULT 10
 ADR12436

ID ADR12436 standard; peptide; 9 AA.

XX ADR12436;

XX 04-NOV-2004 (first entry)

XX Vaccinia virus immunisation peptide 165 variant #4.

XX virucide; vaccine; immunisation; vaccinia; variola; immune response.

OS Vaccinia virus; strain Ankara.

PN WO2004067032-A2.

XX 12-AUG-2004.

XX 26-JAN-2004; 2004WO-US002141.

XX 24-JAN-2003; 2003US-0442846P.

XX (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.

XX Terajima M, Cruz J, Ennis FA;

XX WPI; 2004-594031/57.

XX Immunizing an individual against infection by vaccinia and/or variola
 PT virus comprises inducing an immune response against a polypeptide
 PT comprising peptide 74A or 165.

PS Disclosure; SEQ ID NO 22; 32pp; English.

XX The invention relates to a method of immunizing an individual against
 CC infection by vaccinia and/or variola virus by inducing an immune response
 CC against a polypeptide comprising peptide 74A or 165, or its immunogenic
 CC fragments or mutants. The method is useful for immunizing an individual
 CC against infection by vaccinia and/or variola virus. This sequence
 CC represents a vaccinia virus peptide used in the method of the invention.

XX Sequence 9 AA;

Query Match 66.7%; Score 6; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
 |||||
 Db 4 DTFYV 9

RESULT 11
 ADR12443

ID ADR12443 standard; peptide; 9 AA.

XX ADR12443;

XX 04-NOV-2004 (first entry)

XX Vaccinia virus immunisation peptide 165 variant #11.

XX virucide; vaccine; immunisation; vaccinia; variola; immune response.

OS Vaccinia virus; strain Ankara.

PN WO2004067032-A2.

XX 12-AUG-2004.

XX 26-JAN-2004; 2004WO-US002141.

CC plant with a recombinant DNA construct comprising a promoter region
 CC functional in a plant cell operably joined to a polynucleotide encoding a
 CC polypeptide associated with the property, and growing the transformed
 CC plant. The property is selected from improving plant cold tolerance, for
 CC manipulating growth rate in plant cells by modification of the cell cycle
 CC pathway, for improving plant drought tolerance, for providing increased
 CC resistance to plant disease, for galactomannan production, for production
 CC of plant growth regulators, for improving plant heat tolerance, for
 CC improving plant tolerance to herbicides, for increasing the rate of
 CC homologous recombination in plants, for lignin production, for improving
 CC plant tolerance to extreme osmotic conditions, for improving plant
 CC tolerance to pathogens or pests, for yield improvement by modification of
 CC photosynthesis, for modifying seed oil yield and/or content, for
 CC modifying seed protein yield and/or content, for yield improvement by
 CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
 CC and for yield improvement by providing improved plant growth and
 CC development under at least one stress condition. The polynucleotide may
 CC also encode a plant transcription factor. The methods and compositions of
 CC the present invention are useful in the field of biochemistry and
 CC genetics, in particular for producing transgenic plants with improved
 CC biological characteristics such as increased yield, improved nitrogen
 CC flow, increasing plant tolerance to cold or heat, improving plant
 CC tolerance to extreme osmotic and drought conditions, and improving plant
 CC tolerance to plant pests or pathogens. They can also be used in physical
 CC arrays of molecules, plant breeding markers, computer-based storage and
 CC analysis systems. The present sequence is one of the 5544 plant protein
 CC sequences of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20040216190.

XX Sequence 267 AA;

Query Match 66.7%; Score 6; DB 8; Length 267;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFFY 8
 Db 21 DDTFFY 26
 |||||

RESULT 14

AAG42271
 ID AAG42271 standard; protein; 326 AA.

XX AAG42271;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 52697.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 29-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.
 PR 19-APR-1999; 99US-0130077P.
 PR 21-APR-1999; 99US-0130449P.
 PR 23-APR-1999; 99US-0130510P.
 PR 23-APR-1999; 99US-0130891P.
 PR 28-APR-1999; 99US-0131449P.
 PR 30-APR-1999; 99US-0132048P.
 PR 30-APR-1999; 99US-0132407P.
 PR 04-MAY-1999; 99US-0132484P.
 PR 05-MAY-1999; 99US-0132485P.
 PR 06-MAY-1999; 99US-0132486P.
 PR 06-MAY-1999; 99US-0132487P.
 PR 07-MAY-1999; 99US-0132863P.
 PR 11-MAY-1999; 99US-0134256P.
 PR 11-MAY-1999; 99US-0134218P.
 PR 14-MAY-1999; 99US-0134219P.
 PR 14-MAY-1999; 99US-0134221P.
 PR 14-MAY-1999; 99US-0134370P.
 PR 18-MAY-1999; 99US-0134768P.
 PR 19-MAY-1999; 99US-0134941P.
 PR 20-MAY-1999; 99US-0135124P.
 PR 21-MAY-1999; 99US-0135353P.
 PR 24-MAY-1999; 99US-0135629P.
 PR 25-MAY-1999; 99US-0136021P.
 PR 27-MAY-1999; 99US-0136392P.
 PR 28-MAY-1999; 99US-0136782P.
 PR 01-JUN-1999; 99US-0137222P.
 PR 03-JUN-1999; 99US-0137528P.
 PR 04-JUN-1999; 99US-0137502P.
 PR 07-JUN-1999; 99US-0137724P.
 PR 08-JUN-1999; 99US-0138094P.
 PR 10-JUN-1999; 99US-0138540P.
 PR 14-JUN-1999; 99US-0138847P.
 PR 15-JUN-1999; 99US-0139119P.
 PR 15-JUN-1999; 99US-0139452P.
 PR 16-JUN-1999; 99US-0139453P.
 PR 17-JUN-1999; 99US-0139492P.
 PR 18-JUN-1999; 99US-0139454P.
 PR 18-JUN-1999; 99US-0139455P.
 PR 18-JUN-1999; 99US-0139456P.
 PR 18-JUN-1999; 99US-0139457P.
 PR 18-JUN-1999; 99US-0139458P.
 PR 18-JUN-1999; 99US-0139459P.
 PR 18-JUN-1999; 99US-0139460P.
 PR 18-JUN-1999; 99US-0139461P.
 PR 18-JUN-1999; 99US-0139462P.
 PR 18-JUN-1999; 99US-0139463P.
 PR 18-JUN-1999; 99US-0139750P.
 PR 18-JUN-1999; 99US-0139763P.
 PR 21-JUN-1999; 99US-0139817P.
 PR 22-JUN-1999; 99US-0139899P.
 PR 23-JUN-1999; 99US-0140353P.
 PR 23-JUN-1999; 99US-0140354P.
 PR 24-JUN-1999; 99US-0140695P.
 PR 28-JUN-1999; 99US-0140823P.
 PR 29-JUN-1999; 99US-0140991P.
 PR 30-JUN-1999; 99US-0141287P.
 PR 01-JUL-1999; 99US-0141842P.
 PR 01-JUL-1999; 99US-0142154P.
 PR 02-JUL-1999; 99US-0142055P.
 PR 06-JUL-1999; 99US-0142390P.
 PR 08-JUL-1999; 99US-0142803P.
 PR 09-JUL-1999; 99US-0142920P.
 PR 12-JUL-1999; 99US-0142977P.
 PR 13-JUL-1999; 99US-0143542P.
 PR 14-JUL-1999; 99US-0143624P.
 PR 15-JUL-1999; 99US-0144005P.
 PR 16-JUL-1999; 99US-0144085P.
 PR 16-JUL-1999; 99US-0144086P.
 PR 19-JUL-1999; 99US-0144325P.
 PR 19-JUL-1999; 99US-0144331P.
 PR 19-JUL-1999; 99US-0144332P.
 PR 19-JUL-1999; 99US-0144333P.

PR 30-APR-1999; 99US-01324407P.
PR 04-MAY-1999; 99US-01324484P.
PR 05-MAY-1999; 99US-01324485P.
PR 06-MAY-1999; 99US-01324486P.
PR 07-MAY-1999; 99US-01324487P.
PR 11-MAY-1999; 99US-01328631P.
PR 14-MAY-1999; 99US-01342566P.
PR 14-MAY-1999; 99US-01342188P.
PR 14-MAY-1999; 99US-01342191P.
PR 14-MAY-1999; 99US-01342212P.
PR 14-MAY-1999; 99US-01343706P.
PR 18-MAY-1999; 99US-01343768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-01351244P.
PR 21-MAY-1999; 99US-01353533P.
PR 24-MAY-1999; 99US-01356299P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0140353P.
PR 21-JUN-1999; 99US-0139750P.
PR 21-JUN-1999; 99US-0139763P.
PR 22-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 21-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145090P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 11-AUG-1999; 99US-0148171P.
PR 12-AUG-1999; 99US-0148319P.
PR 13-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 16-AUG-1999; 99US-0148684P.
PR 17-AUG-1999; 99US-0149368P.
PR 18-AUG-1999; 99US-0149175P.
PR 20-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 23-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152263P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154799P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 12-OCT-1999; 99US-0158232P.
PR 13-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159291P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.

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PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 66.7%; Score 6; DB 3; Length 329;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
Db 171 DTFYV 176

RESULT 16
ABU28452
ID ABU28452 standard; protein; 331 AA.
AC ABU28452;
XX
DT 19-JUN-2003 (first entry)
DE Protein encoded by Prokaryotic essential gene #13979.
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX Enterobacter cloacae.
OS WO200277183-A2.
PN
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA32322.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 56376; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense

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CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway; (8)
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 331 AA;

Query Match 66.7%; Score 6; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
Db 179 DTFYV 184

RESULT 17
ABU31900
ID ABU31900 standard; protein; 331 AA.
XX
AC ABU31900;
XX
DT 19-JUN-2003 (first entry)
DE Protein encoded by Prokaryotic essential gene #17427.
XX
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
KW Klebsiella pneumoniae.
OS
XX WO200277183-A2.
PN
PD 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR N-PSDB; ACA35770.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening

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PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 59824; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 331 AA;

Query Match 66.7%; Score 6; DB 6; Length 331;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVY 9

Db 179 DTFYVY 184

RESULT 18

ABO64234

XX ABO64234 standard; protein; 382 AA.

XX ABO64234;

XX 29-JUL-2004 (first entry)

XX Klebsiella pneumoniae polypeptide seqid 10751.

XX Recombinant expression vector; transcription regulatory element;

KW Klebsiella pneumoniae protein; antibacterial; Vaccine.

XX Klebsiella pneumoniae.

XX US6610836-B1.

XX 26-AUG-2003.

XX 27-JAN-2000; 2000US-00489039.

XX 29-JAN-1999; 99US-0117747P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX

PI Breton GL, Osborne M;

XX WPI; 2003-895346/82.

DR N-PSDB; ACH97785.

XX

PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.

XX Disclosure; SEQ ID NO 10751; 932pp; English.

XX The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention

XX Sequence 382 AA;

Query Match 66.7%; Score 6; DB 7; Length 382;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVY 9

Db 230 DTFYVY 235

RESULT 19

ABU33347

XX ABU33347 standard; protein; 399 AA.

XX AC ABU33347;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #18874.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Legionella pneumophila.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyekind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA37217.

XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 61271; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC

CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway; (8)
 CC required for proliferation or that inhibits cellular proliferation; (9)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 399 AA;

Query Match 66.7%; Score 6; DB 6; Length 399;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 |||||
 Db 186 VDDTFY 191

RESULT 20
 AEB39625
 ID AEB39625 standard; protein; 399 AA.

XX AEB39625;

XX 08-SEP-2005 (first entry)

XX L. pneumophila protein SEQ ID NO 3957.

XX detection; infection; Antibacterial; Vaccine.

XX Legionella pneumophila.

XX WO2005049642-A2.

XX 02-JUN-2005.

XX 23-SEP-2004; 2004WO-IB003578.

XX 21-NOV-2003; 2003FR-00013687.

XX (INSP) INST PASTEUR.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX (UVLY-) UNIV LYON 1 BERNARD CLAUDE.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;

PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst P, Vandenesch F;

PI Jarraud S;

XX WPI; 2005-388305/40.

XX New genome of Legionella pneumophila Paris strain and derived

PT polypeptides, useful for detection or identification of the strain and
 PT for treatment and prevention of infections.

XX Claim 3; SEQ ID NO 3957; 660pp; English.

XX The invention relates to an isolated or purified nucleotide sequences (I)
 CC from Legionella pneumophila Paris strain. (I), and their related
 CC sequences or fragments, are useful as primers and probes for detection
 CC and amplification, including differentiation between the Paris and
 CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
 CC (hybrid) polypeptides (II). (II) are also useful for preparation of
 CC specific antibodies (Ab), also used for detection/identification of
 CC Legionella, and some (I), specifically those involved in synthesis of
 CC surface proteins, are targets for identification of inhibitors. (II), or
 CC vectors that contain (I), are useful as vaccines and immunogenic
 CC compositions, for treatment and prevention of infections by L.
 CC pneumophila. The present sequence represents the amino acid sequence of a
 CC L. pneumophila protein.

SQ Sequence 399 AA;

Query Match 66.7%; Score 6; DB 9; Length 399;

Best Local Similarity 100.0%; Pred. No. 44;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7

|||||

Db 186 VDDTFY 191

RESULT 21

ABP78086

ID ABP78086 standard; protein; 400 AA.

XX AC ABP78086;

XX 07-MAR-2003 (first entry)

XX N. gonorrhoeae amino acid sequence SEQ ID 2702.

XX Antibacterial; infection; vaccine; gene therapy.

XX Neisseria gonorrhoeae.

XX WO200279243-A2.

XX 10-OCT-2002.

XX 12-FEB-2002; 2002WO-IB002069.

XX 12-FEB-2001; 2001GB-00003424.

XX (CHIR-) CHIRON SPA.

XX Fontana MR, Pizza M, Masignani V, Monaci E;

XX WPI; 2003-058415/05.

XX N-PSDB; ABZ39056.

XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a
 PT medicament for treating or preventing N. gonorrhoeae infection.

XX Discloure; Page 385; 815pp; English.

XX The present invention relates to proteins from Neisseria gonorrhoeae.
 CC Also disclosed are the nucleic acid molecules encoding the proteins and
 CC antibodies that specifically bind to the proteins. The composition
 CC comprising the protein, nucleic acid or antibody is useful for the
 CC manufacture of a medicament for treating or preventing N. gonorrhoeae
 CC infection, this may be in the form of a vaccine or gene therapy.
 CC Sequences given in records ABP76736-ABP81046 represent nucleic acid
 CC molecules of the invention

SQ Sequence 400 AA;

Query Match 66.7%; Score 6; DB 6; Length 400;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 DB 186 VDDTFY 191
 |||||

RESULT 22
 ABU37336
 ID ABU37336 standard; protein; 400 AA.
 XX
 AC ABU37336;
 XX
 DT 23-OCT-2003 (revised)
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #22863.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Neisseria gonorrhoeae.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA41206.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 65260; 1766pp; English.
 XX

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for the gene product or that has an activity against a biological pathway the gene product or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to
 CC standardise OS field)
 XX

SQ Sequence 400 AA;

Query Match 66.7%; Score 6; DB 6; Length 400;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 DB 186 VDDTFY 191
 |||||

RESULT 23

ABU37892
 ID ABU37892 standard; protein; 400 AA.

XX
 AC ABU37892;

XX
 DT 19-JUN-2003 (first entry)

XX
 DE Protein encoded by Prokaryotic essential gene #23419.

XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX
 OS Neisseria meningitidis.

XX
 PN WO200277183-A2.

XX
 PD 03-OCT-2002.

XX
 PF 21-MAR-2002; 2002WO-US009107.

XX
 PR 21-MAR-2001; 2001US-00815242.

XX
 PR 06-SEP-2001; 2001US-00948993.

XX
 PR 25-OCT-2001; 2001US-0342923P.

XX
 PR 08-FEB-2002; 2002US-00072851.

XX
 PR 06-MAR-2002; 2002US-0362699P.

XX
 PA (ELIT-) ELITRA PHARM INC.

XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX
 DR WPI; 2003-029926/02.

XX
 DR N-PSDB; ACA41762.

XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX
 PS Claim 25; SEQ ID NO 65816; 1766pp; English.

XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 400 AA;

Query Match 66.7%; Score 6; DB 6; Length 400;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 |||||
 Db 186 VDDTFY 191

RESULT 24
 AEB36203
 ID AEB36203 standard; protein; 405 AA.

XX AC AEB36203;

DT 08-SEP-2005 (first entry)

XX L. pneumophila protein SEQ ID NO 535.

XX detection; infection; Antibacterial; Vaccine.

XX Legionella pneumophila.

XX WO2005049642-A2.

XX 02-JUN-2005.

XX 23-SEP-2004; 2004WO-IB003578.

XX 21-NOV-2003; 2003FR-00013687.

XX (INSP) INST PASTEUR.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX (UYLY-) UNIV LYON 1 BERNARD CLAUDE.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
 PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
 PI Jarraud S;

XX WPI; 2605-388305/40.

XX New genome of *Legionella pneumophila* Paris strain and derived
 PT polypeptides, useful for detection or identification of the strain and
 PT for treatment and prevention of infections.

XX Claim 3; SEQ ID NO 535; 660pp; English.

XX The invention relates to an isolated or purified nucleotide sequences (I)

CC from *Legionella pneumophila* Paris strain. (I), and their related
 CC sequences or fragments, are useful as primers and probes for detection
 CC and amplification, including differentiation between the Paris and
 CC Philadelphia strains of *Legionella pneumophila* and to prepare recombinant
 CC (hybrid) polypeptides (II). (II) are also useful for preparation of
 CC specific antibodies (Ab), also used for detection/identification of
 CC *Legionella*, and some (I), specifically those involved in synthesis of
 CC surface proteins, are targets for identification of inhibitors. (II), or
 CC vectors that contain (I), are useful as vaccines and immunogenic
 CC compositions, for treatment and prevention of infections by *L.*
 CC *pneumophila*. The present sequence represents the amino acid sequence of a
 XX *L. pneumophila* protein.

SQ Sequence 405 AA;

Query Match 66.7%; Score 6; DB 9; Length 405;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 |||||
 Db 192 VDDTFY 197

RESULT 25
 ABU41410
 ID ABU41410 standard; protein; 409 AA.

XX AC ABU41410;

DT 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #26937.

DE Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Pseudomonas syringae.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-FSDB; ACA45280.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 69334; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 409 AA;

Query Match 66.7%; Score 6; DB 6; Length 409;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 |||||
 DB 189 VDDTFY 194

RESULT 26
 ADY24554
 ID ADY24554 standard; protein; 479 AA.

AC ADY24554;

XX 21-APR-2005 (first entry)

XX Plant full length insert polypeptide seqid 72338.

XX plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIU//) LIU J.

XX (ZHOU//) ZHOU Y.

XX (KOVA//) KOVALIC D K.

XX (SCRE//) SCREEN S E.

XX (TAB//) TABASKA J E.

XX (CAOY//) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX

DR WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.

PS Claim 1; SEQ ID NO 72338; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the invention.

XX SQ Sequence 479 AA;

Query Match 66.7%; Score 6; DB 8; Length 479;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
 |||||
 DB 321 DTFYV 326

RESULT 27

XX AAG04697

ID AAG04697 standard; protein; 485 AA.

AC AAG04697;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 823.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.

PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0146389P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.

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PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 66.7%; Score 6; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
Db 327 DTFYV 332

RESULT 28
ADN72665
ID ADN72665 standard; protein; 485 AA.
AC ADN72665;
XX
XX
DT 15-JUL-2004 (first entry)
DE
XX
XX Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 560.
DE plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;
KW animal feed product; thale cress; cell wall biosynthesis;
KW nitrogen metabolism; carbon metabolism.
XX
XX Arabidopsis thaliana.
XX
XX WO2004035798-A2.
XX
XX 29-APR-2004.
XX
XX 20-OCT-2003; 2003WO-EP011658.
XX
XX 18-OCT-2002; 2002EP-00079408.
XX
XX (CROP-) CROPDESIGN NV.
XX
XX Inze D, De Veylder L, Vlieghe K;
XX
XX WPI; 2004-348466/32.
XX
XX N-PSDB; ADN72664.
XX
XX Altering plant characteristics, useful for producing plants for enzyme or
PT pharmaceutical production comprises modifying in a plant, expression of
PT one or more nucleic acids and/or modifying level or activity of one or
PT more proteins.
XX
XX Claim 1; SEQ ID NO 560; 134pp; English.
XX
XX This invention relates to a novel method for altering one or more plant
CC characteristics. Specifically, it refers to identifying genes that are up
CC - or down-regulated in transgenic plants overexpressing the heterodimeric

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CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
CC alter plant characteristics accordingly. The present invention describes
CC generating transgenic plants for the production of growth regulators,
CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
CC the altered plant characteristics are selected from increased yield or
CC biomass, enhanced survival capacity, stress tolerance, plant architecture
CC or physiology, altered endoreplication, biochemistry, signal
CC transduction, storage lipid mobilization and/or altered photosynthesis,
CC each relative to the corresponding wild type plants. Accordingly, these
CC sequences can also be useful as positive or negative selectable markers
CC during transformation of cells or tissues. The identified genes play a
CC role in a variety of biological processes such as DNA replication, cell
CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
CC transcription factors. This polypeptide sequence is thale cress protein
CC expressed by a gene upregulated 1.3 fold or more in plants overexpressing
CC the E2Fa/Dpa transcription factor, given in an exemplification of the
CC invention.
XX
SQ Sequence 485 AA;

Query Match 66.7%; Score 6; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
Db 327 DTFYV 332

RESULT 29
AAG04696
ID AAG04696 standard; protein; 496 AA.
XX
XX AAG04696;
XX
XX 17-OCT-2000 (first entry)
DE
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 822.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX
XX 05-MAR-1999; 99US-0123180P.
XX
XX 09-MAR-1999; 99US-0123548P.
XX
XX 23-MAR-1999; 99US-0125788P.
XX
XX 25-MAR-1999; 99US-0126264P.
XX
XX 29-MAR-1999; 99US-0126785P.
XX
XX 01-APR-1999; 99US-0127462P.
XX
XX 06-APR-1999; 99US-0128234P.
XX
XX 08-APR-1999; 99US-0128714P.
XX
XX 16-APR-1999; 99US-0129845P.
XX
XX 19-APR-1999; 99US-0130077P.
XX
XX 21-APR-1999; 99US-0130449P.
XX
XX 23-APR-1999; 99US-0130510P.
XX
XX 23-APR-1999; 99US-0130891P.
XX
XX 28-APR-1999; 99US-0131449P.
XX
XX 30-APR-1999; 99US-0132048P.
XX
XX 30-APR-1999; 99US-0132407P.
XX
XX 04-MAY-1999; 99US-0132484P.
XX
XX 05-MAY-1999; 99US-0132485P.
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Query Match 66.7%; Score 6; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
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Db 338 DTFYV 343

RESULT 30
AAG42270
ID AAG42270 standard; protein; 500 AA.
AC AAG42270;
XX
XX 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52696.
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
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XX 06-SEP-2000.
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Query Match 66.7%; Score 6; DB 3; Length 500;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
Db 342 DTFYV 347

RESULT 31
ABB92358
ID ABB92358 standard; protein; 500 AA.
XX ABB92358;
AC ABB92358;
XX 31-MAY-2002 (first entry)
DT Herbicidally active polypeptide SEQ ID NO 1569.
DE Herbicidally active polypeptide SEQ ID NO 1569.
XX Herbicidally active polypeptide SEQ ID NO 1569.
KW Herbicidally active polypeptide SEQ ID NO 1569.
XX Herbicidally active polypeptide SEQ ID NO 1569.
OS Arabidopsis thaliana.
XX WO200210210-A2.
PN WO200210210-A2.
XX 07-FEB-2002.
XX 28-AUG-2001; 2001WO-EP009892.
XX 28-AUG-2001; 2001WO-EP009892.
XX (FARB ) BAYER AG.
XX Tietjen K, Weidner M;
XX WPI; 2002-269010/31.
PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms.
XX Claim 5; SEQ ID NO 1569; 261pp + Sequence Listing; English.
XX The invention relates to identifying target proteins (ABB90790-ABB94016)
XX for herbicidally active compounds, comprising aligning and comparing
XX nucleic acid or amino acid sequences from plant with nucleic acid or
XX amino acid sequences from non-plant organisms using suitable search
XX parameters, where plant sequences having an E-value greater by a factor
XX of 3 than the E-value of most similar non-plant sequences are selected.
XX The polypeptides or nucleic acids encoding them are useful for
XX identifying modulators. The identified modulators are useful as
XX herbicides
SQ Sequence 500 AA;

Query Match 66.7%; Score 6; DB 5; Length 500;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
Db 342 DTFYV 347

RESULT 32
AAG42269
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PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
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PR 28-OCT-1999; 99US-0161992P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 66.7%; Score 6; DB 3; Length 510;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFYIV 9
Db 352 DTFYIV 357

RESULT 33
ADM48028
ID ADM48028 standard; protein; 510 AA.
XX AC
XX ADM48028;
XX AC
DT 03-JUN-2004 (first entry)
XX AC
XX Polypeptide sequence #78 useful in producing transgenic plants.

XX Plant; maize; rice; sorghum; thale cress; soybean; wheat; transgenic;
KW osmotic stress; sugar transport; cell cycle pathway; plant height;
KW carbohydrate transport; crop productivity; plant growth;
KW stress resistance; disease resistance; insect resistance; heat tolerance;
KW nitrogen assimilation; water stress tolerance;
KW photosynthetic carbon fixation; virus resistance; gene therapy.
XX
OS Zea mays.
XX
PN US2003233670-A1.
XX
PD 18-DEC-2003.
XX
PF 04-DEC-2002; 2002US-00310154.
XX
PR 04-DEC-2001; 2001US-0337358P.
XX
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
XX
PI Edgerton MD, Chomet PS, Laccetti LB;
XX
XX WPI; 2004-061374/06.
XX N-PSDB; ADM47660.
XX
XX New polynucleotide, useful for manipulating plant protein quality,
PT improving plant growth, yield and crop productivity or grain composition
PT or producing plants with improved properties.
XX
XX Claim 8; SEQ ID NO 446; 144pp; English.
XX
CC The present invention relates to polynucleotide sequences, and the
CC proteins they encode. The sequences are isolated from a variety of
CC organisms such as plants (e.g. maize, rice, sorghum, thale cress,
CC soybean, and wheat), cyanobacteria, bacteria, yeast and other fungi. The
CC polynucleotide and polypeptide sequences of the invention are useful in
CC the production of transgenic plants that have improved properties. Also
CC disclosed are methods of producing fertile transgenic plants, preferably
CC maize, with desired phenotypes. The polynucleotide and polypeptide
CC sequences are useful for improving plants by providing protection against
CC osmotic stress, improving altering sugar transport and/or metabolism,
CC modifying the cell cycle pathway, reducing plant height, modifying
CC carbohydrate transport, improving crop productivity, improving plant
CC growth and stress resistance, improving disease resistance, improving
CC insect resistance, improving cold or heat tolerance, improving nitrogen
CC assimilation, improving stalk strength, improving water stress tolerance,
CC improving photosynthetic carbon fixation, improving biotic and abiotic
CC stress resistance, improving resistance to oxidative stress, providing
CC increased vigour, reducing senescence, and conferring virus resistance.
CC The present sequence represents a polypeptide sequence of the invention.
CC Note: The sequence data for this patent is not provided in the printed
CC specification but is obtained in electronic format from the USPTO website
CC at seqdata.uspto.gov.
XX
SQ Sequence 510 AA;
Query Match 66.7%; Score 6; DB 8; Length 510;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFYIV 9
Db 348 DTFYIV 353

RESULT 34
ABB59871
ID ABB59871 standard; protein; 800 AA.
XX AC
XX ABB59871;
XX AC
XX ABB59871;

```

DT 26-MAR-2002 (first entry)
 XX Drosophila melanogaster polypeptide SEQ ID NO 6405.
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 KW Drosophila melanogaster.
 OS WO200171042-A2.
 XX 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US009231.
 XX 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 DR N-PSDB; ABL03974.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX Disclosure; SEQ ID NO 6405; 2lpp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL01840-ABL0175), expressed DNA
 CC sequences (ABL01840-ABL0175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 800 AA;
 SQ
 Query Match 66.7%; Score 6; DB 4; Length 800;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 DDTFFY 8
 Db 755 DDTFFY 760
 RESULT 35
 ABB71398
 ID ABB71398 standard; protein; 900 AA.
 XX AC ABB71398;
 XX 26-MAR-2002 (first entry)
 XX Drosophila melanogaster polypeptide SEQ ID NO 40986.
 DE Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 KW Drosophila melanogaster.
 OS WO200171042-A2.
 XX 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 DR N-PSDB; ABL15501.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX Disclosure; SEQ ID NO 40986; 2lpp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL01840-ABL0175), expressed DNA
 CC sequences (ABL01840-ABL0175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 900 AA;
 SQ
 Query Match 66.7%; Score 6; DB 4; Length 900;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 DTFYV 9
 Db 304 DTFYV 309
 RESULT 36
 ADN21456
 ID ADN21456 standard; protein; 1136 AA.
 XX AC ADN21456;
 XX 02-DEC-2004 (first entry)
 XX Bacterial polypeptide #4109.
 DE Recombinant DNA construct; transformed plant; improved plant property;
 XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX Bacteria.
 OS US2003233675-A1.
 XX 18-DEC-2003.
 XX 20-FEB-2003; 2003US-00369493.
 XX 21-FEB-2002; 2002US-0360039P.
 XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 XX
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 XX Claim 1; SEQ ID NO 4109; 122pp; English.
 XX
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 1136 AA;
 Query Match 66.7%; Score 6; DB 8; Length 1136;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0;
 QY 4 DTFYV 9
 Db 338 DTFYV 343
 |||||
 |||||
 RESULT 37
 AAU89238
 ID AAU89238 standard; peptide; 21 AA.
 AC AAU89238;
 XX
 XX 18-JUN-2002 (first entry)
 DT
 XX Insulin/insulin-like growth factor receptor-binding peptide #1194.
 DE
 XX Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
 KW ophthalmological; insulin; receptor; gene therapy; diabetes;
 KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
 KW diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
 XX
 XX Synthetic.
 OS
 XX WO200172771-A2.
 PN
 XX 04-OCT-2001.
 PD
 XX 29-MAR-2000; 2000WO-US008528.
 PF
 XX 29-MAR-2000; 2000WO-US008528.
 PR
 XX (DGIB-) DGI BIOTECHNOLOGIES LLC.
 XX (NOVO) NOVO NORDISK AS.
 PA

XX Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
 PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
 PI Hansen PH, Ravera M, Hsiao K;
 XX WPI; 2002-025774/03.
 DR
 XX Modulating insulin activity in mammalian cells, for treating e.g.
 PT diabetes and tumors, comprises using peptides that bind to insulin or
 PT insulin-like growth factor receptors.
 XX
 XX Disclosure; Fig 10-2; 390pp; English.
 PS
 XX The invention relates to a method of modulating insulin activity in
 CC mammalian cells by administering a peptide that binds the insulin
 CC receptor (IR). A composition containing a peptide, optionally expressed
 CC from gene therapy vectors, that binds to Site 1 of IR and an insulin
 CC agonist are useful for treating diabetes. Also, peptides that are
 CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
 CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
 CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
 CC receptor agonists are useful for treating neurological diseases,
 CC including stroke and diabetic neuropathy. The peptides are also useful in
 CC screening for compounds that bind to IR or IGF-1 receptor, potential
 CC therapeutics and research reagents. AAU8034-AAU90957 represent IR and/or
 CC IGF-1 receptor-binding peptides and related amino acid sequences of the
 CC invention
 XX
 SQ Sequence 21 AA;
 Query Match 55.6%; Score 5; DB 5; Length 21;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFY 7
 Db 4 DDTFY 8
 |||||
 |||||
 RESULT 38
 ADA04060
 ID ADA04060 standard; peptide; 21 AA.
 XX
 XX ADA04060;
 AC
 XX 06-NOV-2003 (first entry)
 DT
 XX Insulin receptor (IR) related Formula 1 motif peptide SEQ ID NO:691.
 DE
 XX insulin-like growth factor receptor; IGF; modulate; insulin receptor;
 KW IR; insulin; cytostatic; IGF agonist; IGF antagonist; cancer;
 KW leukaemia; sarcoma; lymphoma; carcinoma.
 XX
 XX Synthetic.
 OS
 XX Homo sapiens.
 XX
 XX WO2003027246-A2.
 PN
 XX 03-APR-2003.
 PD
 XX 24-SEP-2002; 2002WO-US030412.
 PF
 XX 24-SEP-2001; 2001US-00962756.
 PR
 XX (NOVO) NOVO NORDISK AS.
 PA (DGIB-) DGI BIOTECHNOLOGIES.
 XX
 XX Pillutla R, Dedova O, Blume AJ, Goldstein NI, Brissette R;
 PI Wang P, Liu H, Hsiao K, Lennick M, Fletcher P;
 XX WPI; 2003-363211/34.
 DR
 XX Modulating insulin-like growth factor receptor (IGFR) activity in IGF-

PT responsive mammalian cells, useful for treating cancer comprises
 PT contacting the cells with an amino acid sequence to modulate the activity
 of IGFR.
 XX
 XX Disclosure; Fig 10; 372pp; English.
 XX
 XX The present invention describes a method for modulating insulin-like
 CC growth factor receptor (IGFR) activity in insulin-like growth factor-
 CC responsive mammalian cells comprising contacting the cells with an amino
 CC acid sequence to modulate the activity of IGFR. In modulating IGFR
 CC activity, the amino acid sequence comprises X1X2X3X4X5 (I), where X1, X2
 CC and X5 = phenylalanine or tyrosine; X3 = aspartic acid, glutamic acid,
 CC glycine or serine; and X4 = tryptophan, tyrosine or phenylalanine. The
 CC amino acid sequence is not insulin, insulin-like growth factor, an anti-
 CC insulin receptor antibody, an anti-insulin-like growth receptor antibody,
 CC or its fragment. Also described: (1) decreasing or increasing IGFR
 CC activity in IGF-responsive mammalian cells by contacting the cells with
 CC an amino acid sequence to decrease or increase the activity of IGFR; (2)
 CC an IGFR modulator, agonist or antagonist; (3) identifying IGFR modulator;
 CC and (4) enhancing survival of an IGF-responsive mammalian cell by
 CC contacting the cell with (I) to enhance the survival of the cell. IGFR
 CC modulators have cytostatic activity, and can be used as IGFR agonists or
 CC IGFR antagonists. The methods, modulators, agonists and antagonists are
 CC useful for treating cancer, e.g. leukemia, sarcoma, lymphoma or
 CC carcinoma. The methods are useful for identifying molecular structures
 CC that are capable of acting as an IGFR agonist or antagonist. The present
 CC sequence represents a peptide given in the exemplification of the present
 XX invention.
 XX
 SQ Sequence 21 AA;

Query Match 55.6%; Score 5; DB 6; Length 21;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 DB 4 DDTFY 8

RESULT 39

ADH95273
 ID ADH95273 standard; protein; 21 AA.

AC ADH95273;

DT 22-APR-2004 (first entry)

DE Insulin receptor motif polypeptide, SEQ ID No 691.

XX insulin receptor; insulin; insulin-like growth factor receptor; agonist;
 KW antagonist; antidiabetic; diabetes; insulin shock.

XX Unidentified.

XX WO2003070747-A2.

XX 28-AUG-2003.

PF 24-SEP-2002; 2002WO-US030312.

XX 24-SEP-2001; 2001US-00962756.

XX (NOVO) NOVO NORDISK AS.

PA (DGI B-) DGI BIOTECHNOLOGIES.

PI Pillutla R, Brissette R, Blume AJ, Schaeffer L, Brandt J;

PI Goldstein NI, Spetzler J, Ostergaard S;

XX WPI; 2003-833235/77.

XX Modulating insulin-like growth factor receptor (IGFR) activity in IGF-
 PT responsive mammalian cells, useful for treating diabetes comprises

PT contacting the cells with an amino acid sequence to modulate the activity
 of IGFR.
 XX
 XX Claim 7; SEQ ID NO 691; 328pp; English.
 XX
 CC The invention relates to a novel method for decreasing or increasing
 CC insulin receptor activity in mammalian cells. The invention further
 CC relates to peptide sequences capable of binding to insulin and/or insulin
 CC -like growth factor receptors with either agonist or antagonist activity.
 CC The peptide sequences are identified from various peptide libraries. The
 CC novel method comprises administering to the mammalian cells an amino acid
 CC having subsequences that binds to site 1 and site 2 of an insulin
 CC receptor. The subsequences are joined C-terminus to N-terminus and
 CC oriented site 1 to site 2. The sequence is not insulin or insulin-like
 CC growth factor. The peptide sequences of the invention have antidiabetic
 CC activity. The peptides are useful for treating diabetes or insulin shock.
 CC This sequence represents an insulin receptor/ insulin growth factor
 CC receptor binding polypeptide relating to the invention.
 XX
 SQ Sequence 21 AA;

Query Match 55.6%; Score 5; DB 7; Length 21;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||

DB 4 DDTFY 8

RESULT 40

ADL67964

ID ADL67964 standard; peptide; 21 AA.

XX AC ADL67964;

XX 20-MAY-2004 (first entry)

XX IGF-1R/IR binding peptide seq id 691.

XX cytostatic; insulin-like growth factor receptor activity;
 KW insulin-like growth factor-responsive mammalian cell;
 KW insulin-like growth factor receptor modulator;
 KW insulin-like growth factor receptor antagonist;
 KW insulin-like growth factor receptor agonist; insulin receptor;
 KW insulin-like growth factor receptor; therapeutic; peptide hormone;
 KW cancer; breast cancer; prostate cancer; colorectal cancer;
 KW ovarian cancer; peptide library; IGF-1R; IR.

XX Unidentified.

OS US2004023887-A1.

XX 05-FEB-2004.

XX 24-SEP-2002; 2002US-00253493.

XX 02-SEP-1998; 98US-00146127.

PR 29-MAR-2000; 2000US-00538038.

PR 24-SEP-2001; 2001US-00962756.

XX (PILL/) PILLUTLA R.

PA (DEDO/) DEDOVA O.

PA (BLUM/) BLUME A J.

PA (GOLD/) GOLDSTEIN N I.

PA (BRIS/) BRISSETTE R.

PA (WANG/) WANG P.

PA (LIUH/) LIU H.

PA (HSIA/) HSIAO K.

PA (LENN/) LENNICK M.

PA (FLET/) FLETCHER P.

XX Pillutla R, Dedova O, Blume AJ, Goldstein NI, Brissette R;

PI Wang P, Liu H, Hsiao K, Lennick M, Fletcher P;
 XX WPI; 2004-132606/13.
 XX Disclosure; SEQ ID NO 691; 242pp; English.
 XX The invention describes the use of molecular structures, preferably
 CC peptides for modulating, increasing or decreasing insulin-like growth
 CC factor receptor activity in insulin-like growth factor-responsive
 CC mammalian cells. Also described are: modulating, decreasing or increasing
 CC insulin-like growth factor receptor activity in insulin-like growth
 CC factor-responsive mammalian cells; an insulin-like growth factor receptor
 CC modulator; an insulin-like growth factor receptor antagonist; an insulin-
 CC like growth factor receptor agonist; identifying an insulin-like growth
 CC factor receptor modulator; and enhancing survival of an insulin-like
 CC growth factor-responsive mammalian cell. The molecular structures of the
 CC peptides are useful for modulating, increasing or decreasing insulin-like
 CC growth factor receptor activity in insulin-like growth factor-responsive
 CC mammalian cells. The peptide sequences are useful for binding to insulin
 CC and/or insulin-like growth factor receptors with either agonist or
 CC antagonist activity. As agonists, the peptides are useful for development
 CC of therapeutics to supplement or replace endogenous peptide hormones. The
 CC antagonist peptides can also be developed as therapeutics. The IR and IGF
 CC -IR agonist and antagonist peptides are useful as lead compounds for
 CC identifying other more potent or selective therapeutics, assay reagents
 CC for identifying other useful ligands, as research tools for further
 CC analysis of IR and IGF-IR. The IGF-IR antagonists are useful as treatment
 CC for cancer, e.g. breast, prostate, colorectal or ovarian cancer. This is
 CC the amino acid sequence of a IGF-IR/IR binding peptide obtained by
 CC panning a peptide library against the insulin-like growth factor 1
 CC receptor (IGF-IR) and insulin receptor (IR). Note: This sequence is also
 CC available in electronic format from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID=20040023887.
 XX Sequence 21 AA;
 SQ

Query Match 55.6%; Score 5; DB 8; Length 21;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db |||||
 4 DDTFY 8

RESULT 41
 ADM37809
 ID ADM37809 standard; peptide; 21 AA.
 XX
 AC ADM37809;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Anti-IR formula 1 motif peptide #427.
 XX
 KW insulin receptor activity; insulin-related disease;
 KW insulin-like growth factor-related disease; diabetes; insulin shock.
 XX
 OS Synthetic.
 XX
 PN US2003236190-A1.
 XX
 PD 25-DEC-2003.
 XX
 PF 24-SEP-2002; 2002US-00253471.
 XX
 PR 02-SEP-1998; 98US-00146127.
 PR 29-MAR-2000; 2000US-00538038.
 PR 24-SEP-2001; 2001US-00962756.
 XX
 XX (PILL/) PILLUTLA R.
 PA (BRIS/) BRISSETTE R.
 PA (BLUM/) BLUME A J.

PA (SCHA/) SCHARPER L.
 PA (BRAN/) BRANDT J.
 PA (GOLD/) GOLDSTEIN N I.
 PA (SPET/) SPETZLER J.
 PA (OSTE/) OSTERGAARD S.
 PA (HANS/) HANSEN P H.
 XX
 XX Pillutla R, Brissette R, Blume AJ, Schaffer L, Brandt J;
 PI Goldstein NI, Spetzler J, Ostergaard S, Hansen PH;
 XX WPI; 2004-081583/08.
 XX Decreasing or increasing insulin receptor activity in mammalian cells
 PT using peptide sequences that bind insulin and/or insulin-like growth
 PT factor receptors, useful for treating diabetes and insulin shock.
 XX
 PS Claim 7; SEQ ID NO 691; 203pp; English.
 XX The invention relates to a method of decreasing insulin receptor activity
 CC in mammalian cells which comprises administering an amino acid sequence
 CC having a subsequence comprising a sequence that binds to Site 1 and Site
 CC 2 of insulin receptor, where the subsequences are linked C-terminus to N-
 CC terminus and oriented Site 1 to Site 2, where the amino acid sequence is
 CC not insulin, insulin-like growth factor or their fragments. The methods
 CC and compositions of the present invention are useful for treating insulin
 CC - or insulin-like growth factor-related diseases or conditions, such as
 CC diabetes and insulin shock. The present sequence is used in the
 CC exemplification of the present invention.
 XX Sequence 21 AA;
 SQ

Query Match 55.6%; Score 5; DB 8; Length 21;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db |||||
 4 DDTFY 8

RESULT 42
 ADA04794
 ID ADA04794 standard; peptide; 27 AA.
 XX
 AC ADA04794;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE IGF-1R binding peptide SEQ ID NO:1425.
 XX
 KW insulin-like growth factor receptor; IGF; modulate; insulin receptor;
 KW IR; insulin; cytostatic; IGF agonist; IGF antagonist; cancer;
 KW leukaemia; sarcoma; lymphoma; carcinoma.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003027246-A2.
 XX
 PD 03-APR-2003.
 XX
 PF 24-SEP-2002; 2002WO-US030412.
 XX
 PR 24-SEP-2001; 2001US-00962756.
 XX
 PA (NOVO) NOVO NORDISK AS.
 PA (DGI-) DGI BIOTECHNOLOGIES.
 XX
 PI Pillutla R, Dedova O, Blume AJ, Goldstein NI, Brissette R;
 PI Wang P, Liu H, Hsiao K, Lennick M, Fletcher P;
 XX WPI; 2003-363211/34.
 XX

PT Modulating insulin-like growth factor receptor (IGFR) activity in IGF-
 PT responsive mammalian cells, useful for treating cancer comprises
 PT contacting the cells with an amino acid sequence to modulate the activity
 of IGFR.

XX Example 11; Fig 43; 372pp; English.

XX
 CC The present invention describes a method for modulating insulin-like
 CC growth factor receptor (IGFR) activity in insulin-like growth factor-
 CC responsive mammalian cells comprising contacting the cells with an amino
 CC acid sequence to modulate the activity of IGFR. In modulating IGFR
 CC activity, the amino acid sequence comprises XIX2K3X4X5 (I), where X1, X2
 CC and X5 = phenylalanine or tyrosine; X3 = aspartic acid, glutamic acid,
 CC glycine or serine; and X4 = tryptophan, tyrosine or phenylalanine. The
 CC amino acid sequence is not insulin, insulin-like growth factor, an anti-
 CC insulin receptor antibody, an anti-insulin-like growth receptor antibody,
 CC or its fragment. Also described: (1) decreasing or increasing IGFR
 CC activity in IGF-responsive mammalian cells by contacting the cells with
 CC an amino acid sequence to decrease or increase the activity of IGFR; (2)
 CC an IGFR modulator, agonist or antagonist; (3) identifying IGFR modulator;
 CC and (4) enhancing survival of an IGF-responsive mammalian cell by
 CC contacting the cell with (1) to enhance the survival of the cell. IGFR
 CC modulators have cytostatic activity, and can be used as IGFR agonists or
 CC IGFR antagonists. The methods, modulators, agonists and antagonists are
 CC useful for treating cancer, e.g. leukaemia, sarcoma, lymphoma or
 CC carcinoma. The methods are useful for identifying molecular structures
 CC that are capable of acting as an IGFR agonist or antagonist. The present
 CC invention represents a peptide given in the exemplification of the present
 XX sequence 27 AA;

SQ Sequence 27 AA;

Query Match 55.6%; Score 5; DB 6; Length 27;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db |||||
 1 DDTFY 5

RESULT 43

ID ADH96007
 AC ADH96007 standard; protein; 27 AA.

XX
 XX ADH96007;

XX 22-APR-2004 (first entry)

XX Insulin growth factor receptor peptide, SEQ ID No 1425.

XX insulin receptor; insulin; insulin-like growth factor receptor; agonist;
 KW antagonist; antidiabetic; diabetes; insulin shock.

XX Unidentified.

XX WO2003070747-A2.

XX 28-AUG-2003.

XX 24-SEP-2002; 2002WO-US030312.

XX 24-SEP-2001; 2001US-00962756.

XX (NOVO) NOVO NORDISK AS.

XX (DGIB-) DGI BIOTECHNOLOGIES.

XX Pillutla R, Brissette R, Blume AJ, Schaeffer L, Brandt J;

PI Goldstein NI, Spetzler J, Ostergaard S;

XX WPI; 2003-833235/77.

XX Modulating insulin-like growth factor receptor (IGFR) activity in IGF-

PT responsive mammalian cells, useful for treating diabetes comprises
 PT contacting the cells with an amino acid sequence to modulate the activity
 of IGFR.

XX Example 14; SEQ ID NO 1425; 328pp; English.

XX
 CC The invention relates to a novel method for decreasing or increasing
 CC insulin receptor activity in mammalian cells. The invention further
 CC relates to peptide sequences capable of binding to insulin and/or insulin
 CC -like growth factor receptors with either agonist or antagonist activity.
 CC The peptide sequences are identified from various peptide libraries. The
 CC novel method comprises administering to the mammalian cells an amino acid
 CC having subsequences that binds to site 1 and site 2 of an insulin
 CC receptor. The subsequences are joined C-terminus to N-terminus and
 CC oriented site 1 to site 2. The sequence is not insulin or insulin-like
 CC growth factor. The peptide sequences of the invention have antidiabetic
 CC activity. The peptides are useful for treating diabetes or insulin shock.
 CC This sequence represents an insulin receptor/ insulin growth factor
 CC receptor binding polypeptide relating to the invention.

XX Sequence 27 AA;

Query Match 55.6%; Score 5; DB 7; Length 27;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db |||||
 1 DDTFY 5

RESULT 44

ID ADL68698

XX ADL68698 standard; peptide; 27 AA.

XX ADL68698;

XX 20-MAY-2004 (first entry)

XX IGF-1R/IR binding peptide seq id 1425.

XX cytostatic; insulin-like growth factor receptor activity;
 KW insulin-like growth factor-responsive mammalian cell;
 KW insulin-like growth factor receptor modulator;
 KW insulin-like growth factor receptor antagonist;
 KW insulin-like growth factor receptor agonist; insulin receptor;
 KW insulin-like growth factor receptor; therapeutic; peptide hormone;
 KW cancer; breast cancer; prostate cancer; colorectal cancer;
 KW ovarian cancer; peptide library; IGF-1R; IR.

XX Unidentified.

XX US2004023887-A1.

XX 05-FEB-2004.

XX 24-SEP-2002; 2002US-00253493.

XX 02-SEP-1998; 98US-00146127.

XX 29-MAR-2000; 2000US-00538038.

XX 24-SEP-2001; 2001US-00962756.

XX (PILL/) PILLUTLA R.

XX (DEDO/) DEDOVA O.

XX (BLUM/) BLUME A J.

XX (GOLD/) GOLDSTEIN N I.

XX (BRIS/) BRISSETTE R.

XX (WANG/) WANG P.

XX (LIUH/) LIU H.

XX (HSIA/) HSIAO K.

XX (LENN/) LENNICK M.

XX (FLET/) FLETCHER P.

XX

PI Pillutla R, Dedova O, Blume AJ, Goldstein NI, Brissette R;
 PI Wang P, Liu H, Hsiao K, Lennick M, Fletcher P;
 XX WPI; 2004-132606/13.
 PS Disclosure; SEQ ID NO 1425; 242pp; English.
 XX
 CC The invention describes the use of molecular structures, preferably
 CC peptides for modulating, increasing or decreasing insulin-like growth
 CC factor receptor activity in insulin-like growth factor-responsive
 CC mammalian cells. Also described are: modulating, decreasing or increasing
 CC insulin-like growth factor receptor activity in insulin-like growth
 CC factor-responsive mammalian cells; an insulin-like growth factor
 CC modulator; an insulin-like growth factor receptor antagonist; an insulin-
 CC like growth factor receptor agonist; identifying an insulin-like growth
 CC factor receptor modulator; and enhancing survival of an insulin-like
 CC growth factor-responsive mammalian cell. The molecular structures of the
 CC peptides are useful for modulating, increasing or decreasing insulin-like
 CC growth factor receptor activity in insulin-like growth factor-responsive
 CC mammalian cells. The peptide sequences are useful for binding to insulin
 CC and/or insulin-like growth factor receptors with either agonist or
 CC antagonist activity. As agonists, the peptides are useful for development
 CC of therapeutics to supplement or replace endogenous peptide hormones. The
 CC antagonist peptides can also be developed as therapeutics. The IR and IGF
 CC -IR agonist and antagonist peptides are useful as lead compounds for
 CC identifying other more potent or selective therapeutics, assay reagents
 CC for identifying other useful ligands, as research tools for further
 CC analysis of IR and IGF-IR. The IGF-IR antagonists are useful as treatment
 CC for cancer, e.g. breast, prostate, colorectal or ovarian cancer. This is
 CC the amino acid sequence of a IGF-IR/IR binding peptide obtained by
 CC panning a peptide library against the insulin-like growth factor 1
 CC receptor (IGF-IR) and insulin receptor (IR). Note: This sequence is also
 CC available in electronic format from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docID=20040023887.
 XX
 SQ Sequence 27 AA;

Query Match 55.6%; Score 5; DB 8; Length 27;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db |||||
 1 DDTFY 5

RESULT 45
 ADM38543
 ID ADM38543 standard; peptide; 27 AA.
 AC ADM38543;
 XX
 XX 03-JUN-2004 (first entry)
 DT
 DE Insulin and IGF-1 receptor associated peptide #164.
 DE
 XX insulin receptor activity; insulin-related disease;
 KW insulin-like growth factor-related disease; diabetes; insulin shock.
 KW
 XX Synthetic.
 OS
 XX US2003236190-A1.
 PN
 XX 25-DEC-2003.
 PD
 XX 24-SEP-2002; 2002US-00253471.
 PF
 XX 02-SEP-1998; 98US-00146127.
 PR
 XX 29-MAR-2000; 2000US-00538038.
 PR
 XX 24-SEP-2001; 2001US-00962756.
 XX
 XX (PILL/) PILLUTLA R.
 PA (BRIS/) BRISSETTE R.

PA (BLUM/) BLUME A J.
 PA (SCHA/) SCHAPPER L.
 PA (BRAN/) BRANDT J.
 PA (GOLD/) GOLDSTEIN N I.
 PA (SPET/) SPETZLER J.
 PA (OSTE/) OSTERGAARD S.
 PA (HAN/) HANSEN P H.
 XX
 PI Pillutla R, Brissette R, Blume AJ, Schaffer L, Brandt J;
 PI Goldstein NI, Spetzler J, Ostergaard S, Hansen PH;
 XX WPI; 2004-081583/08.
 DR Decreasing or increasing insulin receptor activity in mammalian cells
 CC using peptide sequences that bind insulin and/or insulin-like growth
 PT factor receptors, useful for treating diabetes and insulin shock.
 PT
 XX Disclosure; SEQ ID NO 1425; 203pp; English.
 PS
 CC The invention relates to a method of decreasing insulin receptor activity
 CC in mammalian cells which comprises administering an amino acid sequence
 CC having a subsequence comprising a sequence that binds to Site 1 and Site
 CC 2 of insulin receptor, where the subsequences are linked C-terminus to N-
 CC terminus and oriented Site 1 to Site 2, where the amino acid sequence is
 CC not insulin, insulin-like growth factor or their fragments. The methods
 CC and compositions of the present invention are useful for treating insulin
 CC or insulin-like growth factor-related diseases or conditions, such as
 CC diabetes and insulin shock. The present sequence is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 27 AA;

Query Match 55.6%; Score 5; DB 8; Length 27;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db |||||
 1 DDTFY 5

RESULT 46
 ABO57827
 ID ABO57827 standard; protein; 59 AA.
 XX
 AC ABO57827;
 XX
 XX 29-JUL-2004 (first entry)
 DT
 XX Human genome derived single exon protein #4061.
 DE
 XX Human; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 KW
 XX Homo sapiens.
 OS
 XX US2003194704-A1.
 PN
 XX 16-OCT-2003.
 PD
 XX 03-APR-2002; 2002US-00029386.
 PF
 XX 03-APR-2002; 2002US-00029386.
 PR
 XX (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 XX
 XX Penn SG, Rank DR, Hanzel DK;
 PI
 XX WPI; 2004-119264/12.
 DR
 XX New human genome-derived single exon nucleic acid probes useful for human

PT Gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.

XX Claim 45; SEQ ID NO 31461; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 688 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 59 AA;

Query Match 55.6%; Score 5; DB 8; Length 59;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db 48 DDTFY 52

RESULT 47
 AAU44424
 ID AAU44424 standard; protein; 62 AA.
 AC AAU44424;
 XX

DT 27-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #5320.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX 01-NOV-2001.

PD 11-OCT-2002; 2002WO-US032727.

XX PF

XX 20-APR-2001; 2001WO-US012865.

XX 21-APR-2000; 2000US-0199047P.

XX 02-JUN-2000; 2000US-0208841P.

XX 07-JUL-2000; 2000US-0216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

XX N-PSDB; AAS59522.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.

XX Example 1; SEQ ID NO 5619; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 62 AA;

Query Match 55.6%; Score 5; DB 4; Length 62;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 Db 8 VDDTF 12

RESULT 48

ABM40943

ID ABM40943 standard; protein; 62 AA.

XX ABM40943;

XX 20-OCT-2003 (first entry)

XX Propionibacterium acnes predicted ORF-encoded polypeptide #5619.

XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.

XX Propionibacterium acnes.

XX WO2003033515-A1.

XX 24-APR-2003.

```

XX 15-OCT-2001; 2001US-00978825.
XX (CORI-) CORIXA CORP.
XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes WJ, Benson DR, Jones R, Carter D;
PI Barth B, Vallieue-Douglas J;
XX WPI; 2003-381789/36.
DR N-PSDB; ACF64451.
XX
XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.
XX
PS Example 1; SEQ ID NO 5619; 1481pp; English.
XX
XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC polynucleotide of the invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 62 AA;
Query Match 55.6%; Score 5; DB 6; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
DB 8 VDDTF 12
|||||
|||||
RESULT 49
ADM97962
ID ADM97962 standard; peptide; 74 AA.
AC ADM97962;
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Vetispiradiene.
XX
XX sesquiterpene synthase; cubebol synthase; GFTbSC; transformed plant cell;
KW farnesyl-pyrophosphate; valencene; bicyclo-germacrene; cubebol;
KW delta-cadinene; perfumery; GFTpsA; GFTpsB; GFTpsD1; GFTpsD2; GFTpsE.
XX
XX Solanum tuberosum.
OS
XX

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FH Key Location/Qualifiers
FT Misc-difference 5 /note= "Conserved residue"
FT Misc-difference 11. .13 /note= "Conserved residues"
FT Misc-difference 26 /note= "Conserved residue"
FT Misc-difference 28 /note= "Conserved residue"
FT Misc-difference 30. .31 /note= "Conserved residue"
FT Misc-difference 33 /note= "Conserved residues"
FT Misc-difference 35 /note= "Conserved residue"
FT Misc-difference 42. .43 /note= "Conserved residue"
FT Misc-difference 49 /note= "Conserved residues"
FT Misc-difference 54 /note= "Conserved residue"
FT Misc-difference 63. .64 /note= "Conserved residues"
FT Misc-difference 67 /note= "Conserved residue"
FT Misc-difference 74 /note= "Conserved residue"
XX WO2004031376-A2.
XX 15-APR-2004.
XX 02-OCT-2003; 2003WO-IB005072.
XX 04-OCT-2002; 2002US-0415765P.
XX 02-DEC-2002; 2002WO-IB005070.
XX (FIRM ) FIRMENICH SA.
XX Schalk M, Clark A;
XX WPI; 2004-330180/30.
XX
XX New sesquiterpene synthase, useful for converting farnesyl-pyrophosphate
PT to various oxygenated and aliphatic sesquiterpenes including valencene,
PT bicyclogermacrene, cubebol, and delta-cadinene.
XX
XX Disclosure; Fig 4; 66pp; English.
XX
XX This sequence represents a peptide fragment from a sesquiterpene
CC synthase, around residues 280-355. This peptide fragment was used in the
CC production of degenerate primers for the isolation of sesquiterpene
CC synthase coding sequences from grapefruit. The isolated sequences may be
CC used in the production of sesquiterpene synthases by culturing a
CC transformed plant cell in conditions conducive to the production of a
CC sesquiterpene synthase. The sesquiterpene synthases of the invention are
CC useful for converting farnesyl-pyrophosphate to various oxygenated and
CC aliphatic sesquiterpenes, including valencene, bicyclo-germacrene,
CC cubebol, delta-cadinene. Sesquiterpene compounds are used in perfumery. A
CC plant-independent system of production of sesquiterpene compounds would
CC be of interest, to remove the price link to plant availability.
XX
XX Sequence 74 AA;
Query Match 55.6%; Score 5; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
DB 62 VDDTF 66
|||||
|||||

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RESULT 50
ADM97960
ID ADM97960 standard; peptide; 74 AA.
XX AC ADM97960;
XX 01-JUL-2004 (first entry)
XX 5-epi-Aristolochene.
XX sesquiterpene synthase; cubebol synthase; GFTpsC; transformed plant cell;
KW farnesyl-pyrophosphate; valencene; bicyclo-germacrene; cubebol;
KW delta-cadinene; perfumery; GFTpsA; GFTpsB; GFTpsD1; GFTpsD2; GFTpsE.
XX Nicotiana tabacum.
XX
XX Key Location/Qualifiers
FH Misc-difference 5 /note= "Conserved residue"
FT FT Misc-difference 11..13
FT FT Misc-difference 26
FT FT Misc-difference 28
FT FT Misc-difference 30..31
FT FT Misc-difference 33
FT FT Misc-difference 35
FT FT Misc-difference 42..43
FT FT Misc-difference 49
FT FT Misc-difference 54
FT FT Misc-difference 63..64
FT FT Misc-difference 67
FT FT Misc-difference 74
FT FT /note= "Conserved residue"
XX WO2004031376-A2.
XX 15-APR-2004.
XX 02-OCT-2003; 2003WO-IB005072.
XX 04-OCT-2002; 2002US-0415765P.
XX 02-DEC-2002; 2002WO-IB005070.
XX (FIRM) FIRMENICH SA.
XX Schalk M, Clark A;
XX WPI; 2004-330180/30.
XX
XX New sesquiterpene synthase, useful for converting farnesyl-pyrophosphate
PT to various oxygenated and aliphatic sesquiterpenes including valencene,
PT bicyclogermacrene, cubebol, and delta-cadinene.
XX
XX Disclosure; Fig 4; 66pp; English.
XX
XX This sequence represents a peptide fragment from a sesquiterpene
CC synthase, around residues 280-355. This peptide fragment was used in the
CC production of degenerate primers for the isolation of sesquiterpene
CC synthase coding sequences from grapefruit. The isolated sequences may be
CC used in the production of sesquiterpene synthases by culturing a
CC transformed plant cell in conditions conducive to the production of a
CC sesquiterpene synthase. The sesquiterpene synthases of the invention are
CC useful for converting farnesyl-pyrophosphate to various oxygenated and

CC aliphatic sesquiterpenes, including valencene, bicyclo-germacrene,
CC cubebol, delta-cadinene. Sesquiterpene compounds are used in perfumery. A
CC plant-independent system of production of sesquiterpene compounds would
CC be of interest, to remove the price link to plant availability.
XX
XX Sequence 74 AA;
SQ
Query Match 55.6%; Score 5; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 VDPFP 6
Db 62 VDPFP 66
RESULT 51
ADM97963
ID ADM97963 standard; peptide; 74 AA.
XX AC ADM97963;
XX 01-JUL-2004 (first entry)
XX Vetispiradiene.
XX
XX sesquiterpene synthase; cubebol synthase; GFTpsC; transformed plant cell;
KW farnesyl-pyrophosphate; valencene; bicyclo-germacrene; cubebol;
KW delta-cadinene; perfumery; GFTpsA; GFTpsB; GFTpsD1; GFTpsD2; GFTpsE.
XX Hyoscyamus muticus.
XX
XX Key Location/Qualifiers
FH Misc-difference 5 /note= "Conserved residue"
FT FT Misc-difference 11..13
FT FT Misc-difference 26
FT FT Misc-difference 28
FT FT Misc-difference 30..31
FT FT Misc-difference 33
FT FT Misc-difference 35
FT FT Misc-difference 42..43
FT FT Misc-difference 49
FT FT Misc-difference 54
FT FT Misc-difference 63..64
FT FT Misc-difference 67
FT FT Misc-difference 74
FT FT /note= "Conserved residue"
XX WO2004031376-A2.
XX 15-APR-2004.
XX 02-OCT-2003; 2003WO-IB005072.
XX 04-OCT-2002; 2002US-0415765P.
XX 02-DEC-2002; 2002WO-IB005070.
XX (FIRM) FIRMENICH SA.
XX Schalk M, Clark A;
XX

DR WPI; 2004-330180/30.

XX New sesquiterpene synthase, useful for converting farnesyl-pyrophosphate

PT to various oxygenated and aliphatic sesquiterpenes including valencene,

FT bicyclogermacrene, cubebol, and delta-cadinene.

XX Disclosure; Fig 4; 66pp; English.

XX This sequence represents a peptide fragment from a sesquiterpene

CC synthase, around residues 280-355. This peptide fragment was used in the

CC production of degenerate primers for the isolation of sesquiterpene

CC synthase coding sequences from grapefruit. The isolated sequences may be

CC used in the production of sesquiterpene synthases by culturing a

CC transformed plant cell in conditions conducive to the production of a

CC sesquiterpene synthase. The sesquiterpene synthases of the invention are

CC useful for converting farnesyl-pyrophosphate to various oxygenated and

CC aliphatic sesquiterpenes, including valencene, bicyclo-germacrene,

CC cubebol, delta-cadinene. Sesquiterpene compounds are used in perfumery. A

CC plant-independent system of production of sesquiterpene compounds would

CC be of interest, to remove the price link to plant availability.

XX Sequence 74 AA;

Query Match 55.6%; Score 5; DB 8; Length 74;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6

Db 62 VDDTF 66

RESULT 52

AEA51017

ID AEA51017 standard; protein; 74 AA.

XX AEA51017;

AC AEA51017;

DT 11-AUG-2005 (first entry)

XX Tobacco 5-epi-aristolochene synthase protein.

DE Plant; enzyme; 5-epi-aristolochene synthase.

XX Nicotiana tabacum.

OS Location/Qualifiers

FH Region 9..13

FT /note= "Region used to design primer TpsVF1"

FT Region 30..36

FT /note= "Region used to design primer TpsVF2"

FT Region 63..69

FT /note= "Region used to design primer TpsVR3"

XX WO2005052163-A2.

PN 09-JUN-2005.

XX 19-NOV-2004; 2004WO-IB003836.

PF 26-NOV-2003; 2003US-0525512P.

PR 09-DEC-2003; 2003WO-IB006459.

XX (FIRM) FIRMENICH SA.

PA Schalk M;

PI WPI; 2005-418005/42.

XX 19-NOV-2004; 2004WO-IB003836.

PF 26-NOV-2003; 2003US-0525512P.

PR 09-DEC-2003; 2003WO-IB006459.

XX (FIRM) FIRMENICH SA.

PA Schalk M;

PI WPI; 2005-418005/42.

XX New nucleic acid encoding a patchoulol synthase or gamma-curcumene

PT synthase or a polypeptide having sesquiterpene synthase activity, useful

FT for making terpenoids used in perfumery, cosmetics and medicine.

XX

PS Example 7; SEQ ID NO 17; 75pp; English.

XX The present invention relates to patchoulol synthase, gamma-curcumene

CC synthase and sesquiterpene synthase polypeptides and their encoding

CC polynucleotides. The invention is useful for making terpenoids used in

CC perfumery, cosmetics and medicine. The present sequence is the tobacco 5-

CC epi-aristolochene synthase protein.

XX Sequence 74 AA;

Query Match 55.6%; Score 5; DB 9; Length 74;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6

Db 62 VDDTF 66

RESULT 53

AEA51019

ID AEA51019 standard; protein; 74 AA.

XX AEA51019;

AC AEA51019;

DT 11-AUG-2005 (first entry)

XX Potato vetispiradiene synthase protein.

DE Plant; enzyme; vetispiradiene synthase.

XX Solanum tuberosum.

OS Location/Qualifiers

FH Region 9..13

FT /note= "Region used to design primer TpsVF1"

FT Region 30..36

FT /note= "Region used to design primer TpsVF2"

FT Region 63..69

FT /note= "Region used to design primer TpsVR3"

XX WO2005052163-A2.

PN 09-JUN-2005.

XX 19-NOV-2004; 2004WO-IB003836.

PF 26-NOV-2003; 2003US-0525512P.

PR 09-DEC-2003; 2003WO-IB006459.

XX (FIRM) FIRMENICH SA.

PA Schalk M;

PI WPI; 2005-418005/42.

XX New nucleic acid encoding a patchoulol synthase or gamma-curcumene

PT synthase or a polypeptide having sesquiterpene synthase activity, useful

FT for making terpenoids used in perfumery, cosmetics and medicine.

XX Example 7; SEQ ID NO 19; 75pp; English.

XX The present invention relates to patchoulol synthase, gamma-curcumene

CC synthase and sesquiterpene synthase polypeptides and their encoding

CC polynucleotides. The invention is useful for making terpenoids used in

CC perfumery, cosmetics and medicine. The present sequence is the potato

CC vetispiradiene synthase protein.

XX Sequence 74 AA;

Query Match 55.6%; Score 5; DB 9; Length 74;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 62 VDDTF 66

RESULT 54
AEA51020
ID AEA51020 standard; protein; 74 AA.
XX AC AEA51020;
XX 11-AUG-2005 (first entry)
XX Hyoscyamus muticus vetispiradiene synthase protein.
XX DE Plant; enzyme; vetispiradiene synthase.
XX KW Hyoscyamus muticus.
XX OS
XX FH Key Location/Qualifiers
FT Region 9.13
FT /note= "Region used to design primer TpsVF1"
FT Region 30.36
FT /note= "Region used to design primer TpsVF2"
FT Region 63.69
FT /note= "Region used to design primer TpsVR3"
FT
XX WO2005052163-A2.
XX PN
XX 09-JUN-2005.
XX
XX 19-NOV-2004; 2004WO-IB003836.
XX 26-NOV-2003; 2003US-0525512P.
XX 09-DEC-2003; 2003WO-IB006459.
XX (FIRM) FIRMENICH SA.
XX PA
XX Schalk M;
XX PI
XX WPI; 2005-418005/42.
XX
XX New nucleic acid encoding a patchoulol synthase or gamma-curcumene
FT synthase or a polypeptide having sesquiterpene synthase activity, useful
FT for making terpenoids used in perfumery, cosmetics and medicine.
XX
XX Example 7; SEQ ID NO 20; 75pp; English.
XX
XX The present invention relates to patchoulol synthase, gamma-curcumene
CC synthase and sesquiterpene synthase polypeptides and their encoding
CC polynucleotides. The invention is useful for making terpenoids used in
CC perfumery, cosmetics and medicine. The present sequence is the Hyoscyamus
CC muticus vetispiradiene synthase protein.
XX
SQ Sequence 74 AA;
Query Match 55.6%; Score 5; DB 9; Length 74;
Best Local Similarity 100.0%; Pred.No.1.4e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 62 VDDTF 66

RESULT 55
ADC88085
ID ADC88085 standard; protein; 78 AA.
XX AC ADC88085;
XX
XX 01-JAN-2004 (first entry)

XX Ribosomal protein similar to FCWP1 #301.
XX
XX Antifungal protein; ribosomal protein; FCWP1; AlyAPP;
KW Plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;
KW Colletotrichum; Diplodia; Fusarium; Gaeumannomyces; Helminthosporium;
KW Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma;
KW Phymatotrichum; Phytophthora; Plasmodiopsis; Podosphaera; Puccinia; Puthium;
KW Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;
KW Septoria; Thielaviopsis; Venturia; Verticillium.
XX
XX Unidentified.
XX
XX US6573361-B1.
XX
XX 03-JUN-2003.
XX
XX 07-DEC-2000; 2000US-00732210.
XX
XX 07-DEC-1999; 99US-0169340P.
XX 07-DEC-1999; 99US-0169513P.
XX (MONS) MONSANTO TECHNOLOGY LLC.
XX
XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;
XX WPI; 2003-754558/71.
XX
XX Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful
FT for controlling fungal infections in plants.
XX
XX Example 21; SEQ ID NO 338; 27pp; English.
XX
XX The invention relates to an isolated antifungal ribosomal protein from
CC fusarium culmorum, FCWP1. Also included is a fusion protein between the
CC signal peptide of the antifungal protein AlyAPP from Alyssum and FCWP1,
CC encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are
CC useful for controlling fungal infections in plants, such as those caused
CC by Alternaria (e.g. Alternaria brassicola, Alternaria solani),
CC Ascochyta (e.g. Ascochyta pisi); Botrytis (e.g. Botrytis cinerea),
CC Cercospora (e.g. Cercospora kikuchii, Cercospora zea-maydis),
CC Colletotrichum (e.g. Colletotrichum lindemuthianum), Diplodia (e.g.
CC Diplodia maydis), Fusarium (e.g. Fusarium nivale, Fusarium oxysporum,
CC Fusarium graminearum, Fusarium culmorum, Fusarium solani, Fusarium
CC moniliforme, Fusarium roseum), Gaeumannomyces (e.g. Gaeumannomyces
CC graminis f.sp. tritici), Helminthosporium (e.g. Helminthosporium turcicum
CC, Helminthosporium carbonum, Helminthosporium maydis), Macrospominia
CC (e.g. Macrospominia phaseolina, Maganaporthe grisea), Mycosphaerella
CC (e.g. Mycosphaerella figiensis), Nectria (Nectria haematococca),
CC Peronospora (e.g. Peronospora manshurica, Peronospora tabacina), Phoma
CC (e.g. Phoma betae), Phymatotrichum (e.g. Phymatotrichum omnivorum),
CC Phytophthora (e.g. Phytophthora cinnamomi, Phytophthora cactorum),
CC Phytophthora phaseoli, Phytophthora parasitica, Phytophthora
CC citrophthora, Phytophthora megasperma f.sp. sojae, Phytophthora
CC infestans), Plasmodiopsis (e.g. Plasmodiopsis viticola), Puccinia
CC Podosphaera leucotricha), Puccinia (e.g. Puccinia sorghi, Puccinia
CC striformis, Puccinia graminis f.sp. tritici, Puccinia asparagi,
CC Puccinia recondita, Puccinia arachidis), Puthium (e.g. Puthium
CC aphanidermatum), Pyrenophora (e.g. Pyrenophora tritici-repentens),
CC Pyricularia (e.g. Pyricularia oryzae), Pythium (e.g. Pythium ultimum),
CC Rhizoctonia (e.g. Rhizoctonia solani, Rhizoctonia cerealis), Sclerotium
CC (e.g. Sclerotium rolfsii), Sclerotinia (e.g. Sclerotinia sclerotiorum),
CC Septoria (e.g. Septoria lycopersici, Septoria glycoses, Stagonospora
CC nodorum / Phaeosphaeria nodorum, Septoria tritici), Thielaviopsis (e.g.
CC Thielaviopsis basicola), Uncinula (e.g. Uncinula necator), Venturia
CC (e.g. Venturia inaequalis) or Verticillium (e.g. Verticillium dahliae,
CC Verticillium albo-atrum). Mutations in the proteolytic consensus
CC sequences contained within FCWP1 provides improved stability of its
CC antifungal activity. Also disclosed are ribosomal proteins with similar
CC PI (>7) and molecular weight (<20kDa) to FCWP1, which may act as
CC antifungal proteins. The present sequence represents one of the ribosomal
CC proteins similar to FCWP1. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in

CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=6573361B1.
XX
SQ Sequence 78 AA;

Query Match 55.6%; Score 5; DB 7; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
DB 31 KVDDT 35

RESULT 56
ADC88093
ID ADC88093 standard; protein; 80 AA.
XX
AC ADC88093;
XX
DT 01-JAN-2004 (first entry)
XX
DE Ribosomal protein similar to FCWP1 #309.
XX
KW Antifungal protein; ribosomal protein; FCWP1; AlyAPP;
KW plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;
KW Colletotrichum; Diplodia; Fusarium; Gaemanomyces; Helminthosporium;
KW Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma;
KW Phymatotrichum; Phytophthora; Plasmodium; Podosphaera; Puccinia; Puthium;
KW Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;
KW Septoria; Thielaviopsis; Venturia; Verticillium.
OS Unidentified.
XX
XX US6573361-B1.
XX
XX 03-JUN-2003.
XX
XX 07-DEC-2000; 2000US-00732210.
XX
XX 07-DEC-1999; 99US-0169340P.
XX 07-DEC-1999; 99US-0169513P.
XX
XX (MONS) MONSANTO TECHNOLOGY LLC.
XX
XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;
XX WPI; 2003-754558/71.
XX
XX Novel antifungal protein FCWP1, isolated from *Fusarium culmorum*, useful
XX for controlling fungal infections in plants.
XX
XX Example 21; SEQ ID NO 346; 27pp; English.
XX
XX The invention relates to an isolated antifungal ribosomal protein from
XX *Fusarium culmorum*, FCWP1. Also included is a fusion protein between the
XX signal peptide of the antifungal protein AlyAPP from *Alyseum* and FCWP1.
XX encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are
XX useful for controlling fungal infections in plants, such as those caused
XX by *Alternaria* (e.g. *Alternaria brassicicola*, *Alternaria solani*),
XX *Ascochyta* (e.g. *Ascochyta pisi*); *Botrytis* (e.g. *Botrytis cinerea*),
XX *Cercospora* (e.g. *Cercospora kikuchii*, *Cercospora zea-maydis*),
XX *Colletotrichum* (e.g. *Colletotrichum lindemuthianum*), *Diplodia* (e.g.
XX *Diplodia maydis*), *Fusarium* (e.g. *Fusarium nivale*, *Fusarium oxysporum*,
XX *Fusarium graminearum*, *Fusarium culmorum*, *Fusarium solani*, *Fusarium*
XX *moniliforme*, *Fusarium roseum*), *Gaeumanomyces* (e.g. *Gaeumanomyces*
XX *graminis* f.sp. *tritici*), *Helminthosporium* (e.g. *Helminthosporium turcicum*
XX *Helminthosporium carbonum*, *Helminthosporium maydis*), *Macrophomina*
XX (e.g. *Macrophomina phaseolina*, *Maganaporthe grisea*), *Mycosphaerella*
XX (e.g. *Mycosphaerella figiensis*), *Nectria* (*Nectria haematococca*),
XX *Peronospora* (e.g. *Peronospora manshurica*, *Peronospora tabacina*), *Phoma*
XX (e.g. *Phoma betae*), *Phymatotrichum* (e.g. *Phymatotrichum omnivorum*),
XX *Phytophthora* (e.g. *Phytophthora cinnamomi*, *Phytophthora cactorum*,
XX

CC Phytophthora phaseoli , Phytophthora parasitica , Phytophthora
CC citrophthora , Phytophthora megasperma f.sp. sojae , Phytophthora
CC infestans), Plasmodium (e.g. Plasmodium vivax), Podosphaera (e.g.
CC Podosphaera leucotricha), Puccinia (e.g. Puccinia sorghi , Puccinia
CC striiformis , Puccinia graminis f.sp. tritici , Puccinia asparagi ,
CC Puccinia recondita , Puccinia arachidis), Puthium (e.g. Puthium
CC aphanidermatum), Pyrenophora (e.g. Pyrenophora tritici-repentens),
CC Pyricularia (e.g. Pyricularia oryzae), Pythium (e.g. Pythium ultimum),
CC Rhizoctonia (e.g. Rhizoctonia solani , Rhizoctonia cerealis), Sclerotium
CC (e.g. Sclerotium rolfsii), Sclerotinia (e.g. Sclerotinia sclerotiorum),
CC Septoria (e.g. Septoria lycopersici , Septoria glycines , Stagonospora
CC nodorum / Podosphaera nodorum , Septoria tritici), Thielaviopsis (e.g.
CC Thielaviopsis basicola), Uncinula (e.g. Uncinula necator), Venturia
CC (e.g. Venturia inaequalis) or Verticillium (e.g. Verticillium dahliae ,
CC Verticillium albo-atrum). Mutations in the proteolytic consensus
CC sequences contained within FCWP1 provides improved stability of its
CC antifungal activity. Also disclosed are ribosomal proteins with similar
CC PI (>71) and molecular weight (<20kDa) to FCWP1, which may act as
CC antifungal proteins. The present sequence represents one of the ribosomal
CC proteins similar to FCWP1. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=6573361B1.
XX
XX Sequence 80 AA;

Query Match 55.6%; Score 5; DB 7; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
DB 31 KVDDT 35

RESULT 57
ABG28513
ID ABG28513 standard; protein; 109 AA.
XX
AC ABG28513;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #28504.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX N-PSDB; AAS92700.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 20; SEQ ID NO 58872; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 109 AA;

Query Match 55.6%; Score 5; DB 4; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFF 6
 |||||
 Db 85 VDDTFF 89

RESULT 58
 ADX92114
 ID ADX92114 standard; protein; 110 AA.
 XX
 AC ADX92114;

XX 21-APR-2005 (first entry)
 XX Plant full length insert polypeptide seqid 54778.

XX plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 03-NOV-2001; 2001US-00985678.

XX (LIU//) LIU J.

XX (ZHOU//) ZHOU Y.

XX (KOVA//) KOVALIC D K.

XX (SCRE//) SCREEN S E.

XX (TAB//) TABASKA J E.

XX (CAOY//) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.

XX Claim 1; SEQ ID NO 54778; 15pp; English.

PS The invention describes a recombinant DNA construct comprising a
 XX polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.secdta.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

SQ Sequence 110 AA;

Query Match 55.6%; Score 5; DB 8; Length 110;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 |||||
 Db 89 KVDDT 93

RESULT 59

ADM05832

ID ADM05832 standard; protein; 118 AA.

XX ADM05832;

XX 20-MAY-2004 (first entry)

XX Human protein of the invention SEQ ID NO:4517.

XX human; gene therapy; diagnostic marker; pharmaceutical.

XX Homo sapiens.

XX EP1347046-A1.

XX 24-SEP-2003.

XX 12-APR-2002; 2002EP-00008400.

XX 22-MAR-2002; 2002JP-00137785.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX WPI; 2003-723558/69.

DR N-PSDB; ADM03389.

XX New polynucleotides and polypeptides are useful in gene therapy, for

PT developing a diagnostic marker or medicines for regulating their

XX expression and activity, or as a target of gene therapy.

PS Claim 1; SEQ ID NO 4517; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded

CC polypeptide. A polynucleotide of the invention ADM06202-ADM06773 is useful

CC as a primer for synthesizing the polynucleotide or as a probe for

CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are

CC useful in gene therapy, for developing a diagnostic marker or medicines

CC for regulating their expression and activity, or as a target of gene

CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides

CC are useful as pharmaceutical agents. The present sequence represents a

XX protein sequence of the invention.

XX

SQ Sequence 118 AA;

Query Match 55.6%; Score 5; DB 7; Length 118;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8

Db 26 DTFYY 30

|||||

RESULT 60

AEC88762

ID AEC88762 standard; protein; 118 AA.

XX

AC AEC88762;

XX

DT 01-DEC-2005 (first entry)

XX

DE Human cDNA clone protein TESTI20335200, SEQ ID 4517.

XX

KW Osteopathic; Cytostatic; Antiinflammatory; Gastrointestinal-Gen.;

KX Antulcer; Gene Therapy; Osteoporosis; cancer; inflammation; gastritis;

KW stomach ulcer; gastrointestinal ulcer.

XX

OS Homo sapiens.

XX

PN EP1580263-A1.

XX

PD 28-SEP-2005.

XX

PF 12-APR-2002; 2004EP-00027348.

XX

PR 22-MAR-2002; 2002JP-00137785.

XX

PR 12-APR-2002; 2002EP-00008400.

XX

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX

DR WPI; 2005-567421/69.

DR N-PSDB; AEC86319.

XX

PT New full-length cDNA sequences, useful for treating diseases, e.g.

XX osteoporosis, cancer, inflammation, gastritis, or gastroduodenal ulcer.

PS Example 3; SEQ ID NO 4517; 296pp; English.

XX

CC The present invention relates to novel human cDNAs (AEC84246-AEC86688)

CC encoding proteins AEC86689-AEC89131. The cDNAs are useful for analyzing

CC the functions of the proteins, and for developing medicines for diseases

CC e.g. osteoporosis, cancer, inflammation, gastritis, or gastroduodenal

CC ulcer. Note: The sequence data for this patent did not form part of the

CC printed specification but was obtained in electronic format directly from

CC EPO.

XX

SQ Sequence 118 AA;

Query Match 55.6%; Score 5; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

Db 86 KVDDT 90

|||||

RESULT 62

AAW11635

ID AAW11635 standard; protein; 126 AA.

XX

AC AAW11635;

XX

DT 13-MAY-1997 (first entry)

XX

Query Match 55.6%; Score 5; DB 9; Length 118;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8

Db 26 DTFYY 30

|||||

RESULT 61

AAW13923

ID AAW13923 standard; protein; 119 AA.

XX

AC AAW13923;

XX

DT 15-MAY-1997 (first entry)

XX

DE Heavy chain #2 for anti-HB virus antibody.

XX

KW Antibody; heavy chain; light chain; variable region; human; monoclonal;

KX complementarity determining region; human; adr type hepatitis B virus;

KW HB virus; CDR; virus antigen; anti-HB antibody; vaccine.

XX

OS Homo sapiens.

XX

PN JP09020798-A.

XX

PD 21-JAN-1997.

XX

PF 11-JUL-1995; 95JP-00174752.

XX

PR 11-JUL-1995; 95JP-00174752.

XX

PA (ASAH) ASahi Kasei Kogyo KK.

XX

DR WPI; 1997-140911/13.

DR N-PSDB; AAT60118.

XX

PT Human anti-Hepatitis B antibody - used in a adr type HB virus vaccine.

XX

PS Claim 8; Page 11-12; 20pp; Japanese.

CC AAW13921-W13928 represent the sequences for the heavy and light chains of

CC the human monoclonal antibodies of the invention. The antibody of the

CC invention preferably contains the sequence represented by AAW13912 in the

CC complementarity determining region-1 (CDR-1) of the heavy chain variable

CC region. The antibody of the invention also contains the sequence

CC represented by AAW13913 in the CDR-3 of the light chain variable region.

CC The antibody is capable of binding to adr type hepatitis B (HB) virus

CC antigen. A human anti-HB virus monoclonal antibody preparation which is

CC highly safe and is effective to adr type HB virus can be provided, using

CC the monoclonal antibody. It can also be used as a vaccine against HB

CC infection

XX

SQ Sequence 119 AA;

DE Human anti-RSV monoclonal antibody RP-2 VH domain.
 KW Monoclonal antibody; MAbs; RP-1; RP-2; respiratory syncytial virus; RSV;
 KW fusion protein; F-protein; vaccine; immunotherapy; therapy;
 KW Epstein Barr virus; immortalisation; recombinant antibody.
 XX Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Region 1. .30
 FT /label= FR1
 FT /note= "framework region 1"
 FT Region 31. .37
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 38. .51
 FT /label= FR2
 FT /note= "framework region 2"
 FT Region 52. .67
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 68. .99
 FT /label= FR3
 FT /note= "framework region 3"
 FT Region 100. .115
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 FT Region 116. .126
 FT /label= FR4
 FT /note= "framework region 4"
 XX
 PN W09640252-A1.
 XX
 PD 19-DEC-1996.
 XX
 XX 06-JUN-1996; 96WO-US010070.
 XX
 PR 07-JUN-1995; 95US-00488376.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 XX Brams P, Chamat SS, Pan L, Walsh EE, Heard CJ, Newman RA;
 XX WPI; 1997-099892/09.
 XX N-PSDB; AAT61237.
 XX
 PT Human monoclonal antibody specific for respiratory syncytial virus fusion
 PT protein - used for the prevention and treatment of RSV infection.
 XX
 PS Example 6; Fig 7b; 85pp; English.
 XX
 CC Amino acid sequences were deduced for the RP-1 VL, RP-2 VH, RP-2 VL and
 CC RP-1 VH domains (AAW11634-37) of human monoclonal antibodies (hMAbs) RP-1
 CC and RP-2, which show high affinity for respiratory syncytial virus (RSV)
 CC fusion protein. The hMAbs were obt'd. by: antigen priming of naive human
 CC splenocytes in vitro; transferal of primed splenocytes to a SCID mouse;
 CC boosting with antigen; isolating human antibody-producing B-cells from
 CC the SCID mice; and immortalisation of the B-cells using Epstein Barr
 CC virus. DNA (see also AAT61236-39) encoding the RP-1 and RP-2 heavy and
 CC light variable domains can be incorporated into vectors (e.g. NEOSPLA)
 CC and used to transfect eukaryotic (e.g. CHO) cells (see also AAW11638-41)
 CC to provide a constant, stable supply of anti-RSV F-protein hMAbs for use
 CC in the treatment or prevention of RSV infection. (N.B. Fig 7b is referred
 CC to as the RP-1 VH domain in the specification, but is identical to the RP
 CC -2 VH domain of Fig 11b)
 XX
 SQ Sequence 126 AA;
 Query Match 55.6%; Score 5; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFY 7

Db 57 DDTFY 61
 RESULT 63
 ABU07100
 ID ABU07100 standard; protein; 127 AA.
 XX
 AC ABU07100;
 XX
 DT 17-FEB-2003 (first entry)
 XX
 DE Maize Starch synthase III (SSIII) LINKR domain related protein #24.
 XX
 KW Starch; starch synthase; glucan association domain; GLASS; linker domain;
 KW LINKR; glucosyl transferase domain; GLYTR; C-terminal end; CTEND;
 KW granule bound starch synthase; GBSS; morphology; retrogradation;
 KW waterbinding; swelling potential.
 XX
 OS Unidentified.
 XX
 PN W0200279410-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 29-MAR-2002; 2002WO-US009574.
 XX
 PR 30-MAR-2001; 2001US-0279720P.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 XX Commuri P, Keeling PL, Ramirez N, McKean A, Gao Z, Guan H;
 XX WPI; 2003-040678/03.
 XX
 PT New DNA encoding fusion protein consisting of 4 different functional
 PT domains selected from glucan association domain, linker domain, glucosyl
 PT transferase domain, and C-terminal end, useful for producing modified
 PT starches.
 XX
 PS Claim 19; Page 203-210; 265pp; English.
 XX
 CC The invention describes an isolated DNA molecule encoding a fusion
 CC protein consisting of 4 different functional domains selected from glucan
 CC association domain (GLASS), linker domain (LINKR), glucosyl transferase
 CC domain (GLYTR), and C-terminal end (CTEND) which are operably linked to
 CC one another. The DNA molecule is useful for expressing in plants
 CC polypeptides including starch synthase enzymes as fusion proteins with
 CC improved affinity to starch and modified catalytic capabilities and to
 CC the in vivo and in vitro synthesis of glucan chains of modified lengths
 CC as compared to plants producing native starch or starch produced with
 CC native starch synthases. Expression of the starch synthase fusion
 CC proteins along with granule bound starch synthase (GBSS) will lead to a
 CC modified starch having an altered or improved morphology, retrogradation,
 CC waterbinding, or swelling potential of the granules, gel strength,
 CC adhesiveness, cohesiveness, hardness, elasticity, increased or decreased
 CC granule size, degree of branching, crystallinity, degree of cross-
 CC linking, and increased or decreased glucan chain lengths. This is the
 CC amino acid sequence of a starch synthase functional domain associated
 CC protein
 XX
 SQ Sequence 127 AA;
 Query Match 55.6%; Score 5; DB 6; Length 127;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFY 7
 Db 84 DDTFY 88
 RESULT 64

```

AEA24151
ID AEA24151 standard; protein; 128 AA.
XX
AC AEA24151;
XX
DT 11-AUG-2005 (first entry)
XX
DE Anti-HAAH antibody heavy chain variable region #6.
XX
KW Antibody therapy; aspartyl (asparaginyl) beta-hydroxylase; AAH; HAAH;
KW cancer; neoplasm; lung tumor; liver tumor; colon tumor; pancreas tumor;
KW prostate tumor; ovary tumor; brain tumor; breast tumor; cytostatic;
KW antibody; heavy chain variable region.
XX
OS Homo sapiens.
XX
PN WO2005049802-A2.
XX
PD 02-JUN-2005.
XX
PF 15-NOV-2004; 2004WO-US038197.
XX
PR 14-NOV-2003; 2003US-0520114P.
XX
PS 19-APR-2004; 2004US-0563514P.
XX
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Wittrup DK, Yeung YA;
XX
DR WPI; 2005-417728/42.
XX
PT New composition comprising anti-hydroxylase antibodies, useful for
PT diagnosing or treating cancer, e.g. lung, liver, colon, pancreas,
PT prostate, ovary, bile duct, brain, or breast cancer.
XX
PS Disclosure; SEQ ID NO 11; 107pp; English.
XX
CC The invention relates to a composition comprising an isolated human
CC antibody or its fragment or other variant, where the antibody, the
CC fragment or the other variant specifically binds to an aspartyl
CC (asparaginyl) beta-hydroxylase (AAH). The invention also relates to an
CC isolated nucleic acid molecule comprising a sequence encoding a human
CC antibody or its fragment or other variant, where the antibody, the
CC fragment or the other variant specifically binds to human AAH (HAAH), an
CC expression vector comprising the nucleic acid molecule, a host cell
CC comprising the expression vector, a method of modulating an AAH activity
CC in a cell, a method of treating a patient who has a cancer associated
CC with overactive or over expressed AAH, a method for identifying an
CC antibody or its fragment or other variant that specifically binds to an
CC AAH and a method of making a human monoclonal antibody or its fragment or
CC other variant that specifically binds to an AAH. The composition,
CC antibody, nucleic acid, kit and methods are useful for diagnosing or
CC treating cancer, where the cancer cell is a tumor cell of the lung,
CC liver, colon, pancreas, prostate, ovary, bile duct, brain or breast. This
CC sequence represents an anti-HAAH antibody variable region used in the
CC scope of the invention.
XX
SQ Sequence 128 AA;
Query Match 55.6%; Score 5; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDT 5
DB 87 KVDDT 91
RESULT 65
ABG94245
ID ABG94245 standard; protein; 134 AA.
XX
AC ABG94245;
XX
DT 11-AUG-2005 (first entry)
XX
DE Anti-HAAH antibody heavy chain variable region #6.
XX
KW Antibody therapy; aspartyl (asparaginyl) beta-hydroxylase; AAH; HAAH;
KW cancer; neoplasm; lung tumor; liver tumor; colon tumor; pancreas tumor;
KW prostate tumor; ovary tumor; brain tumor; breast tumor; cytostatic;
KW antibody; heavy chain variable region.
XX
OS Homo sapiens.
XX
PN WO2005049802-A2.
XX
PD 02-JUN-2005.
XX
PF 15-NOV-2004; 2004WO-US038197.
XX
PR 14-NOV-2003; 2003US-0520114P.
XX
PS 19-APR-2004; 2004US-0563514P.
XX
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Wittrup DK, Yeung YA;
XX
DR WPI; 2005-417728/42.
XX
PT New composition comprising anti-hydroxylase antibodies, useful for
PT diagnosing or treating cancer, e.g. lung, liver, colon, pancreas,
PT prostate, ovary, bile duct, brain, or breast cancer.
XX
PS Disclosure; SEQ ID NO 11; 107pp; English.
XX
CC The invention relates to a composition comprising an isolated human
CC antibody or its fragment or other variant, where the antibody, the
CC fragment or the other variant specifically binds to an aspartyl
CC (asparaginyl) beta-hydroxylase (AAH). The invention also relates to an
CC isolated nucleic acid molecule comprising a sequence encoding a human
CC antibody or its fragment or other variant, where the antibody, the
CC fragment or the other variant specifically binds to human AAH (HAAH), an
CC expression vector comprising the nucleic acid molecule, a host cell
CC comprising the expression vector, a method of modulating an AAH activity
CC in a cell, a method of treating a patient who has a cancer associated
CC with overactive or over expressed AAH, a method for identifying an
CC antibody or its fragment or other variant that specifically binds to an
CC AAH and a method of making a human monoclonal antibody or its fragment or
CC other variant that specifically binds to an AAH. The composition,
CC antibody, nucleic acid, kit and methods are useful for diagnosing or
CC treating cancer, where the cancer cell is a tumor cell of the lung,
CC liver, colon, pancreas, prostate, ovary, bile duct, brain or breast. This
CC sequence represents an anti-HAAH antibody variable region used in the
CC scope of the invention.
XX
SQ Sequence 128 AA;
Query Match 55.6%; Score 5; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDT 5
DB 87 KVDDT 91
RESULT 65
ABG94245
ID ABG94245 standard; protein; 134 AA.
XX
AC ABG94245;
XX
DT 10-DEC-2002 (first entry)
XX
DE Apis cerana phospholipase A2 protein.
XX
KW Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KW cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW vaccine; infectious disease; honeybee.
XX
OS Apis cerana.
XX
PS Synthetic.
XX
PN WO200256905-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-IB000166.
XX
PR 19-JAN-2001; 2001US-0262379P.
XX
PR 04-MAY-2001; 2001US-0288549P.
XX
PR 05-OCT-2001; 2001US-0326988P.
XX
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
PI Piossek C;
XX
DR WPI; 2002-627351/67.
XX
PT Molecular antigen array used in the production of vaccines for infectious
PT diseases.
XX
PS Claim 161; Page 386; 441pp; English.
XX
CC This invention relates to a novel ordered and repetitive antigen array
CC used in the production of vaccines for infectious diseases. The invention
CC also discloses a composition comprising a non-natural molecular scaffold
CC comprising a core particle selected from a core particle of a non-natural
CC origin and a core particle of natural origin and an organiser comprising
CC at least one first attachment site, where the organiser is connected to
CC the core particle by at least one covalent bond. Also disclosed is an
CC antigen or antigenic determinant with at least one second attachment
CC site, where the antigen or antigenic determinant is amyloid beta peptide
CC (Abeta1-42) or its fragment and where the second attachment site is
CC selected from an attachment site not naturally occurring with the antigen
CC or antigenic determinant and an attachment site naturally occurring with
CC the antigen or antigenic determinant, where the second attachment site is
CC capable of association through at least one non-peptide bond to the first
CC attachment site and where the antigen or antigenic determinant and the
CC scaffold interact through the association to form an ordered and
CC repetitive antigen array. The invention also comprises a coat protein
CC capable of forming a capsid which comprises mutant Qbeta coat proteins
CC having an amino acid sequence selected from five amino acid sequences
CC fully defined in the specification. The compounds of the invention may
CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC immunisation and as a vaccine. The present sequence represents a protein
CC sequence used to create the compositions of the invention
XX
SQ Sequence 134 AA;
Query Match 55.6%; Score 5; DB 5; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 DDTFY 7
DB 64 DDTFY 68
RESULT 66
ABG80557

```

ID ABG80557 standard; protein; 134 AA.
AC ABG80557;
XX
XX
XX 29-NOV-2002 (first entry)
XX
XX
XX Bee phospholipase A2 #4.
XX
XX Molecular antigen array; vaccine; antigen; antimicrobial;
XX molecular scaffold; amyloid beta; Abeta 1-42; influenza;
XX graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
XX adult respiratory distress syndrome; ARDS; Crohn's disease;
XX allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
XX Grave's disease; systemic lupus erythematosus; osteoporosis;
XX inflammatory immune disease; myasthenia gravis; multiple sclerosis;
XX immunoproliferative disease lymphadenopathy; Alzheimer's disease;
XX angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
XX rheumatoid arthritis; diabetes; infectious disease; factor Xa;
XX enterokinase; cysteine-containing linker.
XX
XX Apis cerana.
XX
XX WO200256907-A2.
XX
XX 25-JUL-2002.
XX
XX 21-JAN-2002; 2002WO-IB000168.
XX
XX 19-JAN-2001; 2001US-0262379P.
XX 04-MAY-2001; 2001US-0288549P.
XX 05-OCT-2001; 2001US-0326998P.
XX 07-NOV-2001; 2001US-0331045P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX (NOVS) NOVARTIS PHARMA AG.
XX (MAUR/) MAURER P.
XX (LECH/) LECHNER P.
XX (ORTM/) ORTMANN R.
XX (LUEO/) LUEOEND R.
XX (STAU/) STAUFENBIEL M.
XX (FREY/) FREY P.
XX
XX Maurer P, Lechner F, Ortman R, Lueoend R, Staufenbiel M, Frey P;
XX Renner WA, Bachmann M, Tisot A, Seibel P, Piossek C;
XX
XX WPI; 2002-636514/68.
XX
XX Molecular antigen array used in the production of vaccines for infectious
XX diseases.
XX
XX Disclosure; Page 363-364; 418pp; English.
XX
XX The invention relates to a composition comprising: (a) a non-natural
XX molecular scaffold comprising: (i) a core particle selected from: (i) a
XX core particle of a non-natural origin; and (ii) a core particle of natural
XX origin; and (ii) an organiser comprising at least one first attachment
XX site, where the organiser is connected to the core particle by at least
XX one covalent bond; (b) an antigen or antigenic determinant with at least
XX one second attachment site, where the antigen or antigenic determinant is
XX amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
XX attachment site is selected from: (i) an attachment site not naturally
XX occurring with the antigen or antigenic determinant; and (ii) an
XX attachment site naturally occurring with the antigen or antigenic
XX determinant, where the second attachment site is capable of association
XX through at least one non-peptide bond to the first attachment site; and
XX where the antigen or antigenic determinant and the scaffold interact
XX through the association to form an ordered and repetitive antigen array.
XX Also included is a process for producing a non-naturally occurring
XX ordered and repetitive antigen array. The composition is used in
XX immunisation and as a vaccine for diseases such as influenza, graft
XX versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult
XX respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
XX acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,

CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
CC gravis, immunoproliferative disease lymphadenopathy,
CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
CC osteoporosis and infectious diseases. The present sequence is an antigen
CC for use in the array of the invention. The antigen is modified to possess
CC a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-
CC or C-terminal linker peptide which serves as the attachment point to a
XX virus like particle or bacterial protein (the scaffold protein)
XX
XX Sequence 134 AA;
XX
XX Query Match 55.6%; Score 5; DB 5; Length 134;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 DDTFY 7
XX |||||
XX Db 64 DDTFY 68
XX
XX RESULT 67
XX ADE62328
XX ID ADE62328 standard; protein; 138 AA.
XX
XX AC ADE62328;
XX
XX 29-JAN-2004 (first entry)
XX
XX DE Rat Protein P51673, SEQ ID NO 8257.
XX
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX OS Rattus norvegicus.
XX
XX PN WO2003016475-A2.
XX
XX PD 27-FEB-2003.
XX
XX PF 14-AUG-2002; 2002WO-US025765.
XX
XX PR 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Wolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX GENBANK; P51673.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 138 AA;

Query Match 55.6%; Score 5; DB 7; Length 138;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFFY 7
 |||||
 Db 48 DDTFFY 52

RESULT 68
 AAU19377
 ID AAU19377 standard; protein; 146 AA.

XX AC AAU19377;

XX DT 04-DEC-2001 (first entry)

XX DE Human G protein-coupled receptor nGPCR-2310.

XX KW Human; G protein-coupled receptor; nGPCR-x; antiviral; analgesic;
 KW cytotactic; cardiant; antidiabetic; anorectic; hypotensive; hypertensive;
 KW antiparkinsonian; nootropic; neuroprotective; antidepressant;
 KW viral infection; HIV-1; human immunodeficiency virus; HIV-2; pain;
 KW cancer; metabolic disease; cardiovascular disease; type 2 diabetes;
 KW obesity; anorexia; hypertension; myocardial infarction;
 KW atherosclerosis; Parkinson's disease; psychosis; neurological disorder;
 KW schizophrenia; migraine; major depression; anxiety; mental disorder;
 KW manic depression; dyskinesia; Huntington's disease; Tourette's Syndrome.

XX OS Homo sapiens.

XX PN WO200166751-A2.

XX PD 13-SEP-2001.

XX PF 08-MAR-2001; 2001WO-US007370.

XX PR 08-MAR-2000; 2000US-0187583P.

XX PR 08-MAR-2000; 2000US-0187584P.

XX PR 08-MAR-2000; 2000US-0187637P.

XX PR 08-MAR-2000; 2000US-0187639P.

XX PR 08-MAR-2000; 2000US-0187640P.

XX PR 08-MAR-2000; 2000US-0187707P.

XX PR 08-MAR-2000; 2000US-0187708P.

XX PR 08-MAR-2000; 2000US-0187709P.

XX PR 08-MAR-2000; 2000US-0187827P.

XX PR 08-MAR-2000; 2000US-0188290P.

XX PR 08-MAR-2000; 2000US-0188292P.

XX PR 08-MAR-2000; 2000US-0188293P.

XX PA (PHAA) PHARMACIA & UPJOHN CO.

XX PI Vogeli G;

XX PI WPI: 2001-536779/59.

XX DR N-PSDB; AAS30949.

XX XX

PT Isolated nucleic acid molecules encoding G protein-coupled receptors
 PT termed nGPCR-x, useful in the treatment and diagnosis of viral
 PT infections, cancers and mental disorders (e.g. Parkinson's disease and
 PT schizophrenia).

XX Claim 31; Page 269; 292pp; English.

XX The invention relates to novel isolated nucleic acid molecules encoding G
 CC protein-coupled receptors termed nGPCR-x. nGPCR-x polynucleotides,
 CC polypeptides, and modulators may be used in the treatment of diseases and
 CC conditions such as infections, such as viral infections caused by HIV-1
 CC (human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and
 CC cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity,
 CC anorexia, hypotension, hypertension, myocardial infarction,
 CC atherosclerosis) Parkinson's disease, and psychotic and neurological
 CC disorders, including schizophrenia, migraine, major depression, anxiety,
 CC mental disorder, manic depression, and dyskinesias, such as Huntington's
 CC disease or Tourette's Syndrome and many other diseases and syndromes
 CC listed in the specification. nGPCR-x polynucleotides and polypeptides, as
 CC well as nGPCR-x modulators, may also be used in diagnostic assays for
 CC such diseases or conditions. The present sequence represents a G protein-
 CC coupled receptor of the invention

XX SQ Sequence 146 AA;

Query Match 55.6%; Score 5; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
 |||||
 Db 32 DTFYY 36

RESULT 69

AAB53696

ID AAB53696 standard; protein; 152 AA.

XX AC AAB53696;

XX DT 09-MAR-2001 (first entry)

XX DE Human colon cancer antigen protein sequence SEQ ID NO:1236.

XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytostatic; cardioactive; neuroprotective; vulnery;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; antineoplastic; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder.

XX OS Homo sapiens.

XX PN WO200055351-A1.

XX PD 21-SEP-2000.

XX PF 08-MAR-2000; 2000WO-US005883.

XX PR 12-MAR-1999; 99US-0124270P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX DR WPI; 2000-587534/55.

XX DR N-PSDB; AAC98453.

XX PT Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer.

PS Claim 11; Page 1823-1824; 2104pp; English.

CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal, and
 CC vulnary, nephrotropic, antiinfective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins may
 CC also be used to prevent diseases such as neural disorders, immune system
 CC disorders, muscular disorders, reproductive disorders, gastrointestinal
 CC disorders, wounds, renal disorders, infectious diseases, and
 CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
 CC sequences used in the exemplification of the present invention

SQ Sequence 152 AA;

Query Match 55.6%; Score 5; DB 3; Length 152;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7
 |||||
 Db 55 DDTFY 59

RESULT 70
 AAB39932
 ID AAB39932 standard; protein; 157 AA.
 AC AAE39932;
 XX
 XX 15-JAN-2004 (first entry)
 DT
 DE Corn phosphoethanolamine cytidyltransferase protein.
 XX
 XX Phosphatidylethanolamine N-methyltransferase; EC 2.1.1.17; transgenic;
 KW enzyme; transgenic plant; phosphoethanolamine cytidyltransferase; corn;
 KW EC 2.7.7.41.
 XX
 XX Zea mays.
 OS
 XX US6596926-B1.
 PN
 XX 22-JUL-2003.
 PD
 XX 22-SEP-2000; 2000US-00668262.
 PF
 XX 23-SEP-1999; 99US-0155626P.
 PR (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 XX Famodu OO, Kinney AJ, Rafalski JA;
 PI WPI; 2003-615553/58.
 DR N-PSDB; AAD60656.
 XX
 XX New isolated polynucleotide encoding a phosphatidylethanolamine N-
 PT methyltransferase biosynthetic enzyme, useful for creating transgenic
 FT plants, as probes for genetic mapping or as a genetic marker.
 FT
 XX Example 3; Col 29-30; 28pp; English.

CC The present invention relates to an isolated polynucleotide encoding a
 CC phosphatidylethanolamine N-methyltransferase (EC 2.1.1.17) biosynthetic
 CC enzyme. The invention is useful in creating transgenic plants in which
 CC the polypeptides are present at higher or lower levels than normal cell
 CC types. The invention is also useful as probes for genetically and
 CC physically mapping the genes. The present sequence is corn phospho-
 CC ethanolamine cytidyltransferase (EC 2.7.7.41) protein from clone cc71se-

CC b.pk0008.g2
 XX
 SQ Sequence 157 AA;

Query Match 55.6%; Score 5; DB 7; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
 |||||
 Db 128 KVDDT 132

RESULT 71
 ADJ26813
 ID ADJ26813 standard; protein; 157 AA.
 XX
 AC ADJ26813;
 XX
 XX 20-MAY-2004 (first entry)
 DT Corn phosphoethanolamine cytidyl transferase protein #1.
 XX
 XX Phosphatidylcholine biosynthesis; PC; protein synthesis; gene expression;
 KW herbicide; phosphoethanolamine cytidyl transferase; corn; enzyme.
 KW
 XX Zea mays.
 OS
 XX US2003177523-A1.
 PN
 XX 18-SEP-2003.
 PD
 XX 01-MAY-2003; 2003US-00427442.
 PF
 XX 23-SEP-1999; 99US-0155626P.
 PR 22-SEP-2000; 2000US-00668262.
 PR
 XX (FAMO/) FAMODU O O.
 PA (KINN/) KINNEY A J.
 PA (RAPA/) RAFALSKI J A.
 XX
 XX Famodu OO, Kinney AJ, Rafalski JA;
 PI WPI; 2003-898656/82.
 DR N-PSDB; ADJ26812.
 DR
 XX New phosphatidylcholine biosynthetic enzyme polypeptide, useful for
 PT studying protein synthesis in plants, for manipulating gene expression or
 FT for providing possible target for herbicides.
 FT
 XX Claim 10; SEQ ID NO 2; 30pp; English.

CC The present invention relates to novel phosphatidylcholine (PC)
 CC biosynthetic enzymes and polynucleotides encoding such proteins. The
 CC nucleic acid sequences of the invention are useful for studying protein
 CC synthesis in plants, for manipulating gene expression or for providing
 CC possible target for herbicides. The present sequence is corn
 CC phosphoethanolamine cytidyl transferase, a phosphatidylcholine
 CC biosynthetic enzyme of the invention.

SQ Sequence 157 AA;

Query Match 55.6%; Score 5; DB 7; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
 |||||
 Db 128 KVDDT 132

RESULT 72
 ABB70518

ID ABB70518 standard; protein; 159 AA.
XX
AC ABB70518;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 38346.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI: 2001-656860/75.
DR N-PSDB; ABL14821.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 38346; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 159 AA;

Query Match 55.6%; Score 5; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 53 KVDDT 57
|||||

RESULT 73
AAW31742
ID AAW31742 standard; protein; 166 AA.
XX
AC AAW31742;
XX
DT 26-MAR-1998 (first entry)
XX
DE Canine obese protein (OB protein) variant lacking Gln28.
XX
KW Canine obese protein; OB protein; body fat reduction; dog; obesity;
KW type II diabetes; elevated blood lipid level; lean body mass;
KW insulin sensitivity; osteoporosis.
XX
OS Synthetic.
OS Canis sp.

XX Key Location/Qualifiers
FH Protein 1..21
FT /label= leader_sequence
FT Protein 22..166
FT /label= mature_peptide
XX
PN WO9732022-A2.
XX
PD 04-SEP-1997.
XX
PF 28-FEB-1997; 97WO-US003209.
XX
PR 01-MAR-1996; 96US-00609408.
XX
PA (AMGE-) AMGEN INC.
XX
PI Hernday N;
XX
DR WPI: 1997-448690/41.
DR N-PSDB; AAT8868.
XX
PT New isolated canine obese (OB) protein and related DNA - used to develop
PT products for treating dogs for e.g. obesity, type II diabetes, elevated
PT blood lipid levels or for increasing lean body mass.
XX
PS Claim 1; Page; 44pp; English.
XX
CC The present sequence represents a canine obese (OB) protein variant which
CC lacks Gln28, with respect to the full length sequence (AAW31741). A
CC variant which possesses a N-terminal Met residue in place of the leader
CC sequence (AAW37096) also exists. The OB protein activity results in a
CC decrease in body fat. The canine OB protein can be used for treating dogs
CC who suffer from, e.g. obesity, type II diabetes, elevated blood lipid
CC levels, or to increase lean body mass. They can also be used for e.g.
CC increasing insulin sensitivity, increasing red blood cells (and
CC oxygenation in the blood) and decreasing bone resorption or osteoporosis.
CC The products can also be used for diagnostic purposes, e.g. for
CC characterising or detecting defects in canine OB genes or gene products.
CC note:- this sequence does not appear in the specification; it was created
CC using information provided
XX
SQ Sequence 166 AA;

Query Match 55.6%; Score 5; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 26 KVDDT 30
|||||

RESULT 74
ABB70366
ID ABB70366 standard; protein; 170 AA.
XX
AC ABB70366;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 37890.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.

XX Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*,
 PT useful for vaccinating against infections, e.g. endocarditis.
 XX Claim 18; Page 665; 2189pp; English.
 XX
 CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
 CC (II), given in AAG81454 to AAG83120, from *Staphylococcus epidermidis*, (I)
 CC and (II) can have antibacterial activity and therefore can be used in
 CC vaccination. The nucleic acids (I) may be used to produce the S.
 CC *epidermidis* polypeptides (II) via the production of vectors containing
 CC them which are used to produce hosts cells which express the
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
 CC used to vaccinate subjects and to raise antibodies against the bacteria.
 CC The polypeptides may also be used to assay for other inhibitors of their
 CC activity and therefore identify compounds that may be used for the
 CC treatment of S. *epidermidis* infections, e.g. endocarditis. AAH53971 to
 CC AAH55090 represent specifically claimed S. *epidermidis* genomic DNA
 CC polynucleotide sequences from the present invention. AAH55091 to AAH55098
 CC represent oligonucleotide sequences and primers which are used in the
 CC exemplification of the present invention. N.B. The present invention
 CC specifically claims all the polynucleotide sequences given in the
 CC sequence listing of the present specification, however the sequence
 CC listing only goes up to SEQ ID NO:4454 so even though sequences are given
 CC in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present
 CC for SEQ ID NO:4455 to 4464
 XX
 SQ Sequence 177 AA;

Query Match 55.6%; Score 5; DB 4; Length 177;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 18 KVDDT 22

RESULT 77
 ADY11020
 ID ADY11020 standard; protein; 182 AA.
 XX
 AC ADY11020;
 XX
 DT 21-APR-2005 (first entry)
 DE Plant full length insert polypeptide seqid 66835.

XX plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 XX protein content.

XX Unidentified.

XX US2004034888-A1.
 XX 19-FEB-2004.
 XX
 XX 28-APR-2003; 2003US-00425114.
 XX
 XX 06-MAY-1999; 99US-00304517.
 XX 05-NOV-2001; 2001US-00985678.

XX (LIU/J) LIU J.
 XX (ZHOU/) ZHOU Y.
 XX (KOVA/) KOVALIC D K.
 XX (SCRE/) SCREEN S E.
 XX (TABA/) TABASKA J E.

PA (CAOY/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX
 DR WPI; 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.

XX Claim 1; SEQ ID NO 66835; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

XX Sequence 182 AA;

Query Match 55.6%; Score 5; DB 8; Length 182;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 134 KVDDT 138

RESULT 78
 ADY11256
 ID ADY11256 standard; protein; 182 AA.
 XX
 AC ADY11256;

XX
 DT 21-APR-2005 (first entry)
 DE Plant full length insert polypeptide seqid 67071.

XX plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 XX protein content.

XX Unidentified.

XX US2004034888-A1.
 XX 19-FEB-2004.
 XX
 XX 28-APR-2003; 2003US-00425114.
 XX
 XX 06-MAY-1999; 99US-00304517.
 XX 05-NOV-2001; 2001US-00985678.

PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOV/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX
 DR WPI; 2004-180133/17.
 XX
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 67071; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 XX
 SQ Sequence 182 AA;
 Query Match 55.6%; Score 5; DB 8; Length 182;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVDDT 5
 Db 134 KVDDT 138
 |||||
 RESULT 79
 ABU30050
 ID ABU30050 standard; protein; 189 AA.
 XX
 AC ABU30050;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #15577.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Enterococcus faecium.
 XX
 PN W0200277183-A2.
 XX
 XX 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.
 PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA33920.
 XX
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 57974; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 189 AA;
 Query Match 55.6%; Score 5; DB 6; Length 189;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVDDT 5
 Db 59 KVDDT 63
 |||||
 RESULT 80
 ADY10671
 ID ADY10671 standard; protein; 189 AA.
 XX
 AC ADY10671;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polypeptide seqid 66486.
 XX
 KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;

KW Galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 XX protein content.
 XX Unidentified.
 OS US2004034888-A1.
 XX
 PN 19-FEB-2004.
 XX
 PD 28-APR-2003; 2003US-00425114.
 XX
 PF 06-MAY-1999; 99US-00304517.
 XX
 PR 05-NOV-2001; 2001US-00985678.
 XX
 XX (LIU/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOV/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 66486; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 XX
 SQ Sequence 189 AA;
 Query Match 55.6%; Score 5; DB 8; Length 189;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVDDT 5
 DB 141 KVDDT 145
 RESULT 81
 ABG21277
 ID ABG21277 standard; protein; 201 AA.
 XX
 AC ABG21277;
 XX
 DT 18-FEB-2602 (first entry)
 XX
 DE Novel human diagnostic protein #21268.
 XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 XX
 PR 23-AUG-2000; 2000US-00649167.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS85464.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 51636; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: the sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 201 AA;
 Query Match 55.6%; Score 5; DB 4; Length 201;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 DB 159 VDDTF 163
 RESULT 82
 ADC94805
 ID ADC94805 standard; protein; 202 AA.
 XX
 AC ADC94805;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE E. faecium protein sequence SEQ ID 4432.
 XX
 KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
 KW abdominal-pelvic infection.

XX OS Enterococcus faecium.
 XX PN US6583275-B1.
 XX PD 24-JUN-2003.
 XX PF 30-JUN-1998; 98US-00107532.
 XX PR 02-JUL-1997; 97US-0051571P.
 XX PR 14-MAY-1998; 98US-0085598P.
 XX PA (GENO-) GENOME THERAPEUTICS CORP.
 XX PI Doucette-Stamm LA, Bush D;
 XX DR WPI; 2003-799836/75.
 XX DR N-PSDB; ADC91151.
 XX CC New isolated nucleic acid derived from Enterococcus faecium encoding an
 PT Enterococcus faecium polypeptide useful for detection, prevention and
 PT treatment of a pathological condition resulting from a bacterial
 PT infection.
 XX CC Example 1; SEQ ID NO 4432; 243pp; English.
 XX CC The invention relates to an isolated nucleic acid derived from
 CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
 CC one of 10 fully defined sequences given in the (or comprising 40
 CC sequential nucleotides chosen from any of the nucleic acids, its
 CC complement or sequences hybridising to it). Also included are a
 CC recombinant vector comprising the nucleic acid operably linked to
 CC transcription regulatory element, a cell comprising the vector and a
 CC single-stranded probe comprising the nucleic acid. The nucleic acids are
 CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
 CC The nucleic acids is useful for diagnosing pathological conditions
 CC resulting from E. faecium bacterial infection (e.g. urinary tract
 CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
 CC infection) and for screening drugs such as agonists and antagonists. The
 CC nucleic acid is useful for recombinant production of Candida albicans -
 CC derived peptides or antisense polypeptides. Pharmaceutical compositions
 CC and vaccines containing the nucleic acid are useful for preventing or
 CC treating Enterococcus faecium infections. The present sequence represents
 CC one if the disclosed E. faecium proteins.
 XX CC
 XX SQ Sequence 202 AA;
 Query Match 55.6%; Score 5; DB 7; Length 202;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVDVT 5
 Db 72 KVDVT 76
 RESULT 83
 AAB96683
 ID AAB96683 standard; protein; 211 AA.
 XX AC AAB96683;
 XX DT 29-OCT-2001 (first entry)
 XX DE Putative P. abyssi dolichol phosphate mannose synthase related protein.
 XX KW Hyperthermophilic archaeon; hyperthermophilic protein.
 XX OS Pyrococcus abyssi.
 XX PN PR2792651-A1.
 XX PD 27-OCT-2000.
 Query Match 55.6%; Score 5; DB 7; Length 202;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVDVT 5
 Db 72 KVDVT 76
 RESULT 83
 AAB96683
 ID AAB96683 standard; protein; 211 AA.
 XX AC AAB96683;
 XX DT 29-OCT-2001 (first entry)
 XX DE Putative P. abyssi dolichol phosphate mannose synthase related protein.
 XX KW Hyperthermophilic archaeon; hyperthermophilic protein.
 XX OS Pyrococcus abyssi.
 XX PN PR2792651-A1.
 XX PD 27-OCT-2000.

XX PF 21-APR-1999; 99FR-00005034.
 XX PR 21-APR-1999; 99FR-00005034.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PA (IFRE-) IFREMER INST FR RECH EXPL MER.
 XX PI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;
 XX PI Querrellou J, Weissenbach J, Saurin W, Heilig R;
 XX DR WPI; 2001-126236/14.
 XX CC New nucleotide sequences isolated from Pyrococcus abyssi encode proteins
 PT useful in industry.
 XX PS Claim 7; Page 1441; 1657pp; French.
 XX CC The present invention relates to the genomic sequence of Pyrococcus
 CC abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is
 CC a hyperthermophilic archaeon, which is isolated from deep-sea
 CC hydrothermal vents. The present sequence is one such P. abyssi protein.
 CC The proteins of the present invention have various potential industrial
 CC uses, since the proteins are stable at very high temperatures, some up to
 CC 110 degrees centigrade. Note: This patent is in the same patent family as
 CC WO200605062, which contains additional sequences as shown in AAB99132-
 CC AAB99143, AAH75903-AAH75920 and AAG66436
 XX SQ Sequence 211 AA;
 Query Match 55.6%; Score 5; DB 4; Length 211;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVDVT 5
 Db 139 KVDVT 143
 RESULT 84
 AAY29015
 ID AAY29015 standard; protein; 230 AA.
 XX AC AAY29015;
 XX DT 24-SEP-1999 (first entry)
 XX DE T. gondii immunogenic protein.
 XX KW Immunogenic protein; Toxoplasma gondii protein; oocyst shedding; cat;
 XX KW T. gondii infection; enteric apicomplexa oocyst; Cryptosporidium oocyst;
 XX KW Toxoplasma oocyst.
 XX OS Toxoplasma gondii.
 XX PN WO9932633-A1.
 XX PD 01-JUL-1999.
 XX PF 18-DEC-1998; 98WO-US027137.
 XX PR 19-DEC-1997; 97US-00994825.
 XX PA (HESK-) HESKA CORP.
 XX PI Milhausen MJ, Lutz SB, Ng RK;
 XX DR WPI; 1999-418930/35.
 XX DR N-PSDB; AAX91216.
 XX PT New isolated Toxoplasma gondii nucleic acids used, e.g. to treat
 PT infection caused by this microorganism.
 XX

PS Claim 29; Page 188-189; 381pp; English.

XX The invention provides isolated Toxoplasma gondii nucleic acids that

CC encode immunogenic polypeptides. The T. gondii nucleic acid molecules,

CC immunogenic proteins and antibodies to the proteins can be used to

CC inhibit T. gondii oocyst shedding in a cat due to infection with T.

CC gondii. They can be used for preventing T. gondii infection and for

CC preventing the spread of T. gondii infection. They can also be used for

CC detecting T. gondii infection. The detection method can be used to detect

CC parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts

CC such as Cryptosporidium oocysts and Toxoplasma oocysts

XX

SQ Sequence 230 AA;

Query Match 55.6%; Score 5; DB 2; Length 230;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

Db 168 KVDDT 172

RESULT 85

AAU25486

ID AAU25486 standard; protein; 230 AA.

XX

AC AAU25486;

XX

DT 17-DEC-2001 (first entry)

XX

DE T. gondii immunogenic protein P4604-54.

XX

XX Immunogenic protein; oocyst; faeces; enteric apicomplexa oocyst;

KW Cryptosporidium oocyst; Toxoplasma oocyst; Giardia cyst; vaccine;

KW oocyte shedding.

XX

OS Toxoplasma gondii.

XX

PN US2001014447-A1.

XX

PD 16-AUG-2001.

XX

PF 18-DEC-1998; 98US-00216393.

XX

PR 19-DEC-1997; 97US-00994825.

XX

PA (MILH/) MILHAUSEN M J.

XX

PI Milhausen MJ;

XX

DR WPI: 2001-529100/58.

XX

DR N-PSDB; AAS42539.

XX

PT Detecting parasite oocysts or cysts in feces, comprises eluting DNA from

PT sample into aqueous solution by heating, amplifying DNA with primers

PT specific for oocysts or cysts being detected, and detecting amplification

PT product.

XX

PS Example 2; Page 67; 188pp; English.

XX

CC The invention relates to detection of parasite oocysts or cysts in a

CC faeces sample comprising contacting the sample with a solid support,

CC drying and then washing the sample with an aqueous wash solution, adding

CC an aqueous elution solution and eluting DNA from the sample by heating

CC and amplifying by PCR oocyst/cyst-specific DNA and detecting the

CC amplification products. The method is useful for detecting parasite

CC oocysts e.g., enteric apicomplexa oocysts such as Cryptosporidium oocysts

CC or Toxoplasma oocysts, or for detecting parasite cysts e.g. Giardia

CC cysts. The method is also useful for developing vaccines to prevent

CC oocyte shedding in cats. The present sequence represents an immunogenic

CC protein from Toxoplasma gondii

XX

SQ Sequence 230 AA;

Query Match 55.6%; Score 5; DB 4; Length 230;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

Db 168 KVDDT 172

RESULT 86

ADG17081

ID ADG17081 standard; protein; 230 AA.

XX

AC ADG17081;

XX

DT 26-FEB-2004 (first entry)

XX

DE T. gondii protein #15.

XX

KW Toxoplasma gondii; oocyst shedding; genetic vaccine; vaccine.

XX

OS Toxoplasma gondii.

XX

PN US2003194393-A1.

XX

PD 16-OCT-2003.

XX

PF 17-DEC-2002; 2002US-00321856.

XX

PR 19-DEC-1997; 97US-00994825.

PR 18-DEC-1998; 98US-00216393.

XX

PA (MILH/) MILHAUSEN M J.

XX

PI Milhausen MJ;

XX

DR WPI: 2003-899768/82.

DR N-PSDB; ADG17080.

XX

PT Novel immunogenic Toxoplasma gondii proteins useful for inhibiting oocyst

PT shedding by cats infected with Toxoplasma gondii.

XX

PS Claim 6; SEQ ID NO 31; 198pp; English.

XX

CC The invention relates to an isolated Toxoplasma gondii protein. The

CC protein is useful for inhibit oocyst shedding by cats infected with

CC Toxoplasma gondii. The protein is useful for preventing or ameliorating

CC diseases caused by infection with T. gondii. The nucleic acid can be used

CC as genetic vaccine which encodes the protein. The protein and the nucleic

CC acid are used as diagnostic reagents for detection of T. gondii

CC infection. The present sequence is used in the exemplification of the

CC invention.

XX

SQ Sequence 230 AA;

Query Match 55.6%; Score 5; DB 7; Length 230;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

Db 168 KVDDT 172

RESULT 87

AAB25468

ID AAB25468 standard; protein; 235 AA.

XX

AC AAB25468;

XX

DT 27-NOV-2000 (first entry)

XX DE Pinus radiata cell signalling involved protein SEQ ID NO:787.
 XX DE
 XX KW Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification;
 KW plant;cell signalling; modulation; transgenic plant; pathogen; growth;
 KW environmental change; development; cell proliferation; differentiation;
 KW elongation; survival; disease resistance; nutrient metabolism.
 XX XX
 OS Pinus radiata.
 XX KW
 XX WO200042171-A1.
 XX XX
 XX PD 20-JUL-2000.
 XX XX
 XX PF 11-JAN-2000; 2000WO-US000724.
 XX XX
 XX PR 12-JAN-1999; 99US-0028986.
 XX PR 01-NOV-1999; 99US-0162866P.
 XX XX
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 XX XX
 XX Strabala TJ, Nieuwenhuizen NJ;
 XX XX
 XX WPI; 2000-476052/41.
 XX XX
 XX Isolated polynucleotide encoding a polypeptide involved in cell signaling
 PT used for generating transgenic plants with modified responses to external
 PT signals.
 XX XX
 XX Claim 3; Page 364; 527pp; English.
 XX PS
 XX CC AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide
 CC and protein sequences isolated from eucalyptus (Eucalyptus grandis) or
 CC pine (Pinus radiata also known as Monterey pine). The protein sequences
 CC are involved in cell signalling. The polynucleotide and protein sequences
 CC can be used to modify the response of plant cells to external signals
 CC e.g. environmental changes or pathogens during the growth and development
 CC of a plant. They can be used to modify cell proliferation,
 CC differentiation, elongation and survival, resistance to disease and
 CC nutrient metabolism. Examples of modifications which can be produced are
 CC altered fruit ripening and senescence of leaves and flowers e.g. to delay
 CC senescence and prolong the life of cut flowers or enhance senescence of
 CC reproductive organs to engineer sterile plants. Other modifications can
 CC be used to delay senescence in selected cell types or organs providing
 CC fruit and vegetables which have a longer shelf life between harvest and
 CC consumption, or to decrease branching frequency in forest tree species
 CC giving long stretches of valuable knot-free clear wood which can be used
 CC in solid timber furniture and veneers
 XX XX
 XX SQ Sequence 235 AA;
 Query Match 55.6%; Score 5; DB 3; Length 235;
 Best Local Similarity 100.0%; Pred. No. 4.2e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFF 7
 DB 117 DDTFF 121
 RESULT 88
 ADQ66091
 ID ADQ66091 standard; protein; 238 AA.
 AC
 XX ADQ66091;
 XX XX
 XX 07-OCT-2004 (first entry)
 XX DE
 XX Novel human protein sequence #1064.
 XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KW gene therapy; diagnostic marker; morbid state; osteoporosis;
 KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;

KW cancer.
 XX OS Homo sapiens.
 XX PN EP1440981-A2.
 XX XX
 XX PD 28-JUL-2004.
 XX XX
 XX PF 21-JAN-2004; 2004EP-00001196.
 XX XX
 XX PR 21-JAN-2003; 2003JP-00102206.
 XX PR 03-MAY-2003; 2003JP-00131392.
 XX XX
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX XX
 XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 XX Yamamoto J, Isono Y, Nagai K, Irie R;
 XX WPI; 2004-535376/52.
 XX DR N-PSDB; ADQ63903.
 XX XX
 XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 XX XX
 XX Claim 1; SEQ ID NO 3252; 2449pp; English.
 XX XX
 XX The invention relates to 2495 novel polynucleotides (I) and their encoded
 CC polypeptides, sequences hybridizing to these nucleotides, sequences
 CC encoding partial polypeptides and sequences having 70% or 90% identity to
 CC the nucleotide and protein sequences. The nucleotides and polypeptides
 CC are useful as diagnostic markers or therapeutic target for the diseases
 CC or morbid states. They are also useful for treating osteoporosis,
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
 CC dementia and various cancers. This sequence corresponds to a protein
 CC sequence of the invention.
 XX XX
 XX SQ Sequence 238 AA;
 Query Match 55.6%; Score 5; DB 8; Length 238;
 Best Local Similarity 100.0%; Pred. No. 4.2e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 DB 43 VDDTF 47
 RESULT 89
 ADY64614
 ID ADY64614 standard; protein; 238 AA.
 XX AC
 XX ADY64614;
 XX XX
 XX DT 02-JUN-2005 (first entry)
 XX XX
 XX DE S. mansoni protein SEQ ID 32.
 XX XX
 XX Schistosomacide; schistosomiasis; psychiatric disorder; vaccine;
 KW diagnosis.
 KW XX
 XX Schistosoma mansoni.
 XX XX
 XX PN WO2005023979-A2.
 XX XX
 XX PD 17-MAR-2005.
 XX XX
 XX PF 10-SEP-2004; 2004WO-BR000170.
 XX XX
 XX PR 11-SEP-2003; 2003US-0502277P.
 XX XX
 XX (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.
 XX XX
 XX Verjovski-Almeida S, Leite LCC, Farias LP, Miyasato PA, Kawano T;

PI Demarco R, Garcia JCL, Martins EAL, Ho PL, Nascimento ALTO;
PI Dias-Neto E, Setubal JC, Menck CFM, Madeira AMEN, Rodrigues V;
PI Gargioni C;
XX WPI; 2005-223357/23.
XX
XX New isolated nucleic acid molecule encoding a Schistosoma mansoni
PT protein, useful for as a vaccine or for preventing, diagnosing, or
PT treating Schistosoma mansoni infection.
XX
PS Disclosure; SEQ ID NO 32; 52pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule encoding a
CC Schistosoma mansoni protein, or its portion which is at least 20 amino
CC acids in length. Also included are an expression vector comprising the
CC nucleic acid operably linked to a promoter, a recombinant cell
CC transformed/transfected with the nucleic acid (or expression vector), an
CC immunogenic composition comprising the nucleic acid in combination with a
CC pharmaceutical adjuvant or carrier, an isolated S. mansoni protein
CC comprising an amino acid sequence encoded by the nucleic acid, an
CC immunogenic composition comprising the isolated S. mansoni protein, an
CC isolated antibody which specifically binds to the isolated S. mansoni
CC protein, a hybridoma cell line which produces the isolated antibody, a
CC method for determining a S. mansoni infection in a subject and a computer
CC readable medium having recorded in it a nucleic acid molecule from S.
CC mansoni genome. The nucleic acid molecule is useful for preventing,
CC diagnosing, or treating S. mansoni infection (schistosomiasis). It can
CC also be used as vaccine against S. mansoni. The present sequence is a
CC Schistosoma mansoni protein of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences. Also, SEQ ID 2141-2152 are
CC mentioned in the specification but are not included in the sequence
CC listing.
XX
SQ Sequence 238 AA;
Query Match 55.6%; Score 5; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDT 5
Db 3 KVDDT 7
|||||
RESULT 90
ADX70680
ID ADX70680 standard; protein; 240 AA.
XX
XX AC ADX70680;
XX
XX DT 21-APR-2005 (first entry)
XX
XX DE Plant full length insert polypeptide seqid 40046.
XX
XX KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.
XX
XX Unidentified.
XX
XX US2004034888-A1.
XX
XX PD 19-FEB-2004.
XX
XX PF 28-APR-2003; 2003US-00425114.
XX

PR 06-MAY-1999; 99US-00304517.
XX 05-NOV-2001; 2001US-00985678.
XX
PA (LIUU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 40046; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 240 AA;
Query Match 55.6%; Score 5; DB 8; Length 240;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
Db 190 VDDTF 194
|||||
RESULT 91
AAG28321
ID AAG28321 standard; protein; 244 AA.
XX
XX AC AAG28321;
XX
XX DT 17-OCT-2000 (first entry)
XX
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 33494.
XX
XX KW protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX OS Arabidopsis thaliana.
XX
XX PN EP1033405-A2.
XX
XX PD 06-SEP-2000.
XX
XX PF 25-FEB-2000; 2000EP-00301439.
XX

PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 03-MAY-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 18-MAY-1999; 99US-0134370P.
PR 19-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
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PR 21-MAY-1999; 99US-0135353P.
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PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
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PR 18-JUN-1999; 99US-0139461P.
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PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139753P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140354P.
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PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142820P.
PR 12-JUL-1999; 99US-0142277P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145088P.
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PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
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PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
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PR 20-AUG-1999; 99US-0149723P.
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PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.

PN WO200154472-A2.
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US001307.
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
XX 02-MAR-2000; 2000US-0186350P.
XX 16-MAR-2000; 2000US-0189874P.
XX 17-MAR-2000; 2000US-0190076P.
XX 18-APR-2000; 2000US-0198123P.
XX 19-MAY-2000; 2000US-0205515P.
XX 07-JUN-2000; 2000US-0209467P.
XX 28-JUN-2000; 2000US-0214886P.
XX 30-JUN-2000; 2000US-0215135P.
XX 07-JUL-2000; 2000US-0216647P.
XX 07-JUL-2000; 2000US-0216880P.
XX 11-JUL-2000; 2000US-0217487P.
XX 11-JUL-2000; 2000US-0217496P.
XX 14-JUL-2000; 2000US-0218290P.
XX 26-JUL-2000; 2000US-0220963P.
XX 26-JUL-2000; 2000US-0220964P.
XX 14-AUG-2000; 2000US-0224518P.
XX 14-AUG-2000; 2000US-0224519P.
XX 14-AUG-2000; 2000US-0225213P.
XX 14-AUG-2000; 2000US-0225214P.
XX 14-AUG-2000; 2000US-0225266P.
XX 14-AUG-2000; 2000US-0225267P.
XX 14-AUG-2000; 2000US-0225268P.
XX 14-AUG-2000; 2000US-0225270P.
XX 14-AUG-2000; 2000US-0225447P.
XX 14-AUG-2000; 2000US-0225757P.
XX 14-AUG-2000; 2000US-0225758P.
XX 14-AUG-2000; 2000US-0225759P.
XX 18-AUG-2000; 2000US-0226279P.
XX 22-AUG-2000; 2000US-0226681P.
XX 22-AUG-2000; 2000US-0226868P.
XX 22-AUG-2000; 2000US-0227182P.
XX 23-AUG-2000; 2000US-0227009P.
XX 30-AUG-2000; 2000US-0228924P.
XX 01-SEP-2000; 2000US-0229287P.
XX 01-SEP-2000; 2000US-0229343P.
XX 01-SEP-2000; 2000US-0229344P.
XX 01-SEP-2000; 2000US-0229345P.
XX 05-SEP-2000; 2000US-0229509P.
XX 05-SEP-2000; 2000US-0229513P.
XX 06-SEP-2000; 2000US-0230437P.
XX 06-SEP-2000; 2000US-0230438P.
XX 08-SEP-2000; 2000US-0231242P.
XX 08-SEP-2000; 2000US-0231243P.
XX 08-SEP-2000; 2000US-0231244P.
XX 08-SEP-2000; 2000US-0231413P.
XX 08-SEP-2000; 2000US-0231414P.
XX 08-SEP-2000; 2000US-0232080P.
XX 08-SEP-2000; 2000US-0232081P.
XX 12-SEP-2000; 2000US-0231968P.
XX 14-SEP-2000; 2000US-0232397P.
XX 14-SEP-2000; 2000US-0232398P.
XX 14-SEP-2000; 2000US-0232399P.
XX 14-SEP-2000; 2000US-0232400P.
XX 14-SEP-2000; 2000US-0232401P.
XX 14-SEP-2000; 2000US-0233063P.
XX 14-SEP-2000; 2000US-0233064P.
XX 14-SEP-2000; 2000US-0233065P.
XX 21-SEP-2000; 2000US-0234223P.
XX 21-SEP-2000; 2000US-0234274P.
XX 25-SEP-2000; 2000US-0234997P.
XX 25-SEP-2000; 2000US-0234998P.
XX 26-SEP-2000; 2000US-0235484P.
XX 27-SEP-2000; 2000US-0235834P.
XX 27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239355P.
PR 13-OCT-2000; 2000US-0239377P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0244647P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUNA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX

XX WPI; 2001-476159/51.
 DR N-PSDB; ADM19614.
 PT Isolated nucleic acid molecule encoding a channel/transporter protein is
 XX used in preventing, treating or ameliorating a medical condition.
 PS Claim 11; SEQ ID NO 900; 809pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule encoding a
 CC channel/transporter protein or sequences at least 95% identical to a
 CC these. The nucleic acids and proteins encoded by them are used to
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 CC in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. The antibodies to the proteins can also be used
 CC in alleviating symptoms associated with the disorders and in diagnostic
 CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
 CC (ELISA). Disorders which are diagnosed or treated include autoimmune
 CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
 CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
 CC arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,
 CC nervous system disorders e.g. Alzheimer's disease, infections caused by
 CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection.
 CC The polypeptides can also be used to aid wound healing and epithelial
 CC cell proliferation, to prevent skin aging due to sunburn, to maintain
 CC organs before transplantation, for supporting cell culture of primary
 CC tissues, to regenerate tissues and in chemotaxis. The polypeptides can
 CC also be used as a food additive or preservative to increase or decrease
 CC storage capabilities. This sequence corresponds to a protein of the
 CC invention.
 XX Sequence 254 AA;
 SQ
 Query Match 55.6%; Score 5; DB 4; Length 254;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 Db |||||
 117 VDDTF 121
 RESULT 94
 AAE37328
 ID AAE37328 standard; protein; 254 AA.
 XX
 AC AAE37328;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Human VLCFAE MOOSE00006 protein from ctg12729.
 XX
 KW Human; very long chain fatty acid biosynthesis enzyme; VLCFA; VLCFAE;
 KW non-insulin dependent diabetes mellitus; NIDDM; adrenoleukodystrophy;
 KW ALD; autosomal dominant macular dystrophy; adMD; Alzheimer's disease;
 KW coronary heart disease; stroke; myocardial infarction; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040392-A2.
 XX
 XX 15-MAY-2003.
 PD
 XX
 PF 04-NOV-2002; 2002WO-IB004610.
 XX
 PR 06-NOV-2001; 2001US-0332864P.
 XX
 PA (DECO-) DECODE GENETICS EHF.
 XX
 PI Betts M, Sigurdson GT;
 DR WPI; 2003-430674/40.

DR N-PSDB; AAD56495.
 XX
 PT New isolated nucleic acid molecule comprising a very long chain fatty
 PT acid biosynthesis enzyme nucleic acid, useful for treating a disease
 PT associated with the biosynthesis enzyme nucleic acid.
 XX
 PS Claim 10; Page 87; 90pp; English.
 XX
 CC The invention relates to very long chain fatty acid (VLCFA) biosynthesis
 CC enzymes (VLCFAE) and polynucleotides encoding such proteins. Sequences
 CC of the invention are useful for treating VLCFAE diseases such as non-
 CC insulin dependent diabetes mellitus (NIDDM), adrenoleukodystrophy (ALD),
 CC autosomal dominant macular dystrophy (adMD), Alzheimer's disease and
 CC coronary heart diseases such as stroke and myocardial infarction. They
 CC are also used in gene therapy. The present sequence is human VLCFAE
 CC protein
 XX Sequence 254 AA;
 SQ
 Query Match 55.6%; Score 5; DB 6; Length 254;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 DTFYY 8
 Db |||||
 201 DTFYY 205
 RESULT 95
 ADX74695
 ID ADX74695 standard; protein; 254 AA.
 XX
 AC ADX74695;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polypeptide seqid 44061.
 XX
 KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX
 OS Unidentified.
 XX
 PN US2004034888-A1.
 XX
 PD 19-FEB-2004.
 XX
 PF 28-APR-2003; 2003US-00425114.
 XX
 PR 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABAS/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 DR WPI; 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.

XX Claim 1; SEQ ID NO 44061; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a

CC polynucleotide consisting of a sequence encoding an amino acid sequence

CC available in electronic form from the US patent office at

CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide

CC of the invention are also useful in physical arrays of molecules and as

CC plant breeding markers. The recombinant DNA construct is useful for

CC improving plant tolerance to cold, heat, drought, herbicides, extreme

CC osmotic conditions, pathogens or pests, for manipulating growth rate in

CC plant cells by modification of the cell cycle pathway, for conferring

CC increased resistance to plant disease, for producing galactomannan,

CC lignin or plant growth regulators, for increasing the rate of homologous

CC recombination in plants, for improving yield by modification of

CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

CC or by providing improved plant growth and development under at least one

CC stress condition or for modifying seed oil or protein yield and/or

CC content. This is the amino acid sequence of a plant full length insert

CC polypeptide that can be used in the recombinant DNA construct of the

CC invention.

XX

SQ Sequence 254 AA;

Query Match 55.6%; Score 5; DB 8; Length 254;

Best Local Similarity 100.0%; Pred. No. 4.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

Db 99 KVDDT 103

RESULT 96

AEA24176

ID AEA24176 standard; protein; 259 AA.

AC AEA24176;

XX

DT 11-AUG-2005 (first entry)

DE Anti-HAAH single-chain Fv antibody fragment #6.

XX

KW Antibody therapy; aspartyl (asparaginy) beta-hydroxylase; AAH; HAAH;

KW cancer; neoplasm; lung tumor; liver tumor; colon tumor; pancreas tumor;

KW prostate tumor; ovary tumor; brain tumor; breast tumor; cytostatic;

KW antibody; Fv.

XX

OS Homo sapiens.

XX

PN WO2005049802-A2.

XX

PD 02-JUN-2005.

XX

PF 15-NOV-2004; 2004WO-US038197.

XX

PR 14-NOV-2003; 2003US-0520114P.

XX

PR 19-APR-2004; 2004US-0563514P.

XX

PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX

PI Wittrup DK, Yeung YA;

XX

XX WPI; 2005-417728/42.

XX

PT New composition comprising anti-hydroxylase antibodies, useful for

PT diagnosing or treating cancer, e.g. lung, liver, colon, pancreas,

PT prostate, ovary, bile duct, brain, or breast cancer.

XX

PS Claim 10; SEQ ID NO 36; 107pp; English.

XX

XX The invention relates to a composition comprising an isolated human

CC antibody or its fragment or other variant, where the antibody, the

CC fragment or the other variant specifically binds to an aspartyl

CC (asparaginy) beta-hydroxylase (AAH). The invention also relates to an

CC isolated nucleic acid molecule comprising a sequence encoding a human

CC antibody or its fragment or other variant, where the antibody, the

CC fragment or the other variant specifically binds to human AAH (HAAH), an

CC expression vector comprising the nucleic acid molecule, a host cell

CC comprising the expression vector, a method of modulating an AAH activity

CC in a cell, a method of treating a patient who has a cancer associated

CC with overactive or over expressed AAH, a method for identifying an

CC antibody or its fragment or other variant that specifically binds to an

CC AAH and a method of making a human monoclonal antibody or its fragment or

CC other variant that specifically binds to an AAH. The composition,

CC antibody, nucleic acid, kit and methods are useful for diagnosing or

CC treating cancer, where the cancer cell is a tumor cell of the lung,

CC liver, colon, pancreas, prostate, ovary, bile duct, brain or breast. This

CC sequence represents an anti-HAAH single-chain Fv antibody fragment used

CC in the scope of the invention.

XX

SQ Sequence 259 AA;

Query Match 55.6%; Score 5; DB 9; Length 259;

Best Local Similarity 100.0%; Pred. No. 4.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

Db 87 KVDDT 91

RESULT 97

ADJ11794

ID ADJ11794 standard; protein; 266 AA.

XX

AC ADJ11794;

XX

DT 20-MAY-2004 (first entry)

XX

DE Rice protein modulated by post-transcriptional gene silencing SeqID 430.

XX

KW rice; post-transcriptional gene silencing; PTGS; plant; trans-activation;

KW cereal; plant-viral interaction.

XX

OS Oryza sp.

XX

PN US2003135888-A1.

XX

PD 17-JUL-2003.

XX

PF 26-SEP-2002; 2002US-00259165.

XX

PR 26-SEP-2001; 2001US-0325277P.

XX

PR 27-NAR-2002; 2002US-0368327P.

XX

PR 04-APR-2002; 2002US-0370620P.

XX

XX (ZHUT/) ZHU T.

PA (WANG/) WANG X.

PA (CHAN/) CHANG H.

PA (BRIG/) BRIGGS S. P.

PA (COOP/) COOPER B.

PA (GLAZ/) GLAZEBROOK J.

PA (GOFF/) GOFF S. A.

PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.

PA (MOUG/) MOUGHAMER T.

PA (PROV/) PROVART N.

PA (RICK/) RICHE D.

XX

PI Zhu T, Wang X, Chang H, Briggs SP, Cooper B, Glazebrook J;

PI Goff SA, Katagiri F, Kreps J, Moughamer T, Provart N, Ricke D;

XX

DR WPI; 2003-829655/77.

XX

DR N-PSDB; ADJ11793.

XX

PT New polynucleotide, useful for modulating gene expression within a cell
PT by posttranscriptional gene silencing.
XX
PS Disclosure; SEQ ID NO 430; 79pp; English.
XX
CC This invention relates to a novel method for identifying isolated
CC polynucleotides that are modulated by post-transcriptional gene silencing
CC (PTGS). Specifically, it refers to the regulation of gene expression in
CC plants via PTGS and the trans-activation of homologous genes due to
CC increased RNA degradation. The present invention describes clusters of
CC polynucleotides from cereals, in particular rice, as well as homologues
CC and the polypeptide sequences derived thereof, where gene expression is
CC altered in response to PTGS. As such, the elucidation of gene silencing
CC mechanisms can lead to more efficiently expressed transgenes, and can
CC also improve the understanding of plant-viral interactions and targeting
CC the suppression of specific plant genes. This polypeptide sequence is a
CC rice protein sequence that is modulated by gene silencing, given in an
CC exemplification of the invention. NOTE: This sequence does not appear in
CC the printed specification but has been obtained in electronic format from
CC the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID=20030135888.
XX
SQ Sequence 266 AA;

Query Match 55.6%; Score 5; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVDDT 5
Db 89 KVVDDT 93
|||||

RESULT 98
ADJ11440
ID ADJ11440 standard; protein; 266 AA.
XX
AC ADJ11440;
XX
DT 20-MAY-2004 (first entry)
XX
DE Rice protein modulated by post-transcriptional gene silencing SeqID 76.
XX
KW rice; post-transcriptional gene silencing; PTGS; plant; trans-activation;
KW cereal; plant-viral interaction.
XX
OS Oryza sp.
XX
PN US2003135888-A1.
XX
PD 17-JUL-2003.
XX
PF 26-SEP-2002; 2002US-00259165.
XX
PR 26-SEP-2001; 2001US-0325277P.
PR 27-MAR-2002; 2002US-0368327P.
PR 04-APR-2002; 2002US-0370620P.
XX
XX (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
XX
XX Zhu T, Wang X, Chang H, Briggs SP, Cooper B, Glazebrook J;
PI Goff SA, Katagiri F, Kreps J, Moughamer T, Provart N, Ricke D;

XX
DR WPI; 2003-829655/77.
DR N-PSDB; ADJ11439.
XX
PT New polynucleotide, useful for modulating gene expression within a cell
PT by posttranscriptional gene silencing.
XX
PS Claim 7; SEQ ID NO 76; 79pp; English.
XX
CC This invention relates to a novel method for identifying isolated
CC polynucleotides that are modulated by post-transcriptional gene silencing
CC (PTGS). Specifically, it refers to the regulation of gene expression in
CC plants via PTGS and the trans-activation of homologous genes due to
CC increased RNA degradation. The present invention describes clusters of
CC polynucleotides from cereals, in particular rice, as well as homologues
CC and the polypeptide sequences derived thereof, where gene expression is
CC altered in response to PTGS. As such, the elucidation of gene silencing
CC mechanisms can lead to more efficiently expressed transgenes, and can
CC also improve the understanding of plant-viral interactions and targeting
CC the suppression of specific plant genes. This polypeptide sequence is a
CC rice protein sequence that is modulated by gene silencing, given in an
CC exemplification of the invention. NOTE: This sequence does not appear in
CC the printed specification but has been obtained in electronic format from
CC the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID=20030135888.
XX
SQ Sequence 266 AA;

Query Match 55.6%; Score 5; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVDDT 5
Db 89 KVVDDT 93
|||||

RESULT 99
ABM88716
ID ABM88716 standard; protein; 278 AA.
XX
AC ABM88716;
XX
DT 02-JUN-2005 (first entry)
XX
DE Rice abiotic stress responsive polypeptide SEQ ID NO:6962.
XX
KW Rice abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
XX
OS Oryza sativa.
XX
PN WO2003008540-A2.
XX
PD 30-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019668.
XX
PR 22-JUN-2001; 2001US-0300112P.
PR 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX
DR WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX

PS Claim 1; SEQ ID NO 6962; 89pp; English.

CC The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, osmotic stress or any of their combinations. The present sequence is used in the exemplification of the invention

XX
SQ Sequence 278 AA;

Query Match 55.6%; Score 5; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
|||||

Db 239 VDDTF 243

RESULT 100

ABU43599

ID ABU43599 standard; protein; 280 AA.

XX
AC ABU43599;

XX
DT 19-JUN-2003 (first entry)

XX
DE Protein encoded by Prokaryotic essential gene #29126.

XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX
OS Staphylococcus haemolyticus.

XX
PN W0200277183-A2.

XX
PD 03-OCT-2002.

XX
PF 21-MAR-2002; 2002WO-US009107.

XX
PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362659P.

XX
PA (ELIT-) ELITRA PHARM INC.

XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX
DR WPI; 2003-029926/02.

DR N-PSDB; ACA47469.

XX
PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX
PS Claim 25; SEQ ID NO 71523; 1766pp; English.

XX
CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway; (8) required for proliferation, or that inhibits cellular proliferation; (9) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 280 AA;

Query Match 55.6%; Score 5; DB 6; Length 280;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
|||||

Db 174 KVDDT 178

RESULT 101

ABO82245

ID ABO82245 standard; protein; 285 AA.

XX
AC ABO82245;

XX
DT 29-JUL-2004 (first entry)

XX
DE Pseudomonas aeruginosa polypeptide #14420.

XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX
OS Pseudomonas aeruginosa.

XX
PN US6551795-B1.

XX
PD 22-APR-2003.

XX
PF 18-FEB-1999; 99US-00252991.

XX
PR 18-FEB-1998; 98US-0074788P.

XX
PR 27-JUL-1998; 98US-0094190P.

XX
PA (GENO-) GENOME THERAPEUTICS CORP.

XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX
DR WPI; 2003-615309/58.

DR N-PSDB; ABD15816.

XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.

XX
PS Disclosure; SEQ ID NO 30991; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABO67826-
 CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html

XX SQ Sequence 285 AA;

Query Match 55.6%; Score 5; DB 7; Length 285;

Best Local Similarity 100.0%; Pred. No. 5e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

QY 1 KVVDDT 5

Db 196 KVVDDT 200
 |||||

RESULT 102

ADR46377

ID ADR46377 standard; protein; 297 AA.

XX ADR46377;

XX 04-NOV-2004 (first entry)
 XX Human EndoG protein.

XX cytotostatic; immunotoxin; cancer; mitochondrial malate dehydrogenase;
 KW enzyme; human; MDH; EndoG.
 XX Homo sapiens.

OS WO2004070012-A2.

PN 19-AUG-2004.

XX 02-FEB-2004; 2004WO-US002974.

XX 02-FEB-2003; 2003US-00444191.

XX 03-FEB-2003; 2003US-0444191P.

XX 08-APR-2003; 2003US-0460855P.

XX (PALO-) PALO ALTO INST MOLECULAR MEDICINE.

XX Wright SC, Larrick JW, Nock SR, Wilson DS;

XX WPI; 2004-60434/58.
 DR N-PSDB; ADR46378.

XX New compositions comprising proteins and encoding nucleic acids having a
 PT DNA nuclease or cell killing activity and are operably linked to cancer
 PT cell binding antibodies or growth factors, useful for treating cancer.

XX Claim 6; SEQ ID NO 24; 225pp; English.

XX The present invention relates to a composition comprising an isolated
 CC amino acid sequence that comprises a portion of human mitochondrial
 CC malate dehydrogenase protein (MDH), particularly the minimum activator of
 CC DNA fragmentation and activator of DNA fragmentation sequences. The
 CC composition is useful for treating cancer chosen from liver cancer,
 CC gastric cancer, head cancer, neck cancer, lung cancer, breast cancer,

CC prostate cancer, cervical cancer, pancreatic cancer, colon cancer,
 CC ovarian cancer, stomach cancer, oesophagus cancer, mouth cancer, tongue
 CC cancer, gum cancer, skin cancer, muscle cancer, heart cancer, bronchial
 CC cancer, cartilage cancer, bone cancer, testis cancer, kidney cancer,
 CC endometrium cancer, uterus cancer, bladder cancer, bone marrow cancer,
 CC lymphoma cancer, spleen cancer, thymus cancer, thyroid cancer, brain
 CC cancer, neuron cancer, gall bladder cancer, ocular cancer, joint cancer,
 CC glioblastoma, mesothelioma, lymphoma, leukaemia, melanoma, squamous cell
 CC carcinoma, osteosarcoma, and Kaposi's sarcoma. The present sequence is a
 XX protein shown in the exemplification of the invention.

XX SQ Sequence 297 AA;

Query Match 55.6%; Score 5; DB 8; Length 297;

Best Local Similarity 100.0%; Pred. No. 5.2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

QY 3 DDTFY 7

Db 156 DDTFY 160
 |||||

RESULT 103

ABM81069

ID ABM81069 standard; protein; 297 AA.

XX ABM81069;

XX 18-NOV-2004 (first entry)
 XX Tumour-associated antigenic target (TAT) polypeptide PRO70290, SEQ:2762.

XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic.

XX Homo sapiens.

OS WO2004030615-A2.

PN 15-APR-2004.

XX 29-SEP-2003; 2003WO-US028547.

XX 02-OCT-2002; 2002US-0414971P.

XX (GETH) GENENTECH INC.

XX Wu TD, Zhang Z, Zhou Y;

XX WPI; 2004-347921/32.
 DR N-PSDB; ACN38936.

XX New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.

XX Claim 12; SEQ ID NO 2762; 7273pp; English.

XX The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a

CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridization probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT polypeptide of the invention
 XX

SQ Sequence 297 AA;

Query Match 55.6%; Score 5; DB 8; Length 297;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7
 |||||
 Db 156 DDTFY 160

RESULT 104

ADB70043
 ID ADB70043 standard; protein; 299 AA.

AC ADB70043;

DT 04-DEC-2003 (first entry)

DE C. neoformans amino acid sequence SEQ ID NO:3087.

KW fungicide; gene therapy; infection.

OS Cryptococcus neoformans.

PN W02003052076-A2.

XX 26-JUN-2003.

XX 17-DEC-2002; 2002WO-US040225.

XX 17-DEC-2001; 2001US-0341261P.

XX (ELIT-) ELITRA PHARM INC.

XX Zamudio C, Eroshkin AM;

XX WPI; 2003-533017/50.

XX N-PSDB; ADB68960.

XX New nucleic acid, useful for preparing a composition for treating an
 PT infection caused by Cryptococcus neoformans.

XX Claim 9; SEQ ID NO 3087; 136pp; English.

XX The invention relates to a novel purified or isolated Cryptococcus
 CC neoformans nucleic acid molecule comprising a sequence encoding a
 CC polypeptide comprising a sequence not given in the specification. A
 CC polynucleotide of the invention has fungicide activity, and may have a
 CC use in gene therapy. The nucleic acid is useful for preparing a
 CC composition for treating an infection caused by Cryptococcus neoformans.
 CC The present sequence represents a C. neoformans sequence of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX SQ Sequence 299 AA;

Query Match 55.6%; Score 5; DB 7; Length 299;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVDT 5
 |||||
 Db 253 KVVDT 257

RESULT 105

ADT58018

ID ADT58018 standard; protein; 300 AA.

XX AC ADT58018;

XX 13-JAN-2005 (first entry)

XX Plant polypeptide, SEQ ID 8095.

KW Plant; transgenic; cold tolerance; growth rate; drought tolerance;
 KW disease resistance; galactomannan production; plant growth regulator;
 KW heat tolerance; herbicide tolerance; lignin production;
 KW extreme osmotic condition tolerance; pathogens resistance;
 KW pest resistance; yield improvement; seed oil yield; seed protein yield.

XX Viridiplantae.

XX US2004216190-A1.

XX 28-OCT-2004.

XX 18-DEC-2003; 2003US-00739930.

XX 28-APR-2003; 2003US-00424599.

XX 28-APR-2003; 2003US-00425115.

XX (KOVA/) KOVALIC D K.

XX Kovalic DK;

XX WPI; 2004-757369/74.

XX New recombinant DNA constructs useful in the field of biochemistry and
 PT genetics, and in particular for producing transgenic plants with improved
 PT biological characteristics.

XX Claim 2; SEQ ID NO 8095; 14pp; English.

XX The invention relates a recombinant DNA construct comprising a
 CC polynucleotide having any of 5544 nucleotide sequences (CDNAs SEQ ID NO:
 CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
 CC (SEQ ID NO: 5545-11088). The CDNAs and proteins are from corn, soybean,
 CC Arabidopsis, wheat and rape but the specification does not indicate which
 CC sequences is derived from which organism. Also included is a method of
 CC producing a plant having an improved property, comprising transforming a
 CC plant with a recombinant DNA construct comprising a promoter region
 CC functional in a plant cell operably joined to a polynucleotide encoding a
 CC polypeptide associated with the property, and growing the transformed
 CC plant. The property is selected from improving plant cold tolerance, for
 CC manipulating growth rate in plant cells by modification of the cell cycle
 CC pathway, for improving plant drought tolerance, for providing increased
 CC resistance to plant disease, for galactomannan production, for production
 CC of plant growth regulators, for improving plant heat tolerance, for
 CC improving plant tolerance to herbicides, for increasing the rate of
 CC homologous recombination in plants, for lignin production, for improving
 CC plant tolerance to extreme osmotic conditions, for improving plant
 CC tolerance to pathogens or pests, for yield improvement by modification of
 CC photosynthesis, for modifying seed oil yield and/or content, for
 CC modifying seed protein yield and/or content, for yield improvement by
 CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
 CC and for yield improvement by providing improved plant growth and
 CC development under at least one stress condition. The polynucleotide may
 CC also encode a plant transcription factor. The methods and compositions of
 CC the present invention are useful in the field of biochemistry and
 CC Genetics, in particular for producing transgenic plants with improved
 CC biological characteristics such as increased yield, improved nitrogen

CC flow, increasing plant tolerance to cold or heat, improving plant
CC tolerance to extreme osmotic and drought conditions, and improving plant
CC tolerance to plant pests or pathogens. They can also be used in physical
CC arrays of molecules, plant breeding markers, computer-based storage and
CC analysis systems. The present sequence is one of the 554 plant protein
CC sequences of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20040216190.
XX
XX
SQ Sequence 300 AA;

Query Match 55.6%; Score 5; DB 8; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 142 KVDDT 146

RESULT 106
ADA35398
ID ADA35398 standard; protein; 301 AA.
XX
AC ADA35398;
XX
DT 20-NOV-2003 (first entry)
XX
DE Acinetobacter baumannii protein #2559.
XX
KW Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
KW plant biocontrol agent.
XX
OS Acinetobacter baumannii.
XX
PN US6562958-B1.
XX
PD 13-MAY-2003.
XX
PF 04-JUN-1999; 99US-00328352.
XX
XX 09-JUN-1998; 98US-0088701P.
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton G, Bush D;
XX
DR WPI; 2003-576092/54.
DR N-PSDB; ADA31272.
XX
PT New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
PT for diagnosing a bacterial disease, as components of antibacterial
PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for
PT plants.
XX
PS Example; SEQ ID NO 6685; 328pp; English.
XX
CC The invention relates to isolated Acinetobacter baumannii nucleic acids.
CC The A. baumannii nucleic acids and polypeptides are useful as reagents
CC for diagnosing a bacterial disease, as components of antibacterial
CC vaccines, as targets for antibacterial drugs, to detect the presence of
CC A. baumannii and other Acinetobacter species in a sample, in screening
CC compounds for the ability to interfere with the A. baumannii life cycle
CC or to inhibit A. baumannii infection, and as biocontrol agents for
CC plants. The present sequence represents the amino acid sequence of an A.
CC baumannii protein.
XX
SQ Sequence 301 AA;

Query Match 55.6%; Score 5; DB 6; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 215 KVDDT 219

RESULT 107
AAG20740
ID AAG20740 standard; protein; 302 AA.
XX
AC AAG20740;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23044.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.

PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142300P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
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PR 22-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
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PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.

PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 28-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 13-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
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PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
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PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 25-OCT-1999; 99US-0161407P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 55.6%; Score 5; DB 3; Length 302;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 151 KVDDT 155

RESULT 108

ADN21573
ID ADN21573 standard; protein; 306 AA.
AC ADN21573;
XX
XX 02-DEC-2004 (first entry)
XX Bacterial polypeptide #4226.
DE
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX US2003233675-A1.
PN
XX 18-DEC-2003.
PD
XX 20-FEB-2003; 2003US-00369493.
PF
XX 21-FEB-2002; 2002US-0360039P.
PR
XX (CAOX/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 4226; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 306 AA;

Query Match 55.6%; Score 5; DB 8; Length 306;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
Db 153 DDTFY 157
RESULT 109
AAG51074
ID AAG51074 standard; protein; 307 AA.
XX
AC AAG51074;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64786.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135533P.
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Db 155 KVDVT 159

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XX 11-AUG-2005 (first entry)
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XX vulnery; CNS-gen.; gene therapy; diagnostic; forensic; mapping;
XX DNA purification; protein purification; osteoarthritis; antiarthritic;
XX osteopathic; musculoskeletal disease; osteoporosis; endocrine disease;
XX periodontal disease; antiinflammatory; mouth disease; burns; injury;
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XX cardiovascular disease; autoimmune disease; immunosuppressive;
XX immune disorder; viral infection; virucide; infection; cancer;
XX cytostatic; neoplasm.
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XX Homo sapiens.
XX
XX WO2005049806-A2.
XX
XX 02-JUN-2005.
XX
XX
XX 11-MAR-2004; 2004WO-US007412.
XX
XX 14-MAR-2003; 2003US-00389559.
XX
XX (NUVE-) NUVELO INC.
XX
XX Tang TY, Wang J, Wang ZW, Zhang J, Ren F, Zhou P, Ma Y;
XX Ghosh M, Xue A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R;
XX Wehrman T, Weng G, Boyle B;
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XX WPI; 2005-417730/42.
XX
XX N-PSDB; AEA19655.
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XX New polynucleotide encoding a polypeptide with biological activity,
XX useful for treating a disease or disorder, e.g. osteoarthritis, burns,
XX CNS and peripheral disease, stroke, autoimmune disorders, viral
XX infection, or cancer.
XX
XX Claim 20; SEQ ID NO 916; 500pp; English.
XX
XX The invention describes a new isolated polynucleotide (I) encoding a
XX polypeptide with biological activity comprising: a nucleotide sequence of
XX SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes
XX to the sequence of (I) under stringent hybridization conditions; or a
XX nucleotide sequence having greater than 9% sequence identity with the
XX sequence of (I). Also described are: a(n) (expression) vector comprising
XX (I); a host cell genetically engineered to comprise (I) operatively
XX associated with a regulatory sequence that modulates expression of the
XX polynucleotide in the host cell; an isolated polypeptide comprising a
XX sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide
XX is: a polypeptide encoded by (I); or a polypeptide encoded by a
XX polynucleotide hybridizing under stringent conditions with any one of SEQ
XX ID NOS: 1-567; a composition comprising the polypeptide of (3) and a
XX carrier; an antibody directed against the polypeptide of (3); a method
XX for detecting (I) in a sample; a method for detecting the polypeptide of
XX (3) in a sample; a method for identifying a compound that binds to the
XX polypeptide of (3); a method of producing the polypeptide of (3); and a
XX collection of polynucleotides, where the collection comprising of at
XX least one of SEQ ID NOS: 1-567. (I) is a polynucleotide comprising any of
XX the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological
XX activity, which comprises any of the amino acid sequence of SEQ ID NOS:
XX 568-1134. All sequences are fully defined in the specification. The
XX sequences and methods are useful in diagnostics, forensic, and gene
XX mapping, in identifying of mutations responsible for genetic disorders or
XX other traits, in assessing biodiversity, and for producing many other
XX types of data and products dependent on DNA and amino acid sequences. The
XX composition and method are useful for treating a disease or disorder,
XX e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and
XX peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,
XX autoimmune disorders, viral infection, or cancer. This is the amino acid
XX sequence of a novel polypeptide of the invention.
XX
XX Sequence 308 AA;
SQ

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Query Match 55.6%; Score 5; DB 9; Length 308;
Best Local Similarity 100.0%; Pred. No. 5.4e-02;
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DT 17-OCT-2000 (first entry)

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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

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PN EP1033405-A2.

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PD 06-SEP-2000.

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PF 25-FEB-2000; 2000EP-00301439.

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PR 28-OCT-1999; 99US-0161992P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 55.6%; Score 5; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KVDOT 5

Db 160 KVDOT 164

RESULT 113

ADT55972

ID ADT55972 standard; protein; 311 AA.

XX AC ADT55972;

XX DT 13-JAN-2005 (first entry)

XX DE Plant polypeptide, SEQ ID 6049.

XX KW Plant; transgenic; cold tolerance; growth rate; drought tolerance;
XX KW disease resistance; galactomannan production; plant growth regulator;
XX KW heat tolerance; herbicide tolerance; lignin production;
XX KW extreme osmotic condition tolerance; pathogens resistance;
XX KW pest resistance; yield improvement; seed oil yield; seed protein yield.

XX OS Viridiplantae.

XX PN US2004216190-A1.

XX PD 28-OCT-2004.

XX PF 18-DEC-2003; 2003US-00739930.

XX PR 28-APR-2003; 2003US-00424599.

XX PR 28-APR-2003; 2003US-00425115.

XX PA (KOVA/) KOVALIC D K.

XX PI Kovalic DK;

XX DR WPI; 2004-757369/74.

XX PT New recombinant DNA constructs useful in the field of biochemistry and
XX PT genetics, and in particular for producing transgenic plants with improved
XX PT biological characteristics.

XX PS Claim 2; SEQ ID NO 6049; 14pp; English.

XX CC The invention relates a recombinant DNA construct comprising a
XX CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
XX CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
XX CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
XX CC Arabidopsis, wheat and rape but the specification does not indicate which
XX CC sequences is derived from which organism. Also included is a method of
XX CC producing a plant having an improved property, comprising transforming a
XX CC plant with a recombinant DNA construct comprising a promoter region
XX CC functional in a plant cell operably joined to a polynucleotide encoding a
XX CC polypeptide associated with the property, and growing the transformed a
XX CC plant. The property is selected from improving plant cold tolerance, for
XX CC manipulating growth rate in plant cells by modification of the cell cycle
XX CC pathway, for improving plant drought tolerance, for providing increased
XX CC resistance to plant disease, for galactomannan production, for production
XX CC of plant growth regulators, for improving plant heat tolerance, for
XX CC improving plant tolerance to herbicides, for increasing the rate of
XX CC homologous recombination in plants, for lignin production, for improving
XX CC plant tolerance to extreme osmotic conditions, for improving plant
XX CC tolerance to pathogens or pests, for yield improvement by modification of
XX CC photosynthesis, for modifying seed oil yield and/or content, for
XX CC modifying seed protein yield and/or content, for yield improvement by
XX CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
XX CC and for yield improvement by providing improved plant growth and
XX CC development under at least one stress condition. The polynucleotide may
XX CC also encode a plant transcription factor. The methods and compositions of
XX CC the present invention are useful in the field of biochemistry and
XX CC genetics, in particular for producing transgenic plants with improved
XX CC biological characteristics such as increased yield, improved nitrogen
XX CC flow, increasing plant tolerance to cold or heat, improving plant
XX CC tolerance to extreme osmotic and drought conditions, and improving plant
XX CC tolerance to plant pests or pathogens. They can also be used in physical
XX CC arrays of molecules, plant breeding markers, computer-based storage and

CC analysis systems. The present sequence is one of the 5544 plant protein
CC sequences of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20040216190.

XX
SQ Sequence 311 AA;
Query Match 55.6%; Score 5; DB 8; Length 311;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVDDT 5
Db 160 KVVDDT 164
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RESULT 114
ABB49170
ID ABB49170 standard; protein; 313 AA.
XX
AC ABB49170;
XX
DT 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes protein #1874.
XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.
XX
OS Listeria monocytogenes.
XX
PN WO200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-FR001118.
XX
PR 11-APR-2000; 2000FR-00004629.
XX
PA (INSP) INST PASTEUR.
XX
PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
PI Dussurget O, Chetouani F, Nedjari H, Glaeser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Rierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Maduenio E, De Pablos B, Wehlend J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX
DR WPI; 2002-010914/01.
XX
PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and related
PT polypeptides.
XX
PS Claim 6; SEQ ID NO 1875; 192pp; French.

CC The present invention relates to the genome sequence of Listeria
CC monocytogenes EGP-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.

CC monocytogenes and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 313 AA;

Query Match 55.6%; Score 5; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DTFYY 8
Db 24 DTFYY 28
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RESULT 115
ADN99771
ID ADN99771 standard; protein; 313 AA.
XX
AC ADN99771;
XX
DT 29-JUL-2004 (first entry)
XX
DE Novel human protein sequence #587.
XX
KW anti-inflammatory; dermatological; neuroprotective; immunomodulator;
KW antibacterial; virucide; antipsoriatic; cytostatic; gene therapy;
KW vaccine; inflammatory; CNS; immune disorder; cancer; psoriasis; diabetes;
KW early aging; hormonal imbalance; ischemic heart disease;
KW ulcerative colitis.
XX
OS Homo sapiens.
XX
PN WO2004038003-A2.
XX
PD 06-MAY-2004.
XX
PF 24-OCT-2003; 2003WO-US033947.
XX
PR 25-OCT-2002; 2002US-0421061P.
PR 25-OCT-2002; 2002US-0421080P.
PR 25-OCT-2002; 2002US-0421552P.
PR 25-OCT-2002; 2002US-0421614P.
PR 30-OCT-2002; 2002US-0422177P.
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PR 27-NOV-2002; 2002US-0429651P.
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PR 05-DEC-2002; 2002US-0430965P.
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XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
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PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Kothakota S, Lin H, Linnemann T, Pierce K, Wang Y;
PI Wong JGP, Wu G, Zhang H, Zeng C;
XX
DR WPI; 2004-365511/34.
DR N-PSDB; ADN98987.
XX
PT New nucleic acid molecules, useful in preparing a composition for
PT treating or preventing e.g. inflammatory, CNS, bacterial or viral
PT disorders, cancer, psoriasis, diabetes, ischemic heart disease or
PT ulcerative colitis.
XX
PS Claim 14; SEQ ID NO 1371; 532pp; English.
XX
CC The invention relates to a nucleic acid molecule comprising a
CC polynucleotide sequence or its complement that encodes a polypeptide. The
CC nucleic acid is useful in preparing a composition for treating or
CC preventing inflammatory, CNS, immune, bacterial or viral disorder,
CC cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic
CC heart disease or ulcerative colitis. This sequence corresponds to a
CC protein of the invention.
XX
SQ Sequence 313 AA;
Query Match 55.6%; Score 5; DB 8; Length 313;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
Db 118 VDDTF 122
RESULT 116
AAG14586
ID AAG14586 standard; protein; 316 AA.
XX
XX AAG14586;
XX
DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 14506.
DE Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
KW Arabidopsis thaliana.
OS
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX
XX 06-SEP-2000.
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PR 03-AUG-1999; 99US-0147038P.
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XX 18-OCT-2000 (first entry)

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XX Protein identification; signal transduction pathway; metabolic pathway;
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XX termination sequence.

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KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
KW gene therapy; channel/transporter protein; rheumatoid arthritis;
KW neoplasm; cardiac arrest; cerebrovascular disorder; cerebral ischemia;
KW angiogenesis; nervous system disorder; Alzheimer's disease;
KW ocular disorder; corneal infection; wound healing;
KW epithelial cell proliferation; skin aging; sunburn; transplantation;
KW chemotaxis; food additive.
XX
OS Homo sapiens.
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 (HUMA-) HUMAN GENOME SCI INC.
 PA
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PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-476159/51.
 DR N-PSDB; ADM19368.
 XX
 PT Isolated nucleic acid molecule encoding a channel/transporter protein is
 PT used in preventing, treating or ameliorating a medical condition.
 XX
 PS Claim 11; SEQ ID NO 654; 809pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule encoding a
 CC channel/transporter protein or sequences at least 95% identical to a
 CC these. The nucleic acids and proteins encoded by them are used to
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 CC in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. The antibodies to the proteins can also be used
 CC in alleviating symptoms associated with the disorders and in diagnostic
 CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
 CC (ELISA). Disorders which are diagnosed or treated include autoimmune
 CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
 CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
 CC arrest, cerebrovascular disorders, e.g. cerebral ischemia, angiodenesis,
 CC nervous system disorders e.g. Alzheimer's disease, infections caused by
 CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection.
 CC The polypeptides can also be used to aid wound healing and epithelial
 CC cell proliferation, to prevent skin aging due to sunburn, to maintain
 CC organs before transplantation, for supporting cell culture of primary
 CC tissues, to regenerate tissues and in chemotaxis. The polypeptides can
 CC also be used as a food additive or preservative to increase or decrease
 CC storage capabilities. This sequence corresponds to a protein of the
 CC invention.
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 SQ Sequence 316 AA;
 Query Match 55.8%; Score 5; DB 4; Length 316;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 121 VDDTF 125
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 XX 26-MAR-2002 (first entry)
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 XX pharmaceutical.
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US009231.
 PF
 XX 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 DR

DR N-PSDB; ABL12206.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 31101; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 317 AA;
 Query Match 55.6%; Score 5; DB 4; Length 317;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVDDT 5
 Db 86 KVDDT 90
 RESULT 120
 ABB60330
 ID ABB60330 standard; protein; 322 AA.
 XX
 AC ABB60330;
 XX
 XX 26-MAR-2002 (first entry)
 DT
 DE Drosophila melanogaster polypeptide SEQ ID NO 7782.
 XX
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 XX 23-MAR-2001; 2001WO-US009231.
 PF
 XX 23-MAR-2000; 2000US-0191637P.
 PR
 PR 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI
 XX WPI; 2001-656860/75.
 DR
 DR N-PSDB; ABL04433.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 PT
 XX
 PS Disclosure; SEQ ID NO 7782; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 322 AA;
 Query Match 55.6%; Score 5; DB 4; Length 322;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 Db 15 VDDTF 19
 RESULT 121
 ADY25260
 ID ADY25260 standard; protein; 323 AA.
 XX
 AC ADY25260;
 XX
 XX 21-APR-2005 (first entry)
 DT
 DE Plant full length insert polypeptide seqid 73044.
 XX
 XX plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX
 OS Unidentified.
 XX
 XX US2004034888-A1.
 PN
 XX 19-FEB-2004.
 PD
 XX 28-APR-2003; 2003US-00425114.
 PF
 XX 06-MAY-1999; 99US-00304517.
 PR
 PR 05-NOV-2001; 2001US-00985678.
 XX
 XX (LIU/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 PI
 XX WPI; 2004-180133/17.
 DR
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 XX Claim 1; SEQ ID NO 73044; 15pp; English.
 PS
 XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.secdatas.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring

CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

XX
 SQ Sequence 323 AA;

Query Match 55.6%; Score 5; DB 8; Length 323;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDVT 5

|||||

Db 168 KVDVT 172

RESULT 122

AAG20738

ID AAG20738 standard; protein; 326 AA.

XX

AC AAG20738;

XX

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 23042.

XX

KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-00301439.

XX

PR 25-FEB-1999; 99US-0121825P.

PR

PR 05-MAR-1999; 99US-0123180P.

PR

PR 09-MAR-1999; 99US-0123548P.

PR

PR 23-MAR-1999; 99US-0125788P.

PR

PR 25-MAR-1999; 99US-0126264P.

PR

PR 29-MAR-1999; 99US-0126785P.

PR

PR 01-APR-1999; 99US-0127462P.

PR

PR 06-APR-1999; 99US-0128234P.

PR

PR 08-APR-1999; 99US-0128714P.

PR

PR 16-APR-1999; 99US-0129845P.

PR

PR 19-APR-1999; 99US-0130077P.

PR

PR 21-APR-1999; 99US-0130449P.

PR

PR 23-APR-1999; 99US-0130510P.

PR

PR 23-APR-1999; 99US-0130891P.

PR

PR 28-APR-1999; 99US-0131449P.

PR

PR 30-APR-1999; 99US-0132048P.

PR

PR 04-MAY-1999; 99US-0132407P.

PR

PR 05-MAY-1999; 99US-0132485P.

PR

PR 06-MAY-1999; 99US-0132486P.

PR

PR 07-MAY-1999; 99US-0132487P.

PR

PR 11-MAY-1999; 99US-0132566P.

PR

PR 14-MAY-1999; 99US-0134218P.

PR

PR 14-MAY-1999; 99US-0134219P.

PR

PR 14-MAY-1999; 99US-0134221P.

PR

PR 18-MAY-1999; 99US-0134370P.

PR

PR 19-MAY-1999; 99US-0134768P.

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PR 20-MAY-1999; 99US-0134941P.

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PR 20-MAY-1999; 99US-0135124P.

PR

PR 21-MAY-1999; 99US-0135353P.

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PR 25-MAY-1999; 99US-0136021P.

PR 27-MAY-1999; 99US-0136392P.

PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-0137222P.

PR 03-JUN-1999; 99US-0137528P.

PR 04-JUN-1999; 99US-0137502P.

PR 07-JUN-1999; 99US-0137724P.

PR 08-JUN-1999; 99US-0138094P.

PR 10-JUN-1999; 99US-0138540P.

PR 10-JUN-1999; 99US-0138847P.

PR 14-JUN-1999; 99US-0139119P.

PR 16-JUN-1999; 99US-0139452P.

PR 16-JUN-1999; 99US-0139453P.

PR 17-JUN-1999; 99US-0139492P.

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PR 18-JUN-1999; 99US-0139455P.

PR 18-JUN-1999; 99US-0139456P.

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PR 18-JUN-1999; 99US-0139458P.

PR 18-JUN-1999; 99US-0139459P.

PR 18-JUN-1999; 99US-0139460P.

PR 18-JUN-1999; 99US-0139461P.

PR 18-JUN-1999; 99US-0139462P.

PR 18-JUN-1999; 99US-0139463P.

PR 18-JUN-1999; 99US-0139750P.

PR 18-JUN-1999; 99US-0139763P.

PR 21-JUN-1999; 99US-0139817P.

PR 22-JUN-1999; 99US-0139899P.

PR 23-JUN-1999; 99US-0140353P.

PR 24-JUN-1999; 99US-0140695P.

PR 28-JUN-1999; 99US-0140823P.

PR 28-JUN-1999; 99US-0140991P.

PR 30-JUN-1999; 99US-0141287P.

PR 01-JUL-1999; 99US-0141842P.

PR 02-JUL-1999; 99US-0142154P.

PR 02-JUL-1999; 99US-0142055P.

PR 06-JUL-1999; 99US-0142390P.

PR 09-JUL-1999; 99US-0142803P.

PR 12-JUL-1999; 99US-0142920P.

PR 13-JUL-1999; 99US-0142977P.

PR 14-JUL-1999; 99US-0143542P.

PR 15-JUL-1999; 99US-0143624P.

PR 16-JUL-1999; 99US-0144005P.

PR 16-JUL-1999; 99US-0144085P.

PR 16-JUL-1999; 99US-0144086P.

PR 19-JUL-1999; 99US-0144325P.

PR 19-JUL-1999; 99US-0144331P.

PR 19-JUL-1999; 99US-0144332P.

PR 19-JUL-1999; 99US-0144333P.

PR 19-JUL-1999; 99US-0144334P.

PR 20-JUL-1999; 99US-0144352P.

PR 20-JUL-1999; 99US-0144632P.

PR 20-JUL-1999; 99US-0144884P.

PR 21-JUL-1999; 99US-0144814P.

PR 21-JUL-1999; 99US-0145086P.

PR 21-JUL-1999; 99US-0145088P.

PR 22-JUL-1999; 99US-0145085P.

PR 22-JUL-1999; 99US-0145087P.

PR 22-JUL-1999; 99US-0145089P.

PR 22-JUL-1999; 99US-0145192P.

PR 23-JUL-1999; 99US-0145145P.

PR 23-JUL-1999; 99US-0145218P.

PR 23-JUL-1999; 99US-0145224P.

PR 26-JUL-1999; 99US-0145276P.

PR 27-JUL-1999; 99US-0145913P.

PR 27-JUL-1999; 99US-0145918P.

PR 27-JUL-1999; 99US-0145919P.

PR 28-JUL-1999; 99US-0145951P.

PR 02-AUG-1999; 99US-0146386P.


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CC present invention
XX Sequence 328 AA;
SQ
Query Match 55.6%; Score 5; DB 6; Length 328;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7
Db 291 DDTFY 295

RESULT 124
AAG51072
ID AAG51072 standard; protein; 329 AA.
AC AAG51072;
XX
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64784.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 23-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
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PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
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PR 03-JUN-1999; 99US-0137528P.
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PR 07-JUN-1999; 99US-0137724P.
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PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 21-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
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PR 22-JUL-1999; 99US-0145087P.
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PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0146389P.
PR 04-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
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PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
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PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
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PR 23-AUG-1999; 99US-0149802P.
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PR 23-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
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PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
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PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
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PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160815P.
PR 21-OCT-1999; 99US-0160814P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
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PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 55.6%; Score 5; DB 3; Length 329;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 177 KVDDT 181

RESULT 125

ABR52858
ID ABR52858 standard; protein; 329 AA.

XX ABR52858;

XX 20-JUN-2003 (first entry)

XX Protein sequence #SEQ ID 581.

XX Multiprotein complex; eukaryote; drug target; diagnosis.

XX Saccharomyces cerevisiae.

XX EP1258494-A1.

XX 20-NOV-2002.

XX 20-DEC-2001; 2001EP-00130253.

XX 15-MAY-2001; 2001EP-00111774.

XX (CELL-) CELLZONE AG.

PI Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;

PI Marzioch M, Schultz JD, Superti-Furga GD;

XX WPI; 2003-250078/25.

DR N-PSDB; ACC60900.

XX New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical. Preferably a drug target in the treatment or prevention of disease or disorder.

XX Disclosure; SEQ ID NO 581; 17pp + Sequence Listing; English.

XX The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records CC ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins CC which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful CC for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or CC prevention of a disease or disorder. Note: the sequence data for this patent is not represented in the printed specification, but is based on CC sequence information supplied by the European Patent Office. The complete CC document is available on CD-ROM

XX SQ Sequence 329 AA;

Query Match 55.6%; Score 5; DB 6; Length 329;

Best Local Similarity 100.0%; Pred. No. 5.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7

Db 153 DDTFY 157

RESULT 126

ADK62318
ID ADK62318 standard; protein; 329 AA.

XX ADK62318;

XX

DT 06-MAY-2004 (first entry)
 XX Disease treating protein complex-derived protein #285.
 DE
 XX
 KW protein complex; drug target; diagnosis;
 XX Unidentified.
 OS
 XX
 XX EPI338608-A2.
 PN
 XX
 XX 27-AUG-2003.
 PD
 XX
 XX 20-DEC-2002; 2002EP-00102902.
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 XX 20-DEC-2001; 2001EP-00130253.
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 XX (CELL-) CELLZOME AG.
 XX
 XX Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;
 PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
 PI Michon A, Leutwein C, Rick J;
 XX
 XX WPI; 2003-638460/61.
 DR N-PSDB; ADK62319.
 XX
 XX New proteins and protein complexes from eukaryotes, useful as targets in
 PT drug screening, or in diagnosing or screening for the presence of a
 PT disease or disorder, or a predisposition for developing a disease or
 PT disorder in a subject.
 XX
 XX Disclosure; SEQ ID NO 569; 13pp; English.
 XX
 CC The invention relates to novel protein complexes comprising a first and a
 CC second protein, or its derivative, fragment, homologue or variant. The
 CC proteins are selected from given protein complexes, which are not defined
 CC in the specification. The variants are encoded by nucleic acids that
 CC hybridize to the nucleic acids encoding the proteins under low stringency
 CC conditions. The protein complexes are useful as targets for an active
 CC agent of a pharmaceutical. These protein complexes are particularly
 CC useful as drug targets for the treatment or preventing of a disease or
 CC disorder. The complexes and methods above are useful in diagnosing or
 CC screening for the presence of a disease or disorder or a predisposition
 CC for developing a disease or disorder in a subject. These are also useful
 CC in screening for a drug for treatment or prevention of a disease or
 CC disorder. The molecule that modulates the amount, activity or protein
 CC components of the complex is useful for the manufacture of a medicament
 CC for the treatment or prevention of a disease or disorder. This sequence
 CC corresponds to a protein of the invention. (Note: the sequence data for
 CC this patent did not form part of the printed specification but was
 CC obtained from the EPO in electronic format).
 XX
 SQ Sequence 329 AA;
 Query Match 55.6%; Score 5; DB 7; Length 329;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFY 7
 DB 153 DDTFY 157
 RESULT 127
 ADS43699
 ID ADS43699 standard; protein; 329 AA.
 XX
 AC ADS43699;
 XX
 XX 02-DEC-2004 (first entry)
 DT
 XX Bacterial polypeptide #22129.
 DE
 XX Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.
 XX
 XX US2003233675-A1.
 PN
 XX
 XX 18-DEC-2003.
 PD
 XX
 XX 20-FEB-2003; 2003US-00369493.
 XX
 XX 21-FEB-2002; 2002US-0360039P.
 XX
 XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 PI
 XX WPI; 2004-061375/06.
 DR
 XX
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 PT
 XX
 XX Claim 1; SEQ ID NO 22129; 122pp; English.
 PS
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 XX Sequence 329 AA;
 SQ
 Query Match 55.6%; Score 5; DB 8; Length 329;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFY 7
 DB 153 DDTFY 157
 RESULT 128
 ADT87145
 ID ADT87145 standard; protein; 329 AA.
 XX

AC ADT87145;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Yeast Stress-related protein from gene YUL152W.
 XX
 KW Yeast; Stress-related protein; SRP; environmental stress; abiotic stress;
 XX drought; heat; cold; salt.
 XX
 OS Saccharomyces cerevisiae.
 XX
 FN WO2004092398-A2.
 XX
 PD 28-OCT-2004.
 XX
 PF 15-APR-2004; 2004WO-US011888.
 XX
 PR 15-APR-2003; 2003EP-00008080.
 PR 02-MAY-2003; 2003EP-00039728.
 PR 01-AUG-2003; 2003EP-00016672.
 PR 30-SEP-2003; 2003EP-00022225.
 XX
 PR (BADI) BASF PLANT SCI GMEH.
 PA
 XX Puzio P, Chardonnens A, Shirley A, Wang X, Sarria-Millan R;
 PI McKersie B, Chen R;
 XX
 XX WPI: 2004-766883/75.
 DR N-PSDB; ADT87144.
 XX
 PR New isolated nucleic acid molecule comprises a sequence encoding Stress-
 PT Related Protein (SRP), useful for producing transformed plants with
 PT altered metabolic activity resulting in increased tolerance or resistance
 PT to environmental stress.
 XX
 XX Claim 15; SEQ ID NO 123; 911pp; English.
 PS
 CC The invention relates an isolated nucleic acid molecule comprises a
 CC nucleic acid molecule encoding a Stress-Related Protein (SRP), from Yeast
 CC or E. coli and their homologues from Rice, Soybean and Rape. Also
 CC included are a transformed plant cell with altered metabolic activity
 CC compared to a corresponding non-transformed wild type plant cell (where
 CC the metabolic activity is altered by transformation with a SRP coding
 CC nucleic acid and results in increased tolerance and/or resistance to an
 CC environmental stress as compared to a corresponding non-transformed wild
 CC type plant cell), a transgenic plant generated from the plant cell above
 CC (and which is a monocot or dicot plant, or a gymnosperm plant), a seed
 CC produced by a transgenic plant above (where the seed is genetically
 CC homozygous for a transgene conferring altered metabolic activity
 CC resulting in an increased tolerance to environmental stress as compared
 CC to a corresponding non-transformed wild type plant), a nucleic acid
 CC construct which confers the expression of the nucleic acid molecule above
 CC (comprising one or more regulatory elements, where expression of the SRP
 CC coding nucleic acid in a host cell results in altered metabolic activity
 CC resulting in increased tolerance to environmental stress as compared to a
 CC corresponding non-transformed wild type host cell), a vector comprising
 CC the nucleic acid molecule above or the nucleic acid construct, a host
 CC cell which has been transformed stably or transiently with the vector (or
 CC the nucleic acid molecules above, or the nucleic acid construct), an
 CC isolated Stress Related Protein (SRP) selected from the amino acid
 CC sequences fully given in the specification and/or its homologues, a
 CC method of producing a transgenic plant with altered metabolic activity
 CC compared to a corresponding non-transformed wild type plant cell,
 CC modifying stress tolerance of a plant, detecting environmental stress in
 CC plant cells or plants, screening plant cells or plants for increased
 CC tolerance and/or resistance to environmental stress, breeding plant cells
 CC or plants towards increased tolerance and/or resistance to environmental
 CC stress, increasing tolerance of a plant to at least one abiotic stress,
 CC a plant transformed with the nucleic acids above and a seed of the plant.
 CC The altered metabolic activity and/or a SRP encoding nucleic acids or its
 CC homologues are useful as markers for selection of plants or plant cells
 CC with increased tolerance to environmental stress, or for detection of
 CC stress in plants or plant cells. The nucleic acids are useful for

CC producing transformed plants with altered metabolic activity resulting in
 CC increased tolerance and/or resistance to an environmental stress
 CC (drought, heat, cold and salt) as compared to a corresponding non-
 CC transformed wild-type plant cell. The present sequence is a yeast SRP of
 XX the invention.
 SQ Sequence 329 AA;
 Query Match 55.6%; Score 5; DB 8; Length 329;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFY 7
 Db 153 DDTFY 157
 RESULT 129
 ABU44842
 ID ABU44842 standard; protein; 330 AA.
 XX
 AC ABU44842;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #30369.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Salmonella paratyphi.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 PA (ELIT-) ELITRA PHARM INC.
 XX
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 DR WPI: 2003-029926/02.
 DR N-PSDB; ACA48712.
 XX
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 72766; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX SQ Sequence 330 AA;

Query Match 55.6%; Score 5; DB 6; Length 330;

Best Local Similarity 100.0%; Pred. No. 5.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8

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Db 178 DTFYY 182

RESULT 130

ABU50533

ID ABU50533 standard; protein; 330 AA.

AC ABU50533;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #36060.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX *Yersinia pestis*.

XX WO20027183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA54403.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 XX Claim 25; SEQ ID NO 78457; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX SQ Sequence 330 AA;

Query Match 55.6%; Score 5; DB 6; Length 330;

Best Local Similarity 100.0%; Pred. No. 5.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8

|||||

Db 179 DTFYY 183

RESULT 131

AAG14585

ID AAG14585 standard; protein; 331 AA.

AC AAG14585;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 14505.

XX Protein identification; signal transduction pathway; metabolic pathway;
 XX hybridisation assay; genetic mapping; gene expression control; promoter;
 XX termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123549P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 16-APR-1999; 99US-0128714P.

XX 19-APR-1999; 99US-0129845P.

XX 21-APR-1999; 99US-0130077P.

XX 23-APR-1999; 99US-0130449P.

XX 23-APR-1999; 99US-0130510P.

XX 23-APR-1999; 99US-0130891P.

PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132040P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141844P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144323P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144332P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
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PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
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PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
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PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158039P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.


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PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 21-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 55.6%; Score 5; DB 3; Length 331;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 179 KVDDT 183

RESULT 132
ABU47384
ID ABU47384 standard; protein; 331 AA.
XX AC ABU47384;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #32911.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Salmomella typhimurium.
XX SN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
XX DR N-PSDB; ACA51254.
XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids, required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX PS Claim 25; SEQ ID NO 75308; 1766pp; English.
XX PS The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:

```

```

CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 331 AA;

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Query Match 55.6%; Score 5; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
Db 179 DTFYY 183

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RESULT 133
ABU15092
ID ABU15092 standard; protein; 331 AA.
XX AC ABU15092;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #619.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Escherichia coli.
XX SN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
XX DR N-PSDB; ACA18962.

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XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 43016; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 331 AA;

SQ

Query Match 55.6%; Score 5; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DFFYY 8
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DB 179 DFFYY 183

RESULT 134

ABU21270

ID ABU21270 standard; protein; 337 AA.

XX

AC ABU21270;

XX

XX 19-JUN-2003 (first entry)

DT

XX Protein encoded by Prokaryotic essential gene #6797.

DE

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

KW

XX Burkholderia fungorum.

OS

XX WO20027183-A2.

PN

XX 03-OCT-2002.

PD

XX 21-MAR-2002; 2002WO-US009107.

PF

XX 21-MAR-2001; 2001US-00815242.

PR

XX 06-SEP-2001; 2001US-00948993.

PR

XX 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA25140.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 49194; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 337 AA;

SQ

Query Match 55.6%; Score 5; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDPT 5
|||||

DB 117 KVDPT 121

RESULT 135

AAG53800

ID AAG53800 standard; protein; 347 AA.

XX

AC AAG53800;

XX

XX 18-OCT-2000 (first entry)

DT

XX Arabidopsis thaliana protein fragment SEQ ID NO: 68529.

DE

XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.
OS EP1033405-A2.
PN 06-SEP-2000.
XX 25-FEB-1999; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126284P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132883P.
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PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
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PR 20-MAY-1999; 99US-0135124P.
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PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-01377502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
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PR 16-JUN-1999; 99US-0139452P.
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PR 18-JUN-1999; 99US-0139460P.
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PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
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PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
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PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
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PR 19-JUL-1999; 99US-0144325P.
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PR 23-JUL-1999; 99US-0145224P.
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PR 28-JUL-1999; 99US-0145511P.
PR 02-AUG-1999; 99US-0146386P.
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PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
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PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
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PR 18-AUG-1999; 99US-0149426P.
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PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
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PR 27-AUG-1999; 99US-0151080P.
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PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.

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PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
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PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
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PR 21-OCT-1999; 99US-0160741P.
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PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 55.6%; Score 5; DB 3; Length 347;
Best Local Similarity 100.0%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 4 DTFY 8
Db 190 DTFY 194

RESULT 136
ADN00790
ID ADN00790 standard; protein; 348 AA.
XX AC
XX ADN00790;
XX
XX 15-JUL-2004 (first entry)
XX
XX Mycobacterium sapM-related P chrysoeum protein SeqID19.
XX
XX promoter; mycobacterial secreted acid phosphatase; SAPM; sapM promoter;
KW antibacterial; fungicide; vaccine; pathogenic mycobacterial disease;
KW fungal infection.
XX
XX Penicillium chrysogenum.
XX
XX WO200403677-A2.
XX
XX 22-APR-2004.
XX

PR 09-OCT-2003; 2003WO-CA001554.
PR 09-OCT-2002; 2002US-0416957P.
PR (LIUJ/) LIU J.
XX
XX Liu J, Saleh MT, Alexander D;
XX
XX WPI; 2004-364868/34.
DR N-PSDB; ADN00788.
XX
XX New mycobacterial secreted acid phosphatase, useful in diagnosing,
PT treating or preventing a pathogenic mycobacterial disease or fungal
PT infection.
XX
XX Disclosure; SEQ ID NO 19; 87pp; English.
XX
XX This invention relates to a novel isolated DNA sequence which comprises a
CC promoter or a promoter fragment of a mycobacterial secreted acid
CC phosphatase (SAPM) gene, where the promoter or the promoter fragment is
CC sufficient to control expression of a nucleotide sequence of interest and
CC is inducible under low-pH conditions and where the promoter or the
CC promoter fragment hybridise to a sapM promoter, for example a
CC Mycobacterium tuberculosis sapM promoter, a M bovis sapM promoter, a M
CC avium sapM promoter or a M marinum sapM promoter, each comprising a M
CC sequence of 500 bp, under high stringency hybridisation conditions. The
CC invention may be useful for the production of compounds with an
CC antibacterial or fungicide activity or for the production of a vaccine
CC against Mycobacterium species comprising a mycobacterial secreted acid
CC phosphatase (SAPM) or an antibody specific for a mycobacterial secreted
CC acid phosphatase. The DNA sequence, methods, compounds, vaccine and
CC compositions are useful in diagnosing, treating or preventing a
CC pathogenic mycobacterial disease or fungal infection. The present
CC sequence is that of a P chrysoeum protein fragment which is related to
CC the invention.
XX
XX Sequence 348 AA;

Query Match 55.6%; Score 5; DB 8; Length 348;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DTFY 7
Db 214 DTFY 218

RESULT 137
AAG28320
ID AAG28320 standard; protein; 368 AA.
XX
XX AC
XX AAG28320;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 33493.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.

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PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-013049P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 18-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135333P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139117P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
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PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
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PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142820P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143342P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.

PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 16-AUG-1999; 99US-0148684P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 25-AUG-1999; 99US-0149930P.
PR 26-AUG-1999; 99US-0150566P.
PR 27-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151080P.
PR 31-AUG-1999; 99US-0151303P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.

| | | | | | |
|--|--|----------------|----|--------------|----------------|
| PR | 08-OCT-1999; | 99US-0158232P. | PR | 21-APR-1999; | 99US-0130449P. |
| PR | 12-OCT-1999; | 99US-0158369P. | PR | 23-APR-1999; | 99US-0130510P. |
| PR | 13-OCT-1999; | 99US-0159293P. | PR | 28-APR-1999; | 99US-0130891P. |
| PR | 13-OCT-1999; | 99US-0159294P. | PR | 30-APR-1999; | 99US-0131449P. |
| PR | 13-OCT-1999; | 99US-0159295P. | PR | 04-MAY-1999; | 99US-0132048P. |
| PR | 14-OCT-1999; | 99US-0159329P. | PR | 05-MAY-1999; | 99US-0132407P. |
| PR | 14-OCT-1999; | 99US-0159330P. | PR | 06-MAY-1999; | 99US-0132485P. |
| PR | 14-OCT-1999; | 99US-0159331P. | PR | 07-MAY-1999; | 99US-0132486P. |
| PR | 14-OCT-1999; | 99US-0159637P. | PR | 11-MAY-1999; | 99US-0132487P. |
| PR | 18-OCT-1999; | 99US-0159638P. | PR | 11-MAY-1999; | 99US-0132863P. |
| PR | 21-OCT-1999; | 99US-0160741P. | PR | 14-MAY-1999; | 99US-0134256P. |
| PR | 21-OCT-1999; | 99US-0160767P. | PR | 14-MAY-1999; | 99US-0134218P. |
| PR | 21-OCT-1999; | 99US-0160768P. | PR | 14-MAY-1999; | 99US-0134219P. |
| PR | 21-OCT-1999; | 99US-0160770P. | PR | 14-MAY-1999; | 99US-0134221P. |
| PR | 21-OCT-1999; | 99US-0160814P. | PR | 14-MAY-1999; | 99US-0134221P. |
| PR | 21-OCT-1999; | 99US-0160815P. | PR | 18-MAY-1999; | 99US-0134370P. |
| PR | 22-OCT-1999; | 99US-0160815P. | PR | 19-MAY-1999; | 99US-0134768P. |
| PR | 22-OCT-1999; | 99US-0160980P. | PR | 20-MAY-1999; | 99US-0134941P. |
| PR | 22-OCT-1999; | 99US-0160981P. | PR | 21-MAY-1999; | 99US-0135124P. |
| PR | 22-OCT-1999; | 99US-0160989P. | PR | 21-MAY-1999; | 99US-0135353P. |
| PR | 25-OCT-1999; | 99US-0161404P. | PR | 24-MAY-1999; | 99US-0135629P. |
| PR | 25-OCT-1999; | 99US-0161405P. | PR | 25-MAY-1999; | 99US-0136021P. |
| PR | 25-OCT-1999; | 99US-0161406P. | PR | 27-MAY-1999; | 99US-0136392P. |
| PR | 26-OCT-1999; | 99US-0161359P. | PR | 28-MAY-1999; | 99US-0136782P. |
| PR | 26-OCT-1999; | 99US-0161360P. | PR | 01-JUN-1999; | 99US-0137222P. |
| PR | 26-OCT-1999; | 99US-0161361P. | PR | 03-JUN-1999; | 99US-0137528P. |
| PR | 28-OCT-1999; | 99US-0161920P. | PR | 04-JUN-1999; | 99US-0137502P. |
| PR | 28-OCT-1999; | 99US-0161922P. | PR | 07-JUN-1999; | 99US-0137724P. |
| PR | 28-OCT-1999; | 99US-0161993P. | PR | 08-JUN-1999; | 99US-0138094P. |
| PR | 29-OCT-1999; | 99US-0162142P. | PR | 10-JUN-1999; | 99US-0138540P. |
| Query Match 55.6%; Score 5; DB 3; Length 368; | | | | | 99US-0138847P. |
| Best Local Similarity 100.0%; Pred.No. 6.4e-02; | | | | | 99US-0139119P. |
| Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | 99US-0139452P. |
| QY | 4 DTFYY 8 | | | | 99US-0139453P. |
| | | | | | 99US-0139453P. |
| Db | 326 DTFYY 330 | | | | 99US-0139454P. |
| RESULT 138 | | | | | |
| AAG28319 | | | | | |
| ID | AAG28319 standard; protein; 370 AA. | | | | |
| XX | | | | | |
| AC | AAG28319; | | | | |
| XX | | | | | |
| DT | 17-OCT-2000 (first entry) | | | | |
| XX | | | | | |
| DE | Arabidopsis thaliana protein fragment SEQ ID NO: 33492. | | | | |
| XX | | | | | |
| KW | Protein identification; signal transduction pathway; metabolic pathway; | | | | |
| KW | hybridisation assay; genetic mapping; gene expression control; promoter; | | | | |
| KW | termination sequence. | | | | |
| XX | | | | | |
| OS | Arabidopsis thaliana. | | | | |
| XX | | | | | |
| PN | EP1033405-A2. | | | | |
| XX | | | | | |
| PD | 06-SEP-2000. | | | | |
| XX | | | | | |
| PF | 25-FEB-2000; 2000EP-00301439. | | | | |
| XX | | | | | |
| XX | 25-FEB-1999; 99US-0121825P. | | | | |
| PR | 05-MAR-1999; 99US-0123180P. | | | | |
| PR | 09-MAR-1999; 99US-0123548P. | | | | |
| PR | 23-MAR-1999; 99US-0125788P. | | | | |
| PR | 25-MAR-1999; 99US-0126264P. | | | | |
| PR | 29-MAR-1999; 99US-0126785P. | | | | |
| PR | 01-APR-1999; 99US-0127462P. | | | | |
| PR | 06-APR-1999; 99US-0128234P. | | | | |
| PR | 08-APR-1999; 99US-0128714P. | | | | |
| PR | 16-APR-1999; 99US-0129845P. | | | | |
| PR | 19-APR-1999; 99US-0130077P. | | | | |

PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145086P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147182P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149810P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 23-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.

PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 28-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 55.8%; Score 5; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 8
| | | |
Db 328 DTFY 332

RESULT 139

ADH87165

ID ADH87165 standard; protein; 370 AA.

XX ADH87165;

XX 22-APR-2004 (first entry)

XX Enterococcus faecalis polypeptide #1645.

XX Enterococcus faecalis infection; transcription regulatory element;
antibacterial.

XX Enterococcus faecalis.

XX US6617156-B1.

XX 09-SEP-2003.

XX 13-AUG-1998; 98US-00134000.

XX 15-AUG-1997; 97US-0055778P.

XX (DOUC/) DOUCETTE-STAMM L A.
XX (BUSH/) BUSH D.

XX Doucette-Stamm LA, Bush D;

XX WPI; 2003-895394/82.

XX N-PSDB; ADH83760.

XX New nucleic acid comprising a sequence encoding an Enterococcus faecalis
polypeptide, useful for preparing a composition for diagnosing or
treating E. faecalis infection.

XX Disclosure; SEQ ID NO 5050; 193pp; English.

XX The invention relates to Enterococcus faecalis polynucleotides and
polypeptides. The invention also relates to a recombinant expression
vector comprising a polynucleotide operably linked to a transcription

CC regulatory element, a cell comprising a recombinant vector, a method for
 CC producing an E. faecalis polypeptide, an isolated nucleic acid comprising
 CC a sequence not given in the specification, a recombinant vector
 CC comprising the nucleic acid and a cell comprising the recombinant vector.
 CC The polynucleotides can be used to detect the presence of E. faecalis in
 CC a sample. The sequences are useful for preparing a composition for
 CC diagnosing or treating Enterococcus faecalis infection. This sequence
 CC represents an E. faecalis polypeptide of the invention.
 XX
 SQ Sequence 370 AA;

Query Match 55.6%; Score 5; DB 7; Length 370;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 145 KVDDT 149
 |||||

RESULT 140
 AAB08467
 ID AAB08467 standard; protein; 373 AA.

AC AAB08467;
 XX
 XX 20-DEC-2000 (first entry)

DE Amino acid sequence of a lysophosphatidic acid acetyltransferase.
 XX
 KW Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant;
 KW triacylglycerol; oil content.
 XX
 OS Glycine max.

XX WO200049156-A2.
 PN
 XX 24-AUG-2000.
 XX

PF 22-FEB-2000; 2000WO-US004526.

XX 22-FEB-1999; 99US-0121119P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ, Ripp KG;

XX WPI; 2000-558300/51.
 DR N-PSDB; AAA64189.

XX New nucleic acid fragment encoding a lysophosphatidic acid
 PT acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants
 PT which encode LPAAT at higher or lower levels than normal.

XX Claim 10; Page 82-83; 102pp; English.

XX The present sequence represents a lysophosphatidic acid acetyltransferase
 CC (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic
 CC plants which encode LPAAT at higher or lower levels than normal or in
 CC cell types or developmental stages in which they are not normally found.
 CC This would have the effect of altering the level of specific
 CC triacylglycerols in those cells, for e.g. overexpression of an LPAAT
 CC similar to the maize LPAAT will result in higher oil content in the seed,
 CC stem and leaf. LPAAT chimeric genes may be used for co-suppression of
 CC genes encoding LPAAT. The polynucleotides may also be used as probes for
 CC genetically and physically mapping the genes that are a part of, and as
 CC markers for traits linked to those genes
 XX

SQ Sequence 373 AA;

Query Match 55.6%; Score 5; DB 3; Length 373;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 Db 56 VDDTF 60
 |||||

RESULT 141
 ADD02198
 ID ADD02198 standard; protein; 378 AA.

XX ADD02198;

XX 01-JAN-2004 (first entry)

XX B2L viral envelope protein #1.

XX B2L; viral envelope protein; Parapox virus; cell proliferative disorder;
 KW immune response; inflammatory response; cancer; immunostimulant;
 KW immunosuppressive; antiinflammatory; cytostatic.

XX Parapoxvirus ovis strain N22.

XX US2003109483-A1.

XX 12-JUN-2003.

XX 06-DEC-2002; 2002US-00313332.

XX 07-DEC-2001; 2001US-0336694P.

XX (CASS/) CASSELL D.

PA (TEPP/) TEPPER J S.

PA (SAMU/) SAMUELS I.

PA (DUBO/) DUBOIS-STRINGFELLOW N.

XX Cassell D, Tepper JS, Samuels I, Dubois-Stringfellow N;

XX WPI; 2003-801275/75.

DR N-PSDB; ADD02199.

XX Enhancing an immune response to endogenous antigens e.g. for treating
 PT cancer, comprises administering a B2L Parapox viral envelope protein.

XX Disclosure; SEQ ID NO 1; 22pp; English.

XX The invention relates to a method for enhancing an immune response to
 CC endogenous antigens comprising administering a B2L viral envelope protein
 CC of a Parapox virus to a subject. The method is used to enhance an immune
 CC response to endogenous antigens, associated with a cell proliferative
 CC disorder or infectious pathogens. The method is used to treat a patient
 CC having a cell proliferative disorder or to elicit an immune or
 CC inflammatory response in a subject. The method is also used for
 CC identifying compounds with the ability to modify a subject's immune
 CC and/or inflammatory response. The method is used to treat cancer and can
 CC enhance a subject's immune response to non-administered antigens. This
 CC sequence represents a B2L protein of the invention. Note: The
 CC specification states that this sequence is encoded by the DNA displayed
 CC in SEQ ID NO:2, but this does not appear to be the case.

XX SQ Sequence 378 AA;

Query Match 55.6%; Score 5; DB 7; Length 378;

Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 Db 325 VDDTF 329
 |||||

RESULT 142
 ADD02200
 ID ADD02200 standard; protein; 378 AA.

XX AC ADD02200;
 XX DT 01-JAN-2004 (first entry)
 XX DE B2L viral envelope protein #2.
 XX KW B2L; viral envelope protein; Parapox virus; cell proliferative disorder;
 XX KW immune response; inflammatory response; cancer; immunostimulant;
 XX KW immunosuppressive; antiinflammatory; cytostatic.
 XX OS Parapoxvirus ovis strain D1701.
 XX PN US2003109483-A1.
 XX PD 12-JUN-2003.
 XX PF 06-DEC-2002; 2002US-00313332.
 XX PR 07-DEC-2001; 2001US-0336694P.
 XX PA (CASS/) CASSELL D.
 XX PA (TEPP/) TEPPER J S.
 XX PA (SAMU/) SAMUELS I.
 XX PA (DUBO/) DUBOIS-STRINGFELLOW N.
 XX PI Cassell D, Tepper JS, Samuels I, Dubois-Stringfellow N;
 XX DR WPI; 2003-801275/75.
 XX DR N-PSDB; ADD02201.
 XX PT Enhancing an immune response to endogenous antigens e.g. for treating
 XX PT cancer, comprises administering a B2L Parapox viral envelope protein.
 XX PS Disclosure; SEQ ID NO 3; 22pp; English.
 XX CC The invention relates to a method for enhancing an immune response to
 XX CC endogenous antigens comprising administering a B2L viral envelope protein
 XX CC of a Parapox virus to a subject. The method is used to enhance an immune
 XX CC response to infectious pathogens, associated with a cell proliferative
 XX CC disorder or infectious pathogens. The method is used to treat a patient
 XX CC having a cell proliferative disorder, or to elicit an immune or
 XX CC inflammatory response in a subject. The method is also used for
 XX CC identifying compounds with the ability to modify a subject's immune
 XX CC and/or inflammatory response. The method is used to treat cancer and can
 XX CC enhance a subject's immune response to non-administered antigens. This
 XX CC sequence represents a B2L protein of the invention.
 XX SQ Sequence 378 AA;
 Query Match 55.6%; Score 5; DB 7; Length 378;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 Db 325 VDDTF 329
 RESULT 143
 ADJ63965
 ID ADJ63965 standard; protein; 378 AA.
 XX AC ADJ63965;
 XX DT 06-MAY-2004 (first entry)
 XX DE Parapox virus B2L protein from parapox virus from strain D1701.
 XX KW Immune response; B2L viral envelope protein; Parapox virus; adjuvant;
 XX KW PP30 protein; virucide; cytostatic; tuberculostatic; virucide; anti-HIV;
 XX KW vaccine; tumour; flu; tuberculosis; respiratory syncytial virus; anthrax;
 XX KW HIV infection.

XX OS Orf virus; D1701.
 XX PH Key Location/Qualifiers
 XX FT Misc-difference 9 /note= "Encoded by GTG"
 XX PN US2003194737-A1.
 XX PD 16-OCT-2003.
 XX PF 15-APR-2003; 2003US-00414609.
 XX PR 15-APR-2002; 2002US-00123058.
 XX PA (JOHN/) JOHNSTON S A.
 XX PA (MCGU/) MCGUIRE M J.
 XX PI Johnston SA, McGuire MJ;
 XX DR WPI; 2003-844451/78.
 XX PT Enhancing an immune response to an antigen by administering to a subject
 XX PT mammal a B2L viral envelope protein of a Parapox virus and an antigen and
 XX PT detecting a resultant enhanced, specific immune response to the antigen.
 XX PS Disclosure; SEQ ID NO 4; 10pp; English.
 XX CC This invention relates to a novel composition for enhancing an immune
 XX CC response to an antigen comprising administering to a subject mammal a B2L
 XX CC viral envelope protein of a Parapox virus and an antigen, and detecting a
 XX CC resultant enhanced, specific immune response to the antigen. The B2L
 XX CC protein is unassociated with other envelope components naturally
 XX CC associated with the B2L protein in the virus, and acts as adjuvant to
 XX CC enhance the immune response to the antigen. The invention also discloses
 XX CC a pharmaceutical composition for enhancing an immune response to an
 XX CC antigen, the composition preferably comprises the PP30 protein of a
 XX CC Parapox virus or the nucleic acid encoding the protein and the antigen or
 XX CC the nucleic acid encoding the antigen. The composition of the invention or
 XX CC may have virucide, cytostatic, tuberculostatic, virucide or anti-HIV
 XX CC activity and may be used as a vaccine. The protein is PP30 protein of a
 XX CC Parapox virus. The method of the invention is useful for enhancing an
 XX CC immune response to an antigen for treating or preventing tumour, flu,
 XX CC tuberculosis, or respiratory syncytial virus, anthrax or HIV infections.
 XX CC The present sequence represents the parapoxvirus B2L viral envelope
 XX CC protein from Parapox virus strain D1701 used to create the composition of
 XX CC the invention.
 XX SQ Sequence 378 AA;
 Query Match 55.6%; Score 5; DB 7; Length 378;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 Db 325 VDDTF 329
 RESULT 144
 ADJ63963
 ID ADJ63963 standard; protein; 378 AA.
 XX AC ADJ63963;
 XX DT 06-MAY-2004 (first entry)
 XX DE Parapox virus B2L protein.
 XX KW Immune response; B2L viral envelope protein; Parapox virus; adjuvant;
 XX KW PP30 protein; virucide; cytostatic; tuberculostatic; virucide; anti-HIV;
 XX KW vaccine; tumour; flu; tuberculosis; respiratory syncytial virus; anthrax;
 XX KW HIV infection; virus.

XX OS Orf virus; OV NZ2.
 XX PF US2003194737-A1.
 XX PN 16-OCT-2003.
 XX PD 15-APR-2003; 2003US-004114609.
 XX PF 15-APR-2002; 2002US-00123058.
 XX PR (JOHN/) JOHNSTON S A.
 XX PA (MCGU/) MCGUIRE M J.
 XX XX Johnston SA, Mcguire MJ;
 XX WPI; 2003-844451/78.
 XX DR N-PSDB; ADJ63962.
 XX XX
 PT Enhancing an immune response to an antigen by administering to a subject
 PT mammal a B2L viral envelope protein of a Parapox virus and an antigen and
 PT detecting a resultant enhanced, specific immune response to the antigen.
 XX
 PS Disclosure; SEQ ID NO 2; 10pp; English.
 XX
 CC This invention relates to a novel composition for enhancing an immune
 CC response to an antigen comprising administering to a subject mammal a B2L
 CC viral envelope protein of a Parapox virus and an antigen, and detecting a
 CC resultant enhanced, specific immune response to the antigen. The B2L
 CC protein is unassociated with other envelope components naturally
 CC associated with the B2L protein in the virus, and acts as adjuvant to
 CC enhance the immune response to the antigen. The invention also discloses
 CC a pharmaceutical composition for enhancing an immune response to an
 CC antigen, the composition preferably comprises the PP30 protein of a
 CC Parapox virus or the nucleic acid encoding the protein and the invention
 CC the nucleic acid encoding the antigen. The composition of the invention
 CC may have virucide, cytostatic, tuberculostatic, virucide or anti-HIV
 CC activity and may be used as a vaccine. The protein is PP30 protein of a
 CC Parapox virus. The method of the invention is useful for enhancing an
 CC immune response to an antigen for treating or preventing tumour, flu,
 CC tuberculosis, or respiratory syncytial virus, anthrax or HIV infections.
 CC The present sequence represents the parapoxvirus B2L viral envelope
 CC protein used to create the composition of the invention.
 XX
 SQ Sequence 378 AA;
 Query Match 55.6%; Score 5; DB 7; Length 378;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 DB 325 VDDTF 329
 RESULT 145
 ADG46065
 ID ADG46065 standard; protein; 378 AA.
 XX
 AC ADG46065;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Parapoxvirus B2WL polypeptide #1.
 XX
 KW Immune system stimulation; immunostimulatory polypeptide; Parapoxvirus;
 KW B2WL; PP30; dendritic cell accumulation; skin; adjuvant activity;
 KW immune response; gene vaccine; immunostimulant.
 XX
 OS Orf virus; strain D1701.
 XX
 PN US2003194695-A1.
 XX

PD 16-OCT-2003.
 XX
 PF 15-APR-2002; 2002US-00123058.
 XX
 PR 15-APR-2002; 2002US-00123058.
 XX
 PA (JOHN/) JOHNSTON S A.
 XX (MCGU/) MCGUIRE M J.
 XX
 PI Johnston SA, Mcguire MJ;
 XX WPI; 2004-041264/04.
 XX DR N-PSDB; ADG46064.
 XX
 XX Stimulation of an immune system involves use of an immunostimulatory
 PT polypeptide from parapox virus.
 XX
 PS Claim 3; SEQ ID NO 2; 26pp; English.
 XX
 CC The present invention relates to a method of stimulation the immune
 CC system. The method involves administration of an immunostimulatory
 CC polypeptide from Parapoxvirus. Two immunostimulatory peptides are
 CC identified in the present invention and designated B2WL and PP30. Also
 CC disclosed are the polynucleotide sequences encoding them. The B2WL
 CC polynucleotide induces dendritic cell accumulation when expressed in
 CC skin, and the PP30 polynucleotide exhibits adjuvant activity in the
 CC absence of stimulating dendritic cell accumulation at the site of
 CC inoculation. When co-inoculated, both genes acts as adjuvants in
 CC stimulating an immune response. The sequences of the invention are useful
 CC for stimulation of an immune system in a subject, preferably mammal,
 CC especially human or mouse. The method enhances immune response induced by
 CC gene vaccines. The present sequence represents Parapoxvirus B2WL
 CC polypeptide.
 XX
 SQ Sequence 378 AA;
 Query Match 55.6%; Score 5; DB 8; Length 378;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 DB 325 VDDTF 329
 RESULT 146
 ADG46067
 ID ADG46067 standard; protein; 378 AA.
 XX
 AC ADG46067;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Parapoxvirus B2WL polypeptide #2.
 XX
 KW Immune system stimulation; immunostimulatory polypeptide; Parapoxvirus;
 KW B2WL; PP30; dendritic cell accumulation; skin; adjuvant activity;
 KW immune response; gene vaccine; immunostimulant.
 XX
 OS Orf virus; strain D1701.
 XX
 PN US2003194695-A1.
 XX
 PD 16-OCT-2003.
 XX
 PF 15-APR-2002; 2002US-00123058.
 XX
 PR 15-APR-2002; 2002US-00123058.
 XX
 XX (JOHN/) JOHNSTON S A.
 XX (MCGU/) MCGUIRE M J.
 XX
 PI Johnston SA, Mcguire MJ;

XX WPI; 2004-041264/04.
 DR N-PSDB; ADG46066.
 XX
 PT Stimulation of an immune system involves use of an immunostimulatory
 PT polypeptide from parapox virus.
 XX
 PS Claim 3; SEQ ID NO 4; 26pp; English.
 XX
 CC The present invention relates to a method of stimulation the immune
 CC system. The method involves administration of an immunostimulatory
 CC polypeptide from Parapoxvirus. Two immunostimulatory peptides are
 CC identified in the present invention and designated B2WL and PP30. Also
 CC disclosed are the polynucleotide sequences encoding them. The B2WL
 CC polynucleotide induces dendritic cell accumulation when expressed in
 CC skin, and the PP30 polynucleotide exhibits adjuvant activity in the
 CC absence of stimulating dendritic cell accumulation at the site of
 CC inoculation. When co-inoculated, both genes acts as adjuvants in
 CC stimulating an immune response. The sequences of the invention are useful
 CC for stimulation of an immune system in a subject, preferably mammal,
 CC especially human or mouse. The method enhances immune response induced by
 CC gene vaccines. The present sequence represents Parapoxvirus B2WL
 CC polypeptide.
 XX
 SQ Sequence 378 AA;
 Query Match 55.6%; Score 5; DB 8; Length 378;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 Db 325 VDDTF 329
 RESULT 147
 ADK01346
 ID ADK01346 standard; protein; 378 AA.
 XX
 AC ADK01346;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE D1701 B2L protein.
 XX
 KW B2L viral envelope protein; Parapoxvirus; immune response;
 KW tumour antigen; flu; tuberculosis; respiratory syncytial virus; anthrax;
 KW HIV; immunostimulant; virucide; anti-HIV; D1701.
 XX
 OS Parapoxvirus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 9 /note= "Encoded by GTG"
 FT
 XX US2004054159-A1.
 FN
 XX 18-MAR-2004.
 PD
 XX 15-APR-2003; 2003US-00414759.
 PF
 XX 07-DEC-2001; 2001US-0336694P.
 PR
 XX 06-DEC-2002; 2002WO-US038971.
 XX
 PA (JOHN/) JOHNSTON S A.
 PA (MCGU/) MCGUIRE M J.
 XX
 PI Johnston SA, Mcguire MJ;
 XX
 XX WPI; 2004-247782/23.
 DR
 DR N-PSDB; ADK01347.
 XX
 PT Enhancing an immune response to an antigen, useful in preventing and/or

PT treating flu, tuberculosis, respiratory syncytial virus, anthrax and HIV,
 PT by administering B2L viral envelope protein of a Parapox virus and an
 PT antigen.
 XX
 PS Disclosure; SEQ ID NO 4; 8pp; English.
 XX
 CC The invention relates to a method of enhancing an immune response to an
 CC antigen comprising administering to a mammal an amount of a B2L viral
 CC envelope protein of a Parapoxvirus and an antigen. The B2L protein acts
 CC as an adjuvant to enhance the immune response to the antigen. The antigen
 CC is a tumour antigen administered as an attenuated or killed pathogen
 CC comprising the antigen. The B2L protein and the antigen are administered
 CC sequentially or simultaneously as a fusion protein. The method and
 CC composition are useful in enhancing an immune response to an antigen such
 CC as a tumour antigen. The composition is useful in preventing and/or
 CC treating flu, tuberculosis, respiratory syncytial virus, anthrax and HIV.
 CC This sequence represents the D1701 B2L protein, used in the scope of the
 CC invention.
 XX
 SQ Sequence 378 AA;
 Query Match 55.6%; Score 5; DB 8; Length 378;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 Db 325 VDDTF 329
 RESULT 148
 ADK01346
 ID ADK01346 standard; protein; 378 AA.
 XX
 AC ADK01346;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Envelope antigen p37K polypeptide.
 XX
 KW B2L viral envelope protein; Parapoxvirus; immune response;
 KW tumour antigen; flu; tuberculosis; respiratory syncytial virus; anthrax;
 KW HIV; envelope antigen; p37K; immunostimulant; virucide; anti-HIV.
 XX
 OS Parapoxvirus.
 XX
 PN US2004054159-A1.
 XX
 PD 18-MAR-2004.
 XX
 PF 15-APR-2003; 2003US-00414759.
 XX
 XX 07-DEC-2001; 2001US-0336694P.
 PR
 XX 06-DEC-2002; 2002WO-US038971.
 XX
 PA (JOHN/) JOHNSTON S A.
 PA (MCGU/) MCGUIRE M J.
 XX
 PI Johnston SA, Mcguire MJ;
 XX
 XX WPI; 2004-247782/23.
 DR
 DR N-PSDB; ADK01345.
 XX
 PT Enhancing an immune response to an antigen, useful in preventing and/or
 PT treating flu, tuberculosis, respiratory syncytial virus, anthrax and HIV,
 PT by administering B2L viral envelope protein of a Parapox virus and an
 PT antigen.
 XX
 PS Disclosure; SEQ ID NO 2; 8pp; English.
 XX
 CC The invention relates to a method of enhancing an immune response to an
 CC antigen comprising administering to a mammal an amount of a B2L viral
 CC envelope protein of a Parapoxvirus and an antigen. The B2L protein acts

CC as an adjuvant to enhance the immune response to the antigen. The antigen
 CC is a tumour antigen administered as an attenuated or killed pathogen
 CC comprising the antigen. The B2L protein and the antigen are administered
 CC sequentially or simultaneously as a fusion protein. The method and
 CC composition are useful in enhancing an immune response to an antigen such
 CC as a tumour antigen. The composition is useful in preventing and/or
 CC treating flu, tuberculosis, respiratory syncytial virus, anthrax and HIV.
 CC This sequence represents the envelope antigen p37K, used in the scope of
 CC the invention.

XX SQ Sequence 378 AA;

Query Match 55.6%; Score 5; DB 8; Length 378;

Best Local Similarity 100.0%; Pred. No. 6.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6

|||||

325 VDDTF 329

RESULT 149

ADT99512
 ID ADT99512 standard; protein; 378 AA.

XX AC ADT99512;

XX DT 13-JAN-2005 (first entry)

XX DE Parapox ovis strain N22 B2L viral envelope protein.

XX KW Immune response; B2L; viral envelope protein; immunostimulatory protein;
 KW PP30; tumour antigen; flu; tuberculosis; respiratory syncytial virus;
 KW anthrax; vaccine; immunostimulant; virucide; antitubercular;
 KW tuberculostatic; anti-HIV.

XX OS Parapox ovis.

XX PN US2004213807-A1.

XX PD 28-OCT-2004.

XX PF 28-MAY-2004; 2004US-00857546.

XX PR 07-DEC-2001; 2001US-0336694P.

XX PR 15-APR-2002; 2002US-00123058.

XX PR 06-DEC-2002; 2002WO-US038971.

XX PR 15-APR-2003; 2003US-00414609.

XX PA (JOHN/) JOHNSTON S A.

XX PA (MCGU/) MCGUIRE M J.

XX PI Johnston SA, McGuire MJ;

XX DR WPI; 2004-765577/75.

XX DR N-PSDB; ADT99511.

XX PT Enhancing an immune response to an antigen comprises administering a
 PT Parapox B2L protein and an antigen to the mammal.

XX PS Disclosure; SEQ ID NO 2; 10pp; English.

XX CC The present invention provides a method for enhancing a subject's immune
 CC response to an administered antigen and/or an active component of a
 CC vaccine by administering an amount of a B2L viral envelope protein and an
 CC immunostimulatory protein PP30 of a Parapox virus. The method and
 CC composition of the invention is useful for enhancing an immune response
 CC to an antigen such as a tumour antigen. The invention is useful as an
 CC adjuvant for vaccine for preventing and/or treating flu, tuberculosis,
 CC respiratory syncytial virus, anthrax and human immunodeficiency virus
 CC (HIV). The invention is also useful in the preparation of vaccine. The
 CC present sequence is Parapox ovis B2L viral envelope protein.

XX

SQ Sequence 378 AA;

Query Match 55.6%; Score 5; DB 8; Length 378;

Best Local Similarity 100.0%; Pred. No. 6.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6

|||||

325 VDDTF 329

RESULT 150

ADT99514

ID ADT99514 standard; protein; 378 AA.

XX AC ADT99514;

XX DT 13-JAN-2005 (first entry)

XX DE Parapox ovis strain D1701 B2L viral envelope protein.

XX KW Immune response; B2L; viral envelope protein; immunostimulatory protein;
 KW PP30; tumour antigen; flu; tuberculosis; respiratory syncytial virus;
 KW anthrax; vaccine; immunostimulant; virucide; antitubercular;
 KW tuberculostatic; anti-HIV.

XX OS Parapox ovis.

XX FH Key Location/Qualifiers

XX FT Misc-difference 9

XX FT /note= "Encoded by GTG"

XX US2004213807-A1.

XX PD 28-OCT-2004.

XX PF 28-MAY-2004; 2004US-00857546.

XX PR 07-DEC-2001; 2001US-0336694P.

XX PR 15-APR-2002; 2002US-00123058.

XX PR 06-DEC-2002; 2002WO-US038971.

XX PR 15-APR-2003; 2003US-00414609.

XX PA (JOHN/) JOHNSTON S A.

XX PA (MCGU/) MCGUIRE M J.

XX PI Johnston SA, McGuire MJ;

XX DR WPI; 2004-765577/75.

XX DR N-PSDB; ADT99513.

XX PT Enhancing an immune response to an antigen comprises administering a
 PT Parapox B2L protein and an antigen to the mammal.

XX PS Disclosure; SEQ ID NO 4; 10pp; English.

XX CC The present invention provides a method for enhancing a subject's immune
 CC response to an administered antigen and/or an active component of a
 CC vaccine by administering an amount of a B2L viral envelope protein and an
 CC immunostimulatory protein PP30 of a Parapox virus. The method and
 CC composition of the invention is useful for enhancing an immune response
 CC to an antigen such as a tumour antigen. The invention is useful as an
 CC adjuvant for vaccine for preventing and/or treating flu, tuberculosis,
 CC respiratory syncytial virus, anthrax and human immunodeficiency virus
 CC (HIV). The invention is also useful in the preparation of vaccine. The
 CC present sequence is Parapox ovis B2L viral envelope protein.

XX SQ Sequence 378 AA;

Query Match 55.6%; Score 5; DB 8; Length 378;

Best Local Similarity 100.0%; Pred. No. 6.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
Db 325 VDDTF 329

Search completed: May 17, 2006, 06:20:35
Job time : 279 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 17, 2006, 06:24:29 ; Search time 24.5 Seconds
(without alignments)
35.345 Million cell updates/sec

Title: US-10-764-985-2

Perfect score: 9

Sequence: 1 KVDDTFYV 9

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 9 | 100.0 | 150 | 1 | WZVZB1 |
| 2 | 9 | 100.0 | 150 | 2 | H36837 |
| 3 | 9 | 100.0 | 150 | 2 | H28446 |
| 4 | 9 | 100.0 | 150 | 2 | F72151 |
| 5 | 7 | 77.8 | 770 | 2 | S75042 |
| 6 | 6 | 66.7 | 206 | 2 | C36365 |
| 7 | 6 | 66.7 | 400 | 2 | H81169 |
| 8 | 6 | 66.7 | 400 | 2 | H81936 |
| 9 | 6 | 66.7 | 482 | 2 | S31478 |
| 10 | 6 | 66.7 | 485 | 2 | C86143 |
| 11 | 6 | 66.7 | 535 | 2 | T47790 |
| 12 | 6 | 66.7 | 1256 | 2 | T26101 |
| 13 | 6 | 66.7 | 1286 | 2 | T16507 |
| 14 | 5 | 55.6 | 72 | 2 | S53874 |
| 15 | 5 | 55.6 | 90 | 2 | D97355 |
| 16 | 5 | 55.6 | 118 | 2 | S25001 |
| 17 | 5 | 55.6 | 128 | 2 | G85757 |
| 18 | 5 | 55.6 | 134 | 2 | A59055 |
| 19 | 5 | 55.6 | 134 | 2 | AC0079 |
| 20 | 5 | 55.6 | 139 | 2 | I53298 |
| 21 | 5 | 55.6 | 140 | 2 | T50420 |
| 22 | 5 | 55.6 | 156 | 1 | UQT07A |
| 23 | 5 | 55.6 | 156 | 2 | S25305 |
| 24 | 5 | 55.6 | 211 | 2 | A75176 |
| 25 | 5 | 55.6 | 263 | 2 | A83956 |
| 26 | 5 | 55.6 | 264 | 2 | B96612 |
| 27 | 5 | 55.6 | 275 | 2 | C83482 |
| 28 | 5 | 55.6 | 279 | 2 | H75326 |
| 29 | 5 | 55.6 | 284 | 2 | T21974 |

| | | | | | |
|-----|---|------|-----|---|--------|
| 30 | 5 | 55.6 | 284 | 2 | AG3556 |
| 31 | 5 | 55.6 | 297 | 2 | T09542 |
| 32 | 5 | 55.6 | 300 | 2 | B56118 |
| 33 | 5 | 55.6 | 304 | 2 | AH0763 |
| 34 | 5 | 55.6 | 306 | 2 | G97132 |
| 35 | 5 | 55.6 | 311 | 2 | T49312 |
| 36 | 5 | 55.6 | 313 | 2 | AD1285 |
| 37 | 5 | 55.6 | 313 | 2 | AG1656 |
| 38 | 5 | 55.6 | 313 | 2 | S51729 |
| 39 | 5 | 55.6 | 315 | 2 | AG0503 |
| 40 | 5 | 55.6 | 316 | 1 | F64966 |
| 41 | 5 | 55.6 | 316 | 2 | A99881 |
| 42 | 5 | 55.6 | 316 | 2 | F85826 |
| 43 | 5 | 55.6 | 317 | 2 | T29624 |
| 44 | 5 | 55.6 | 329 | 1 | NCBYN1 |
| 45 | 5 | 55.6 | 330 | 2 | T33944 |
| 46 | 5 | 55.6 | 330 | 2 | AI0491 |
| 47 | 5 | 55.6 | 331 | 2 | D91184 |
| 48 | 5 | 55.6 | 331 | 2 | B86031 |
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| 50 | 5 | 55.6 | 350 | 2 | C56118 |
| 51 | 5 | 55.6 | 358 | 2 | AC2367 |
| 52 | 5 | 55.6 | 372 | 2 | JC1069 |
| 53 | 5 | 55.6 | 372 | 2 | C83766 |
| 54 | 5 | 55.6 | 399 | 2 | G83857 |
| 55 | 5 | 55.6 | 406 | 2 | JS0343 |
| 56 | 5 | 55.6 | 412 | 2 | JN0319 |
| 57 | 5 | 55.6 | 417 | 2 | JC2389 |
| 58 | 5 | 55.6 | 422 | 2 | B31776 |
| 59 | 5 | 55.6 | 425 | 2 | T36585 |
| 60 | 5 | 55.6 | 426 | 2 | E86575 |
| 61 | 5 | 55.6 | 426 | 2 | D72049 |
| 62 | 5 | 55.6 | 435 | 2 | G87334 |
| 63 | 5 | 55.6 | 440 | 2 | JS0374 |
| 64 | 5 | 55.6 | 452 | 2 | H81777 |
| 65 | 5 | 55.6 | 455 | 2 | D81202 |
| 66 | 5 | 55.6 | 465 | 2 | T00090 |
| 67 | 5 | 55.6 | 468 | 2 | T24724 |
| 68 | 5 | 55.6 | 475 | 2 | T01260 |
| 69 | 5 | 55.6 | 483 | 2 | JC7179 |
| 70 | 5 | 55.6 | 483 | 2 | T47974 |
| 71 | 5 | 55.6 | 483 | 2 | D86385 |
| 72 | 5 | 55.6 | 484 | 2 | S40051 |
| 73 | 5 | 55.6 | 486 | 2 | AB1584 |
| 74 | 5 | 55.6 | 492 | 2 | A82632 |
| 75 | 5 | 55.6 | 506 | 2 | G90430 |
| 76 | 5 | 55.6 | 508 | 2 | T22836 |
| 77 | 5 | 55.6 | 518 | 2 | S49620 |
| 78 | 5 | 55.6 | 518 | 2 | T50745 |
| 79 | 5 | 55.6 | 520 | 2 | A56118 |
| 80 | 5 | 55.6 | 524 | 2 | A32617 |
| 81 | 5 | 55.6 | 528 | 2 | T34417 |
| 82 | 5 | 55.6 | 535 | 2 | F90418 |
| 83 | 5 | 55.6 | 540 | 2 | S54586 |
| 84 | 5 | 55.6 | 545 | 2 | T06264 |
| 85 | 5 | 55.6 | 547 | 2 | I39593 |
| 86 | 5 | 55.6 | 548 | 2 | T51035 |
| 87 | 5 | 55.6 | 550 | 2 | T03714 |
| 88 | 5 | 55.6 | 566 | 2 | D90250 |
| 89 | 5 | 55.6 | 572 | 1 | ERBP22 |
| 90 | 5 | 55.6 | 574 | 2 | T37452 |
| 91 | 5 | 55.6 | 574 | 2 | H42527 |
| 92 | 5 | 55.6 | 574 | 2 | H42527 |
| 93 | 5 | 55.6 | 574 | 2 | A36857 |
| 94 | 5 | 55.6 | 574 | 2 | T28615 |
| 95 | 5 | 55.6 | 574 | 2 | C72174 |
| 96 | 5 | 55.6 | 575 | 1 | ERBP29 |
| 97 | 5 | 55.6 | 579 | 2 | S46210 |
| 98 | 5 | 55.6 | 617 | 2 | JC5721 |
| 99 | 5 | 55.6 | 628 | 2 | T45864 |
| 100 | 5 | 55.6 | 683 | 2 | AC0741 |
| 101 | 5 | 55.6 | 683 | 2 | AB0217 |
| 102 | 5 | 55.6 | 686 | 2 | C90948 |

heat resistant agg
endonuclease G (EC
vetispiradiene syn
probable transcrip
uncharacterized ph
hypothetical prote
glycerate dehydrog
NSP3 protein - hum
probable regulator
probable transcrip
probable transcrip
hypothetical prote
nuclease NUC1 (EC
hypothetical prote
probable membrane
hypothetical prote
hypothetical 37.6K
hypothetical 37.6K
vetispiradiene syn
glucose-1-phosphat
nonstructure prote
adenine glycosylas
tryptophan synthas
tryptophan synthas
acid phosphatase (
acid phosphatase (
hypothetical prote
probable membrane
phosphate permease
acyl-CoA dehydroge
UDP-N-acetylmutamo
UDP-N-acetylmutamo
glycosyltransferas
hypothetical prote
probable ammonium
acid phosphatase (
hypothetical prote
hypothetical prote
starch synthase (E
hypothetical prote
ammonium transport
conserved hypotet
hypothetical prote
phytoene dehydroge
phytoene dehydroge
vetispiradiene syn
phytoene dehydroge
delayed rectifier
ABC transporter, p
probable membrane
3-dehydroquinatate d
exaA protein - Aer
B17R protein - vac
B18R protein - vac
B19R protein - var
hypothetical prote
D8R protein - vari
DNA-directed DNA p
3-dehydroquinatate d
vacuolar protein s
probable tyrosine
oligopeptidase B (
oligopeptidase B (
proteinase II (imp

| | | | | | | | | | | | | | |
|-----|---|------|-------|---|--------|---------------------|-----|---|------|-----|---|--------|--------------------|
| 103 | 5 | 55.6 | 686 | 2 | G85796 | proteinase II [imp | 176 | 4 | 44.4 | 85 | 2 | F96949 | hypothetical prote |
| 104 | 5 | 55.6 | 696 | 2 | A12849 | GGDEF family prote | 177 | 4 | 44.4 | 85 | 2 | AG2583 | hypothetical prote |
| 105 | 5 | 55.6 | 696 | 2 | G97626 | hypothetical prote | 178 | 4 | 44.4 | 85 | 2 | E97664 | hypothetical prote |
| 106 | 5 | 55.6 | 705 | 2 | T51034 | hypothetical prote | 179 | 4 | 44.4 | 85 | 2 | F97365 | hypothetical prote |
| 107 | 5 | 55.6 | 724 | 1 | B32571 | ribosomal protein | 180 | 4 | 44.4 | 86 | 2 | G98244 | hypothetical prote |
| 108 | 5 | 55.6 | 735 | 2 | I51901 | ribosomal protein | 181 | 4 | 44.4 | 85 | 2 | T41003 | transcription init |
| 109 | 5 | 55.6 | 735 | 2 | A53300 | ribosomal protein | 182 | 4 | 44.4 | 87 | 2 | A84679 | hypothetical prote |
| 110 | 5 | 55.6 | 739 | 2 | A81430 | outer membrane pro | 183 | 4 | 44.4 | 87 | 2 | B45823 | shiga-like toxin I |
| 111 | 5 | 55.6 | 752 | 1 | A32571 | ribosomal protein | 184 | 4 | 44.4 | 87 | 2 | S52290 | HLA-A30 variant ex |
| 112 | 5 | 55.6 | 752 | 2 | T27276 | hypothetical prote | 185 | 4 | 44.4 | 87 | 2 | T44104 | hypothetical prote |
| 113 | 5 | 55.6 | 778 | 2 | D87965 | protein Y63D3A.6b | 186 | 4 | 44.4 | 87 | 2 | T18045 | hypothetical prote |
| 114 | 5 | 55.6 | 807 | 2 | T00990 | hypothetical prote | 187 | 4 | 44.4 | 89 | 1 | JN0726 | Shiga-like toxin I |
| 115 | 5 | 55.6 | 841 | 2 | S69563 | suppressor protein | 188 | 4 | 44.4 | 89 | 1 | XVBP9 | Shiga-like toxin c |
| 116 | 5 | 55.6 | 938 | 2 | T01809 | hypothetical prote | 189 | 4 | 44.4 | 89 | 1 | XVEBBD | Shigella toxin cha |
| 117 | 5 | 55.6 | 955 | 2 | S44622 | C50C3.3 protein - | 190 | 4 | 44.4 | 89 | 2 | S58344 | Shiga-like toxin I |
| 118 | 5 | 55.6 | 956 | 2 | B71468 | probable insulinas | 191 | 4 | 44.4 | 89 | 2 | F90779 | Shiga toxin 2 subu |
| 119 | 5 | 55.6 | 971 | 2 | T39912 | conserved hypothet | 192 | 4 | 44.4 | 89 | 2 | H85640 | Shiga toxin 2 subu |
| 120 | 5 | 55.6 | 971 | 2 | T43656 | mating-type switch | 193 | 4 | 44.4 | 89 | 2 | E91000 | Shiga toxin I subu |
| 121 | 5 | 55.6 | 973 | 2 | B89009 | protein T27C4.4 [i | 194 | 4 | 44.4 | 89 | 2 | G85845 | Shiga toxin I subu |
| 122 | 5 | 55.6 | 1045 | 2 | B83393 | RND multidrug effl | 195 | 4 | 44.4 | 89 | 2 | I69156 | Shiga-like toxin I |
| 123 | 5 | 55.6 | 1152 | 2 | AE1852 | hypothetical prote | 196 | 4 | 44.4 | 89 | 2 | S01033 | Shiga-like toxin I |
| 124 | 5 | 55.6 | 1185 | 2 | AG2457 | transcription-repa | 197 | 4 | 44.4 | 89 | 2 | B53887 | Shiga-like toxin I |
| 125 | 5 | 55.6 | 1245 | 2 | D71613 | GAF domain protein | 198 | 4 | 44.4 | 89 | 2 | A47759 | retrovirus-related |
| 126 | 5 | 55.6 | 1269 | 2 | T14476 | pelA protein - sli | 199 | 4 | 44.4 | 91 | 2 | T28436 | hypothetical prote |
| 127 | 5 | 55.6 | 1294 | 2 | S58307 | hypothetical 149.2 | 200 | 4 | 44.4 | 91 | 2 | T15032 | hypothetical prote |
| 128 | 5 | 55.6 | 1308 | 2 | E71622 | probable membrane | 201 | 4 | 44.4 | 91 | 2 | S07895 | hypothetical prote |
| 129 | 5 | 55.6 | 1338 | 2 | T40993 | protein kinase cek | 202 | 4 | 44.4 | 93 | 2 | A60232 | T-cell surface gly |
| 130 | 5 | 55.6 | 1361 | 2 | S50943 | hypothetical prote | 203 | 4 | 44.4 | 93 | 2 | T44779 | hypothetical prote |
| 131 | 5 | 55.6 | 1552 | 2 | G86344 | T22111.2 protein - | 204 | 4 | 44.4 | 94 | 2 | G75143 | hypothetical prote |
| 132 | 5 | 55.6 | 1614 | 2 | T29861 | hypothetical prote | 205 | 4 | 44.4 | 94 | 2 | A81453 | ferredoxin Cj033c |
| 133 | 5 | 55.6 | 1679 | 2 | S48385 | hypothetical prote | 206 | 4 | 44.4 | 96 | 1 | I64010 | C4-dicarboxylate t |
| 134 | 5 | 55.6 | 1860 | 2 | T17485 | peptide synthetase | 207 | 4 | 44.4 | 97 | 2 | S72333 | hypothetical prote |
| 135 | 5 | 55.6 | 2025 | 2 | T03884 | hypothetical prote | 208 | 4 | 44.4 | 97 | 2 | T29534 | hypothetical prote |
| 136 | 5 | 55.6 | 3085 | 2 | T00327 | polyprotein - infe | 209 | 4 | 44.4 | 98 | 2 | S17604 | Ig heavy chain V r |
| 137 | 5 | 55.6 | 3871 | 2 | T22812 | hypothetical prote | 210 | 4 | 44.4 | 98 | 2 | E64763 | probable alpha hel |
| 138 | 5 | 55.6 | 10797 | 2 | T30192 | probable peptide s | 211 | 4 | 44.4 | 98 | 2 | D90680 | probable alpha hel |
| 139 | 4 | 44.4 | 25 | 2 | B53415 | lectin chain B - I | 212 | 4 | 44.4 | 98 | 2 | H85530 | hypothetical prote |
| 140 | 4 | 44.4 | 33 | 2 | C64536 | hypothetical prote | 213 | 4 | 44.4 | 98 | 2 | T14691 | hypothetical prote |
| 141 | 4 | 44.4 | 37 | 2 | I56058 | cell surface glyco | 214 | 4 | 44.4 | 99 | 2 | T09998 | 12-oxophytodienoat |
| 142 | 4 | 44.4 | 37 | 2 | S21665 | S-layer protein - | 215 | 4 | 44.4 | 99 | 2 | A55819 | nonhistone chromos |
| 143 | 4 | 44.4 | 37 | 2 | E72269 | hypothetical prote | 216 | 4 | 44.4 | 99 | 2 | A31090 | hypothetical prote |
| 144 | 4 | 44.4 | 38 | 2 | S71381 | lebetin 2 isoform | 217 | 4 | 44.4 | 99 | 2 | AG3070 | hypothetical prote |
| 145 | 4 | 44.4 | 46 | 2 | BH1717 | hypothetical protei | 218 | 4 | 44.4 | 99 | 2 | B98216 | hypothetical prote |
| 146 | 4 | 44.4 | 49 | 2 | J00643 | GTP-binding protei | 219 | 4 | 44.4 | 100 | 2 | H95366 | NADH2 dehydrogenas |
| 147 | 4 | 44.4 | 50 | 2 | A60718 | phospholipase A2 h | 220 | 4 | 44.4 | 100 | 2 | T49323 | hypothetical prote |
| 148 | 4 | 44.4 | 50 | 2 | B60718 | phospholipase A2 h | 221 | 4 | 44.4 | 101 | 2 | B97800 | hypothetical prote |
| 149 | 4 | 44.4 | 53 | 2 | B84236 | hypothetical prote | 222 | 4 | 44.4 | 103 | 2 | T26137 | hypothetical prote |
| 150 | 4 | 44.4 | 58 | 2 | S05489 | alpha-amylase (EC | 223 | 4 | 44.4 | 103 | 2 | AH2487 | hypothetical prote |
| 151 | 4 | 44.4 | 58 | 2 | S76577 | hypothetical prote | 224 | 4 | 44.4 | 103 | 2 | H89764 | conserved hypothet |
| 152 | 4 | 44.4 | 61 | 2 | F98014 | hypothetical prote | 225 | 4 | 44.4 | 104 | 1 | K9RB | Ig kappa-B9 chain |
| 153 | 4 | 44.4 | 63 | 2 | G84589 | hypothetical prote | 226 | 4 | 44.4 | 104 | 2 | H91204 | hypothetical prote |
| 154 | 4 | 44.4 | 63 | 2 | AD3041 | hypothetical prote | 227 | 4 | 44.4 | 104 | 2 | T18823 | hypothetical prote |
| 155 | 4 | 44.4 | 64 | 2 | H81811 | hypothetical prote | 228 | 4 | 44.4 | 105 | 2 | S06985 | probable nitrogen |
| 156 | 4 | 44.4 | 64 | 2 | T34580 | hypothetical prote | 229 | 4 | 44.4 | 106 | 2 | E84056 | thioredoxin H1 BH3 |
| 157 | 4 | 44.4 | 65 | 2 | S51099 | MHC class I histoc | 230 | 4 | 44.4 | 107 | 2 | B53307 | thioredoxin - Stre |
| 158 | 4 | 44.4 | 65 | 2 | A81810 | hypothetical prote | 231 | 4 | 44.4 | 107 | 2 | A59825 | hypothetical prote |
| 159 | 4 | 44.4 | 66 | 2 | S09855 | hypothetical prote | 232 | 4 | 44.4 | 107 | 2 | A82040 | hypothetical prote |
| 160 | 4 | 44.4 | 67 | 2 | I53485 | GTP-binding protei | 233 | 4 | 44.4 | 107 | 2 | D87337 | hypothetical prote |
| 161 | 4 | 44.4 | 67 | 2 | T44097 | hypothetical prote | 234 | 4 | 44.4 | 108 | 2 | A84658 | hypothetical prote |
| 162 | 4 | 44.4 | 67 | 2 | S66426 | plasma-sensitiv | 235 | 4 | 44.4 | 109 | 2 | T17831 | hypothetical prote |
| 163 | 4 | 44.4 | 67 | 2 | F97130 | probable transcrip | 236 | 4 | 44.4 | 110 | 2 | C85063 | hypothetical prote |
| 164 | 4 | 44.4 | 69 | 2 | AH2888 | hypothetical prote | 237 | 4 | 44.4 | 110 | 2 | F89797 | hypothetical prote |
| 165 | 4 | 44.4 | 71 | 2 | H65284 | conserved hypothet | 238 | 4 | 44.4 | 111 | 2 | S69911 | Ig V-D-J region (R |
| 166 | 4 | 44.4 | 72 | 2 | A65292 | archaeal histone A | 239 | 4 | 44.4 | 112 | 2 | S51123 | genome polyprotein |
| 167 | 4 | 44.4 | 74 | 2 | B90467 | conserved hypothet | 240 | 4 | 44.4 | 112 | 2 | H90595 | ribosome-binding f |
| 168 | 4 | 44.4 | 76 | 2 | A69033 | hypothetical prote | 241 | 4 | 44.4 | 112 | 2 | A13327 | hypothetical cytos |
| 169 | 4 | 44.4 | 76 | 2 | T14724 | hypothetical prote | 242 | 4 | 44.4 | 113 | 2 | G86823 | nitrogen regulator |
| 170 | 4 | 44.4 | 80 | 2 | S78295 | acyl carrier prote | 243 | 4 | 44.4 | 113 | 2 | T06155 | hypothetical prote |
| 171 | 4 | 44.4 | 80 | 2 | B84285 | hypothetical prote | 244 | 4 | 44.4 | 113 | 2 | S09830 | hypothetical prote |
| 172 | 4 | 44.4 | 81 | 2 | C72349 | acyl carrier prote | 245 | 4 | 44.4 | 113 | 2 | G96942 | hypothetical prote |
| 173 | 4 | 44.4 | 81 | 2 | C81337 | hypothetical prote | 246 | 4 | 44.4 | 114 | 2 | S26319 | Ig heavy chain V r |
| 174 | 4 | 44.4 | 83 | 2 | B84679 | hypothetical prote | 247 | 4 | 44.4 | 114 | 2 | T44547 | hypothetical prote |
| 175 | 4 | 44.4 | 83 | 2 | F89920 | conserved hypothet | 248 | 4 | 44.4 | 114 | 2 | T49086 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|---|------|-----|---|--------|--------------------|-----|---|------|-----|---|--------|--------------------|
| 249 | 4 | 44.4 | 114 | 2 | E90274 | hypothetical prote | 322 | 4 | 44.4 | 140 | 2 | T28576 | 6R protein - vario |
| 250 | 4 | 44.4 | 115 | 2 | S78053 | ig heavy chain-V-D | 323 | 4 | 44.4 | 140 | 2 | F64516 | hypothetical prote |
| 251 | 4 | 44.4 | 115 | 2 | S60397 | hypothetical prote | 324 | 4 | 44.4 | 140 | 2 | F90342 | hypothetical prote |
| 252 | 4 | 44.4 | 115 | 2 | AD3601 | hypothetical prote | 325 | 4 | 44.4 | 140 | 2 | F97027 | hypothetical prote |
| 253 | 4 | 44.4 | 115 | 2 | AB1172 | hypothetical prote | 326 | 4 | 44.4 | 141 | 2 | S06483 | hemoglobin I, extr |
| 254 | 4 | 44.4 | 116 | 1 | E69393 | probable erpK prot | 327 | 4 | 44.4 | 141 | 2 | T26567 | hypothetical prote |
| 255 | 4 | 44.4 | 116 | 1 | A10746 | flagellar transcri | 328 | 4 | 44.4 | 142 | 1 | F70437 | nucleoside-diphosp |
| 256 | 4 | 44.4 | 116 | 2 | H97213 | reductase/isomeras | 329 | 4 | 44.4 | 142 | 1 | JC5612 | troponin I beta - |
| 257 | 4 | 44.4 | 116 | 2 | T05517 | abscisic acid-indu | 330 | 4 | 44.4 | 142 | 2 | JC5611 | troponin I alpha - |
| 258 | 4 | 44.4 | 117 | 2 | JK0053 | lysozyme (EC 3.2.1 | 331 | 4 | 44.4 | 142 | 2 | C70059 | hypothetical prote |
| 259 | 4 | 44.4 | 117 | 2 | B97063 | uncharacterized pr | 332 | 4 | 44.4 | 142 | 2 | H89829 | conserved hypotet |
| 260 | 4 | 44.4 | 117 | 2 | AB3201 | hypothetical prote | 333 | 4 | 44.4 | 142 | 4 | S13768 | MHC class I hiatoc |
| 261 | 4 | 44.4 | 118 | 2 | T23280 | hypothetical prote | 334 | 4 | 44.4 | 143 | 2 | A95333 | hypothetical prote |
| 262 | 4 | 44.4 | 118 | 2 | T60377 | interphotoreceptor | 335 | 4 | 44.4 | 144 | 2 | H82837 | conserved hypotet |
| 263 | 4 | 44.4 | 118 | 2 | T60377 | RNA polymerase II | 336 | 4 | 44.4 | 144 | 2 | C95308 | hypothetical prote |
| 264 | 4 | 44.4 | 118 | 2 | I59405 | hypothetical prote | 337 | 4 | 44.4 | 145 | 2 | B98057 | hypothetical prote |
| 265 | 4 | 44.4 | 119 | 2 | S29887 | ribosomal protein | 338 | 4 | 44.4 | 146 | 2 | I47196 | ig heavy chain var |
| 266 | 4 | 44.4 | 119 | 2 | C95877 | hypothetical prote | 339 | 4 | 44.4 | 146 | 2 | H72167 | A35R protein - var |
| 267 | 4 | 44.4 | 120 | 2 | T17514 | hypothetical prote | 340 | 4 | 44.4 | 146 | 2 | I46506 | zona pellucida bin |
| 268 | 4 | 44.4 | 120 | 2 | A64804 | hypothetical prote | 341 | 4 | 44.4 | 147 | 2 | F98018 | flavodoxin [import |
| 269 | 4 | 44.4 | 121 | 2 | B69380 | ybfG protein - Esc | 342 | 4 | 44.4 | 147 | 2 | H95150 | flavodoxin [import |
| 270 | 4 | 44.4 | 121 | 2 | F97650 | chemotaxis respons | 343 | 4 | 44.4 | 147 | 2 | A43547 | T-cell surface gly |
| 271 | 4 | 44.4 | 122 | 2 | A02222 | hypothetical prote | 344 | 4 | 44.4 | 147 | 2 | AH2414 | hypothetical prote |
| 272 | 4 | 44.4 | 123 | 2 | A29652 | flagellar protein | 345 | 4 | 44.4 | 147 | 2 | G48552 | ORF-US441 - infect |
| 273 | 4 | 44.4 | 123 | 2 | H70482 | inter-alpha-trypsi | 346 | 4 | 44.4 | 147 | 2 | T40381 | hypothetical prote |
| 274 | 4 | 44.4 | 123 | 2 | H71558 | hypothetical prote | 347 | 4 | 44.4 | 147 | 2 | E82923 | early glycoprotein |
| 275 | 4 | 44.4 | 123 | 2 | D64549 | hypothetical prote | 348 | 4 | 44.4 | 148 | 1 | VGBE48 | hypothetical prote |
| 276 | 4 | 44.4 | 124 | 2 | AB1465 | hypothetical prote | 349 | 4 | 44.4 | 148 | 2 | AF1288 | probable flavodoxi |
| 277 | 4 | 44.4 | 124 | 2 | AB0561 | dihydroneopterin a | 350 | 4 | 44.4 | 148 | 2 | AE1660 | probable flavodoxi |
| 278 | 4 | 44.4 | 124 | 2 | F85543 | conserved hypotet | 351 | 4 | 44.4 | 148 | 2 | AI3263 | 6-pyruvoyltetrahyd |
| 279 | 4 | 44.4 | 124 | 2 | B90593 | hypothetical prote | 352 | 4 | 44.4 | 148 | 2 | S78271 | hypothetical prote |
| 280 | 4 | 44.4 | 124 | 2 | D64776 | hypothetical prote | 353 | 4 | 44.4 | 148 | 2 | AE1036 | probable phage tai |
| 281 | 4 | 44.4 | 124 | 2 | F42520 | ybaJ protein - Esc | 354 | 4 | 44.4 | 148 | 2 | B71529 | probable phage tai |
| 282 | 4 | 44.4 | 125 | 2 | S72665 | ig V-D-J region (R | 355 | 4 | 44.4 | 148 | 2 | CGWN2C | hypothetical prote |
| 283 | 4 | 44.4 | 125 | 2 | B86051 | hypothetical prote | 356 | 4 | 44.4 | 149 | 1 | GMWN2C | globin IIC, extrac |
| 284 | 4 | 44.4 | 126 | 2 | T10191 | hypothetical prote | 357 | 4 | 44.4 | 149 | 2 | D84292 | transcription regu |
| 285 | 4 | 44.4 | 126 | 2 | S53585 | hypothetical prote | 358 | 4 | 44.4 | 150 | 2 | T33928 | hypothetical prote |
| 286 | 4 | 44.4 | 127 | 2 | B86158 | 60S ribosomal prot | 359 | 4 | 44.4 | 151 | 2 | C64064 | iron-sulfur cofact |
| 287 | 4 | 44.4 | 127 | 2 | AG1024 | hypothetical prote | 360 | 4 | 44.4 | 152 | 1 | VGBEY9 | early glycoprotein |
| 288 | 4 | 44.4 | 127 | 2 | AH3491 | hypothetical cytos | 361 | 4 | 44.4 | 153 | 2 | D96906 | hypothetical prote |
| 289 | 4 | 44.4 | 128 | 2 | S58156 | hypothetical prote | 362 | 4 | 44.4 | 153 | 2 | E86872 | galactoside O-acet |
| 290 | 4 | 44.4 | 129 | 2 | JB0400 | ribosomal protein | 363 | 4 | 44.4 | 153 | 2 | E88955 | protein K04F1.8 [i |
| 291 | 4 | 44.4 | 129 | 2 | G98225 | hypothetical prote | 364 | 4 | 44.4 | 153 | 2 | T12454 | hypothetical prote |
| 292 | 4 | 44.4 | 130 | 2 | H97605 | hypothetical prote | 365 | 4 | 44.4 | 155 | 2 | T04026 | probable ubiquitin |
| 293 | 4 | 44.4 | 130 | 2 | A83400 | hypothetical prote | 366 | 4 | 44.4 | 155 | 2 | JS0657 | ubiquitin / riboso |
| 294 | 4 | 44.4 | 130 | 2 | A48892 | abscisic acid-indu | 367 | 4 | 44.4 | 155 | 2 | S40239 | ubiquitin/ribosoma |
| 295 | 4 | 44.4 | 130 | 2 | T22920 | hypothetical prote | 368 | 4 | 44.4 | 155 | 2 | S40240 | ubiquitin / riboso |
| 296 | 4 | 44.4 | 131 | 2 | JQ1767 | SalLR protein - v | 369 | 4 | 44.4 | 155 | 2 | JH0227 | ubiquitin / riboso |
| 297 | 4 | 44.4 | 132 | 1 | JC4159 | ribosomal protein | 370 | 4 | 44.4 | 155 | 2 | JH0226 | leu ribosomal prot |
| 298 | 4 | 44.4 | 132 | 1 | R3HU12 | ribosomal protein | 371 | 4 | 44.4 | 155 | 2 | C75145 | probable ribosomal |
| 299 | 4 | 44.4 | 132 | 1 | R3MS12 | ribosomal protein | 372 | 4 | 44.4 | 155 | 2 | G71184 | hypothetical prote |
| 300 | 4 | 44.4 | 132 | 1 | R3RT12 | ribosomal protein | 373 | 4 | 44.4 | 155 | 2 | T35423 | hypothetical prote |
| 301 | 4 | 44.4 | 132 | 2 | I51557 | ribosomal protein | 374 | 4 | 44.4 | 156 | 2 | H89787 | ubiquitin extensio |
| 302 | 4 | 44.4 | 132 | 2 | A69844 | hypothetical prote | 375 | 4 | 44.4 | 156 | 2 | T52335 | ubiquitin extensio |
| 303 | 4 | 44.4 | 132 | 2 | C91773 | chemotaxis signal | 376 | 4 | 44.4 | 156 | 2 | T52334 | ubiquitin extensio |
| 304 | 4 | 44.4 | 133 | 2 | A11658 | glutathione transf | 377 | 4 | 44.4 | 156 | 2 | T35689 | hypothetical prote |
| 305 | 4 | 44.4 | 134 | 2 | AE3490 | hit1 protein [impo | 378 | 4 | 44.4 | 156 | 2 | A86473 | 17.2K hypothetical |
| 306 | 4 | 44.4 | 134 | 2 | C90490 | conserved hypotet | 379 | 4 | 44.4 | 157 | 2 | S22489 | IG8-dependent hist |
| 307 | 4 | 44.4 | 134 | 2 | A95304 | ig heavy chain pre | 380 | 4 | 44.4 | 157 | 2 | F72274 | type IV pilin-rela |
| 308 | 4 | 44.4 | 135 | 2 | F80057 | hypothetical prote | 381 | 4 | 44.4 | 157 | 2 | F81274 | probable flagellar |
| 309 | 4 | 44.4 | 135 | 2 | C90699 | hypothetical prote | 382 | 4 | 44.4 | 157 | 2 | F82941 | hypothetical prote |
| 310 | 4 | 44.4 | 135 | 2 | E64781 | hypothetical prote | 383 | 4 | 44.4 | 157 | 2 | G83772 | hypothetical prote |
| 311 | 4 | 44.4 | 135 | 2 | F85549 | hypothetical prote | 384 | 4 | 44.4 | 157 | 2 | T35638 | hypothetical prote |
| 312 | 4 | 44.4 | 136 | 2 | T15031 | hypothetical prote | 385 | 4 | 44.4 | 157 | 2 | C71060 | hypothetical prote |
| 313 | 4 | 44.4 | 136 | 2 | C95291 | hypothetical prote | 386 | 4 | 44.4 | 158 | 2 | T33718 | probable transcrip |
| 314 | 4 | 44.4 | 137 | 2 | H86700 | flavodoxin [import | 387 | 4 | 44.4 | 158 | 2 | AH1930 | hypothetical prote |
| 315 | 4 | 44.4 | 137 | 2 | B72335 | (3R)-hydroxymyrist | 388 | 4 | 44.4 | 158 | 2 | F90273 | hypothetical prote |
| 316 | 4 | 44.4 | 137 | 2 | H95190 | conserved domain p | 389 | 4 | 44.4 | 158 | 2 | E86993 | hypothetical prote |
| 317 | 4 | 44.4 | 138 | 1 | RJHU02 | retinoic acid-bind | 390 | 4 | 44.4 | 158 | 2 | T22645 | hypothetical prote |
| 318 | 4 | 44.4 | 138 | 2 | B97224 | ferric uptake regu | 391 | 4 | 44.4 | 159 | 2 | S32014 | dihydrofolate redu |
| 319 | 4 | 44.4 | 138 | 2 | T12631 | DrS12 protein - co | 392 | 4 | 44.4 | 159 | 2 | S77852 | probable phenylala |
| 320 | 4 | 44.4 | 140 | 1 | S57774 | thioredoxin m prec | 393 | 4 | 44.4 | 161 | 2 | B86678 | hypothetical prote |
| 321 | 4 | 44.4 | 140 | 2 | H36851 | RNA-binding ribonu | 394 | 4 | 44.4 | 161 | 2 | T32499 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|---|------|-----|---|--------|--------------------|-----|---|------|-----|---|--------|---------------------|
| 395 | 4 | 44.4 | 162 | 2 | B70144 | transcription fact | 468 | 4 | 44.4 | 187 | 1 | S77378 | polypeptide deform |
| 396 | 4 | 44.4 | 162 | 2 | I58408 | IK factor - human | 469 | 4 | 44.4 | 187 | 2 | AH2190 | polypeptide deform |
| 397 | 4 | 44.4 | 163 | 2 | PC4186 | hemagglutinin 2 ch | 470 | 4 | 44.4 | 188 | 2 | S55057 | SSX1 protein - hum |
| 398 | 4 | 44.4 | 163 | 2 | D84320 | hypothetical prote | 471 | 4 | 44.4 | 188 | 2 | D87694 | hypothetical prote |
| 399 | 4 | 44.4 | 165 | 2 | AC2463 | hypothetical prote | 472 | 4 | 44.4 | 188 | 2 | G75326 | probable 16S rRNA |
| 400 | 4 | 44.4 | 165 | 2 | C97624 | petP protein limpo | 473 | 4 | 44.4 | 189 | 2 | E95000 | peptidyl-tRNA hydr |
| 401 | 4 | 44.4 | 165 | 2 | AD2847 | transcription regu | 474 | 4 | 44.4 | 189 | 2 | E97872 | aminoacyl-tRNA hyd |
| 402 | 4 | 44.4 | 166 | 2 | I69004 | histocompatibility | 475 | 4 | 44.4 | 189 | 2 | D84289 | hypothetical prote |
| 403 | 4 | 44.4 | 166 | 2 | I69005 | histocompatibility | 476 | 4 | 44.4 | 189 | 2 | T48779 | ankyrin repeat-con |
| 404 | 4 | 44.4 | 166 | 2 | I69006 | histocompatibility | 477 | 4 | 44.4 | 190 | 2 | B72416 | conserved hypothet |
| 405 | 4 | 44.4 | 166 | 2 | I69003 | histocompatibility | 478 | 4 | 44.4 | 190 | 2 | H83172 | hypothetical prote |
| 406 | 4 | 44.4 | 167 | 2 | T09686 | TcRP protein homol | 479 | 4 | 44.4 | 190 | 2 | E83103 | hypothetical prote |
| 407 | 4 | 44.4 | 167 | 2 | T06567 | IGF-dependent hist | 480 | 4 | 44.4 | 190 | 2 | H84112 | hypothetical prote |
| 408 | 4 | 44.4 | 167 | 2 | G70436 | hypothetical prote | 481 | 4 | 44.4 | 190 | 2 | C90529 | nuclease, lipoprot |
| 409 | 4 | 44.4 | 167 | 2 | F90090 | 60S ribosomal prot | 482 | 4 | 44.4 | 191 | 2 | A00016 | conserved hypothet |
| 410 | 4 | 44.4 | 168 | 2 | B86861 | hypothetical prote | 483 | 4 | 44.4 | 191 | 2 | T19026 | hypothetical prote |
| 411 | 4 | 44.4 | 168 | 2 | S68355 | heme dI synthesis | 484 | 4 | 44.4 | 191 | 2 | A96765 | hypothetical prote |
| 412 | 4 | 44.4 | 168 | 2 | T45305 | hypothetical prote | 485 | 4 | 44.4 | 191 | 2 | AB1800 | hypothetical prote |
| 413 | 4 | 44.4 | 169 | 2 | G64250 | plasmid surface ex | 486 | 4 | 44.4 | 192 | 2 | B48111 | EF-hand protein EF |
| 414 | 4 | 44.4 | 169 | 2 | A64396 | hypothetical prote | 487 | 4 | 44.4 | 192 | 2 | G95072 | conserved hypothet |
| 415 | 4 | 44.4 | 169 | 2 | AE1166 | transcription regu | 488 | 4 | 44.4 | 192 | 2 | D37940 | conserved hypothet |
| 416 | 4 | 44.4 | 170 | 2 | G90157 | conserved hypothet | 489 | 4 | 44.4 | 192 | 2 | E75318 | transcription term |
| 417 | 4 | 44.4 | 171 | 1 | A42514 | dual specificity p | 490 | 4 | 44.4 | 192 | 2 | E64942 | hypothetical 21.4 |
| 418 | 4 | 44.4 | 171 | 1 | B47452 | dual specificity p | 491 | 4 | 44.4 | 192 | 2 | B90944 | hypothetical prote |
| 419 | 4 | 44.4 | 171 | 1 | I36845 | dual specificity p | 492 | 4 | 44.4 | 192 | 2 | F85792 | hypothetical prote |
| 420 | 4 | 44.4 | 171 | 1 | QQVZH1 | dual specificity p | 493 | 4 | 44.4 | 193 | 2 | H84051 | RNA polymerase ECF |
| 421 | 4 | 44.4 | 171 | 1 | T28522 | probable dual spec | 494 | 4 | 44.4 | 194 | 2 | F69840 | conserved hypothet |
| 422 | 4 | 44.4 | 171 | 2 | B72161 | JLL protein - vari | 495 | 4 | 44.4 | 195 | 2 | D83237 | hypothetical prote |
| 423 | 4 | 44.4 | 171 | 2 | G83829 | hypothetical prote | 496 | 4 | 44.4 | 195 | 2 | AC2527 | hypothetical prote |
| 424 | 4 | 44.4 | 172 | 2 | S73542 | MG428 homolog Cl2 | 497 | 4 | 44.4 | 195 | 2 | C83076 | type 4 fimbrial bi |
| 425 | 4 | 44.4 | 172 | 2 | F83696 | hypothetical prote | 498 | 4 | 44.4 | 196 | 2 | S40728 | hypothetical prote |
| 426 | 4 | 44.4 | 173 | 2 | AF0743 | crossover junction | 499 | 4 | 44.4 | 197 | 2 | C42148 | GTP-binding protei |
| 427 | 4 | 44.4 | 173 | 2 | A85799 | crossover junction | 500 | 4 | 44.4 | 197 | 2 | E69415 | conserved hypothet |
| 428 | 4 | 44.4 | 173 | 2 | D38113 | crossover junction | 501 | 4 | 44.4 | 197 | 2 | H83910 | hypothetical prote |
| 429 | 4 | 44.4 | 173 | 2 | E90950 | Holliday junction | 502 | 4 | 44.4 | 197 | 2 | T24133 | hypothetical prote |
| 430 | 4 | 44.4 | 174 | 2 | D97760 | NADH2 dehydrogenas | 503 | 4 | 44.4 | 197 | 2 | E84606 | probable WRKY-type |
| 431 | 4 | 44.4 | 174 | 2 | G70877 | probable reck prot | 504 | 4 | 44.4 | 197 | 2 | T33525 | hypothetical prote |
| 432 | 4 | 44.4 | 174 | 2 | T02683 | hypothetical prote | 505 | 4 | 44.4 | 198 | 2 | S48994 | hypothetical prote |
| 433 | 4 | 44.4 | 175 | 2 | F82529 | hypothetical prote | 506 | 4 | 44.4 | 199 | 2 | A83195 | conserved hypothet |
| 434 | 4 | 44.4 | 176 | 2 | AD0716 | probable cytochrom | 507 | 4 | 44.4 | 201 | 2 | A53688 | 5-formyltetrahydro |
| 435 | 4 | 44.4 | 176 | 2 | F84110 | hypothetical prote | 508 | 4 | 44.4 | 201 | 2 | G64013 | hypothetical prote |
| 436 | 4 | 44.4 | 176 | 2 | AG2403 | hypothetical prote | 509 | 4 | 44.4 | 201 | 2 | AC1785 | hydrolase (esteras |
| 437 | 4 | 44.4 | 177 | 2 | AB3221 | oxidoreductase wit | 510 | 4 | 44.4 | 201 | 2 | S16899 | alanine-tRNA ligas |
| 438 | 4 | 44.4 | 177 | 2 | E71327 | hypothetical prote | 511 | 4 | 44.4 | 202 | 2 | E97556 | clpp (AF218420) i |
| 439 | 4 | 44.4 | 177 | 2 | G96794 | probable calmoduli | 512 | 4 | 44.4 | 202 | 2 | AC2776 | ATP-dependent Clp |
| 440 | 4 | 44.4 | 177 | 2 | T06170 | resistance protein | 513 | 4 | 44.4 | 202 | 2 | H86689 | prophage ps2 prote |
| 441 | 4 | 44.4 | 177 | 2 | D95278 | conserved hypothet | 514 | 4 | 44.4 | 203 | 2 | H89892 | orateate phosphorib |
| 442 | 4 | 44.4 | 177 | 2 | T31499 | hypothetical prote | 515 | 4 | 44.4 | 204 | 2 | T14834 | plastoquinol-plast |
| 443 | 4 | 44.4 | 178 | 2 | G84357 | probable acetyltra | 516 | 4 | 44.4 | 204 | 2 | D72864 | Acorf-115 protein |
| 444 | 4 | 44.4 | 179 | 2 | G83451 | hypothetical prote | 517 | 4 | 44.4 | 204 | 2 | T41853 | ACMPV orf115 - Bo |
| 445 | 4 | 44.4 | 180 | 2 | H84154 | hypothetical prote | 518 | 4 | 44.4 | 204 | 2 | E70525 | hypothetical prote |
| 446 | 4 | 44.4 | 181 | 2 | I79640 | MHC cell surface a | 519 | 4 | 44.4 | 205 | 2 | T11657 | rho GDP dissociati |
| 447 | 4 | 44.4 | 181 | 2 | I59188 | MHC cell surface g | 520 | 4 | 44.4 | 205 | 2 | T10384 | hypothetical prote |
| 448 | 4 | 44.4 | 181 | 2 | A05087 | lectin beta-1 chai | 521 | 4 | 44.4 | 205 | 2 | A83427 | homoserine kinase |
| 449 | 4 | 44.4 | 181 | 2 | A05088 | lectin beta-2 chai | 522 | 4 | 44.4 | 205 | 2 | JC2558 | flagellar filament |
| 450 | 4 | 44.4 | 181 | 2 | E84676 | hypothetical prote | 523 | 4 | 44.4 | 206 | 2 | JN0874 | GTP-binding protei |
| 451 | 4 | 44.4 | 182 | 2 | A59411 | human leukocyte an | 524 | 4 | 44.4 | 206 | 2 | I37529 | HLA-Cw7 - human (f |
| 452 | 4 | 44.4 | 182 | 2 | D70859 | hypothetical prote | 525 | 4 | 44.4 | 206 | 2 | I37528 | HLA-Cw1 - human (f |
| 453 | 4 | 44.4 | 183 | 2 | B63240 | hypothetical prote | 526 | 4 | 44.4 | 206 | 2 | D95082 | amino acid ABC tra |
| 454 | 4 | 44.4 | 183 | 2 | T21289 | hypothetical prote | 527 | 4 | 44.4 | 206 | 2 | C84408 | hypothetical prote |
| 455 | 4 | 44.4 | 183 | 2 | AD1474 | probable secreted, | 528 | 4 | 44.4 | 206 | 2 | T38251 | hypothetical prote |
| 456 | 4 | 44.4 | 183 | 2 | T47707 | hypothetical prote | 529 | 4 | 44.4 | 206 | 2 | T01366 | hypothetical prote |
| 457 | 4 | 44.4 | 183 | 2 | G97035 | secreted protein, | 530 | 4 | 44.4 | 207 | 2 | A56395 | nitrophorin 1 prec |
| 458 | 4 | 44.4 | 184 | 2 | E98229 | sarcosine oxidase | 531 | 4 | 44.4 | 207 | 2 | D72215 | hypothetical prote |
| 459 | 4 | 44.4 | 184 | 2 | AB3056 | sarcosine oxidase | 532 | 4 | 44.4 | 208 | 2 | S40207 | GTP-binding protei |
| 460 | 4 | 44.4 | 184 | 2 | H66192 | hypothetical prote | 533 | 4 | 44.4 | 208 | 2 | A48567 | calmodulin-ubiquit |
| 461 | 4 | 44.4 | 185 | 2 | S67036 | SPF2 protein - yea | 534 | 4 | 44.4 | 209 | 2 | A86455 | hypothetical prote |
| 462 | 4 | 44.4 | 186 | 2 | F89949 | DNA-3-methyladenin | 535 | 4 | 44.4 | 209 | 2 | S7156 | hypothetical prote |
| 463 | 4 | 44.4 | 186 | 2 | S35057 | NADH2 dehydrogenas | 536 | 4 | 44.4 | 209 | 2 | H69872 | conserved hypothet |
| 464 | 4 | 44.4 | 186 | 2 | E75515 | conserved hypothet | 537 | 4 | 44.4 | 209 | 2 | A85623 | hypothetical prote |
| 465 | 4 | 44.4 | 186 | 2 | B84074 | hypothetical prote | 538 | 4 | 44.4 | 209 | 2 | C90759 | hypothetical prote |
| 466 | 4 | 44.4 | 186 | 2 | AB1493 | probable transcrip | 539 | 4 | 44.4 | 209 | 2 | F64836 | probable membrane |
| 467 | 4 | 44.4 | 186 | 2 | AB1134 | probable transcrip | 540 | 4 | 44.4 | 209 | 2 | C64317 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|---|------|-----|---|--------|--------------------|-----|---|------|-----|---|--------|---------------------|
| 541 | 4 | 44.4 | 210 | 2 | P96551 | hypothetical prote | 614 | 4 | 44.4 | 221 | 2 | A82331 | hypothetical prote |
| 542 | 4 | 44.4 | 210 | 2 | G84899 | hypothetical prote | 615 | 4 | 44.4 | 221 | 2 | C64040 | adenylate kinase (|
| 543 | 4 | 44.4 | 210 | 2 | H72460 | hypothetical prote | 616 | 4 | 44.4 | 222 | 1 | KIBYA | plastoquinol-plast |
| 544 | 4 | 44.4 | 211 | 2 | F75474 | hypothetical prote | 617 | 4 | 44.4 | 222 | 2 | S26193 | plastoquinol-plast |
| 545 | 4 | 44.4 | 211 | 2 | D96960 | uncharacterized pr | 618 | 4 | 44.4 | 222 | 2 | S76297 | plastoquinol-plast |
| 546 | 4 | 44.4 | 211 | 2 | T01627 | probable Arg bindi | 619 | 4 | 44.4 | 222 | 2 | S22470 | plastoquinol-plast |
| 547 | 4 | 44.4 | 211 | 2 | AB3020 | conserved hypothet | 620 | 4 | 44.4 | 222 | 2 | T03540 | cobalamin biosynth |
| 548 | 4 | 44.4 | 211 | 2 | T34501 | hypothetical prote | 621 | 4 | 44.4 | 222 | 2 | B97118 | hypothetical prote |
| 549 | 4 | 44.4 | 212 | 2 | D84203 | hypothetical prote | 622 | 4 | 44.4 | 222 | 2 | AF0658 | phase shock protei |
| 550 | 4 | 44.4 | 212 | 2 | AB2992 | hypothetical prote | 623 | 4 | 44.4 | 222 | 2 | A99864 | phase shock protei |
| 551 | 4 | 44.4 | 212 | 2 | H98291 | hypothetical prote | 624 | 4 | 44.4 | 222 | 2 | B90096 | hypothetical prote |
| 552 | 4 | 44.4 | 213 | 1 | JQ1727 | 22K protein - cani | 625 | 4 | 44.4 | 222 | 2 | A83996 | dolichyl-phosphate |
| 553 | 4 | 44.4 | 213 | 2 | T07603 | NADH2 dehydrogenas | 626 | 4 | 44.4 | 222 | 2 | H85754 | phase shock protei |
| 554 | 4 | 44.4 | 213 | 2 | T44818 | NADH2 dehydrogenas | 627 | 4 | 44.4 | 222 | 2 | C64879 | hemagglutinin HA2 |
| 555 | 4 | 44.4 | 213 | 2 | A26130 | translation initia | 628 | 4 | 44.4 | 223 | 2 | PQ0514 | hypothetical prote |
| 556 | 4 | 44.4 | 213 | 2 | H86692 | hypothetical prote | 629 | 4 | 44.4 | 223 | 2 | F75051 | hypothetical prote |
| 557 | 4 | 44.4 | 214 | 2 | D64442 | conserved hypothet | 630 | 4 | 44.4 | 223 | 2 | E95862 | hypothetical prote |
| 558 | 4 | 44.4 | 214 | 2 | B87424 | outer membrane pro | 631 | 4 | 44.4 | 224 | 2 | C85571 | L4 ribosomal prote |
| 559 | 4 | 44.4 | 215 | 1 | A30807 | plastoquinol-plast | 632 | 4 | 44.4 | 224 | 2 | H72055 | ribosomal protein |
| 560 | 4 | 44.4 | 215 | 1 | CBKL6P | plastoquinol-plast | 633 | 4 | 44.4 | 224 | 2 | S37862 | hypothetical prote |
| 561 | 4 | 44.4 | 215 | 1 | CBLV6 | plastoquinol-plast | 634 | 4 | 44.4 | 224 | 2 | C48652 | transfer protein s |
| 562 | 4 | 44.4 | 215 | 1 | CBNT6 | plastoquinol-plast | 635 | 4 | 44.4 | 225 | 2 | D90570 | hypothetical prote |
| 563 | 4 | 44.4 | 215 | 1 | CBSP6 | plastoquinol-plast | 636 | 4 | 44.4 | 225 | 2 | S36621 | probable drought-1 |
| 564 | 4 | 44.4 | 215 | 1 | CBSP6 | plastoquinol-plast | 637 | 4 | 44.4 | 225 | 2 | F97349 | response regulator |
| 565 | 4 | 44.4 | 215 | 1 | CBZM6R | plastoquinol-plast | 638 | 4 | 44.4 | 225 | 2 | S29950 | surface glycoprote |
| 566 | 4 | 44.4 | 215 | 1 | S09186 | plastoquinol-plast | 639 | 4 | 44.4 | 225 | 2 | S29953 | surface glycoprote |
| 567 | 4 | 44.4 | 215 | 1 | S21253 | plastoquinol-plast | 640 | 4 | 44.4 | 225 | 2 | S29947 | surface glycoprote |
| 568 | 4 | 44.4 | 215 | 1 | S34548 | plastoquinol-plast | 641 | 4 | 44.4 | 225 | 2 | AH0538 | hypothetical prote |
| 569 | 4 | 44.4 | 215 | 1 | XSAC2 | plastoquinol-plast | 642 | 4 | 44.4 | 226 | 2 | G83293 | probable two-compo |
| 570 | 4 | 44.4 | 215 | 2 | S73262 | chloramphenicol O- | 643 | 4 | 44.4 | 226 | 2 | S29948 | surface glycoprote |
| 571 | 4 | 44.4 | 215 | 2 | S78307 | plastoquinol-plast | 644 | 4 | 44.4 | 226 | 2 | AD2198 | hypothetical prote |
| 572 | 4 | 44.4 | 215 | 2 | S14961 | plastoquinol-plast | 645 | 4 | 44.4 | 226 | 2 | B82417 | Cbby family protei |
| 573 | 4 | 44.4 | 215 | 2 | T07266 | plastoquinol-plast | 646 | 4 | 44.4 | 226 | 2 | A70436 | hypothetical prote |
| 574 | 4 | 44.4 | 215 | 2 | T07512 | plastoquinol-plast | 647 | 4 | 44.4 | 226 | 2 | D82597 | phage-related prot |
| 575 | 4 | 44.4 | 215 | 2 | T06863 | plastoquinol-plast | 648 | 4 | 44.4 | 226 | 2 | F71108 | hypothetical prote |
| 576 | 4 | 44.4 | 215 | 2 | AF2233 | plastoquinol-plast | 649 | 4 | 44.4 | 226 | 2 | S29952 | surface glycoprote |
| 577 | 4 | 44.4 | 215 | 2 | B26473 | plastoquinol-plast | 650 | 4 | 44.4 | 226 | 2 | S29951 | surface glycoprote |
| 578 | 4 | 44.4 | 215 | 2 | A49758 | chloramphenicol O- | 651 | 4 | 44.4 | 228 | 2 | AD2874 | tRNA (guanine-N1) - |
| 579 | 4 | 44.4 | 215 | 2 | F96746 | probable drought i | 652 | 4 | 44.4 | 228 | 2 | AD1052 | probable class II |
| 580 | 4 | 44.4 | 215 | 2 | F97825 | S0S ribosomal prot | 653 | 4 | 44.4 | 228 | 2 | H97373 | hypothetical prote |
| 581 | 4 | 44.4 | 215 | 2 | S48826 | NADH2 dehydrogenas | 654 | 4 | 44.4 | 228 | 2 | A13106 | transcription regu |
| 582 | 4 | 44.4 | 215 | 2 | G70575 | hypothetical prote | 655 | 4 | 44.4 | 228 | 2 | C98180 | probable transcript |
| 583 | 4 | 44.4 | 215 | 2 | G97590 | probable membrane | 656 | 4 | 44.4 | 229 | 1 | P8XR10 | nonstructural prot |
| 584 | 4 | 44.4 | 215 | 2 | AF2812 | conserved hypothet | 657 | 4 | 44.4 | 229 | 1 | P8XR10 | nonstructural prot |
| 585 | 4 | 44.4 | 215 | 2 | H97181 | uncharacterized pr | 658 | 4 | 44.4 | 229 | 2 | A20969 | Ig kappa chain pre |
| 586 | 4 | 44.4 | 216 | 2 | T48378 | GTP-binding protei | 659 | 4 | 44.4 | 229 | 2 | H83892 | two-component resp |
| 587 | 4 | 44.4 | 216 | 2 | A71672 | ribosomal protein | 660 | 4 | 44.4 | 229 | 2 | S12593 | nonstructural prot |
| 588 | 4 | 44.4 | 216 | 2 | AG2591 | peptide methionine | 661 | 4 | 44.4 | 229 | 2 | S44640 | hypothetical prote |
| 589 | 4 | 44.4 | 217 | 2 | T12965 | GTP-binding protei | 662 | 4 | 44.4 | 229 | 2 | S58210 | bradyzoite-specifi |
| 590 | 4 | 44.4 | 217 | 2 | T43082 | transfer complex p | 663 | 4 | 44.4 | 230 | 2 | T28284 | hypothetical prote |
| 591 | 4 | 44.4 | 217 | 2 | E70126 | hypothetical prote | 664 | 4 | 44.4 | 230 | 2 | C97104 | hypothetical prote |
| 592 | 4 | 44.4 | 217 | 2 | A82467 | hypothetical prote | 665 | 4 | 44.4 | 231 | 2 | S58245 | BCLV7A protein - hu |
| 593 | 4 | 44.4 | 217 | 2 | C70629 | probable mutT3 pro | 666 | 4 | 44.4 | 231 | 2 | D90427 | hypothetical prote |
| 594 | 4 | 44.4 | 218 | 2 | S37658 | drought-induced pr | 667 | 4 | 44.4 | 231 | 2 | H70157 | hypothetical prote |
| 595 | 4 | 44.4 | 218 | 2 | I72808 | MHC class I HLA-J | 668 | 4 | 44.4 | 231 | 2 | G98264 | hypothetical prote |
| 596 | 4 | 44.4 | 218 | 2 | S52286 | NADH2 dehydrogenas | 669 | 4 | 44.4 | 232 | 1 | S04149 | plastoquinol-plast |
| 597 | 4 | 44.4 | 218 | 2 | H85643 | hypothetical prote | 670 | 4 | 44.4 | 232 | 2 | D97683 | plastoquinol-plast |
| 598 | 4 | 44.4 | 218 | 2 | F90783 | hypothetical prote | 671 | 4 | 44.4 | 232 | 2 | AD2908 | tRNA (guanine-N1) - |
| 599 | 4 | 44.4 | 219 | 1 | H69098 | phosphate transpor | 672 | 4 | 44.4 | 232 | 2 | F55009 | tRNA (guanine-N1) - |
| 600 | 4 | 44.4 | 219 | 2 | T35128 | hypothetical prote | 673 | 4 | 44.4 | 232 | 2 | D97881 | DNA-binding respon |
| 601 | 4 | 44.4 | 219 | 2 | B34323 | GTP-binding protei | 674 | 4 | 44.4 | 232 | 1 | LNLWBA | response regulator |
| 602 | 4 | 44.4 | 219 | 2 | B29224 | GTP-binding protei | 675 | 4 | 44.4 | 233 | 1 | FVVFBA | lectin precursor [|
| 603 | 4 | 44.4 | 219 | 2 | S47177 | lactoylglutathione | 676 | 4 | 44.4 | 233 | 1 | D69630 | flavin precursor - |
| 604 | 4 | 44.4 | 219 | 2 | T08330 | hypothetical prote | 677 | 4 | 44.4 | 233 | 1 | H84322 | menaquinone biosyn |
| 605 | 4 | 44.4 | 220 | 1 | NXEC | exclusion-determin | 678 | 4 | 44.4 | 233 | 2 | T02590 | 30S ribosomal prot |
| 606 | 4 | 44.4 | 220 | 2 | G72472 | hypothetical prote | 679 | 4 | 44.4 | 233 | 2 | C90427 | DNA binding protei |
| 607 | 4 | 44.4 | 220 | 2 | B84304 | hypothetical prote | 680 | 4 | 44.4 | 233 | 2 | T41980 | hypothetical prote |
| 608 | 4 | 44.4 | 220 | 2 | A97216 | superoxide dismuta | 681 | 4 | 44.4 | 234 | 2 | S58581 | plastoquinol-plast |
| 609 | 4 | 44.4 | 220 | 2 | S48450 | hypothetical prote | 682 | 4 | 44.4 | 234 | 2 | D81342 | plastoquinol-plast |
| 610 | 4 | 44.4 | 220 | 2 | T09108 | RNA binding protei | 683 | 4 | 44.4 | 234 | 2 | F70360 | tRNA (guanine-N1) - |
| 611 | 4 | 44.4 | 221 | 2 | D70243 | hypothetical prote | 684 | 4 | 44.4 | 234 | 2 | T07686 | 3-deoxy-manno-octu |
| 612 | 4 | 44.4 | 221 | 2 | S69682 | hypothetical prote | 685 | 4 | 44.4 | 234 | 2 | G83111 | transcription fact |
| 613 | 4 | 44.4 | 221 | 2 | G83998 | mutants block spor | 686 | 4 | 44.4 | 234 | 2 | E96957 | HAD superfamily hy |

| | | | | | | | | | | | | | |
|-----|---|------|-----|---|--------|--------------------|-----|---|------|-----|---|--------|---------------------|
| 687 | 4 | 44.4 | 234 | 2 | AF2214 | hypothenical prote | 760 | 4 | 44.4 | 249 | 2 | AI1196 | B. subtilis yjch p |
| 688 | 4 | 44.4 | 235 | 2 | E69814 | conserved hypotet | 761 | 4 | 44.4 | 249 | 2 | A81892 | probable transpos |
| 689 | 4 | 44.4 | 235 | 2 | E72217 | hypothenical prote | 762 | 4 | 44.4 | 250 | 2 | S07237 | hypothenical prote |
| 690 | 4 | 44.4 | 235 | 2 | AC1800 | hypothenical prote | 763 | 4 | 44.4 | 250 | 2 | G84054 | hypothenical prote |
| 691 | 4 | 44.4 | 235 | 2 | D84919 | hypothenical prote | 764 | 4 | 44.4 | 250 | 2 | F97036 | hypotophan synthas |
| 692 | 4 | 44.4 | 236 | 2 | I57681 | potassium channel | 765 | 4 | 44.4 | 251 | 2 | T43928 | hypotophan synthas |
| 693 | 4 | 44.4 | 236 | 2 | G90007 | purine nucleoside | 766 | 4 | 44.4 | 251 | 2 | S69021 | hypotophan synthas |
| 694 | 4 | 44.4 | 236 | 2 | T02432 | ethylene-responsiv | 767 | 4 | 44.4 | 251 | 2 | A84807 | probable acid phos |
| 695 | 4 | 44.4 | 236 | 2 | T36579 | probable RNA polym | 768 | 4 | 44.4 | 251 | 2 | T14407 | pectin esterase ho |
| 696 | 4 | 44.4 | 236 | 2 | T50280 | probable oxidoredu | 769 | 4 | 44.4 | 251 | 2 | B1298 | hypotophical prote |
| 697 | 4 | 44.4 | 237 | 2 | S64718 | formin-binding pro | 770 | 4 | 44.4 | 251 | 2 | F70683 | probable lipoprote |
| 698 | 4 | 44.4 | 237 | 2 | T27198 | hypotophical prote | 771 | 4 | 44.4 | 251 | 2 | AH2520 | hypotophical prote |
| 699 | 4 | 44.4 | 238 | 2 | AC2043 | heme oxygenase [im | 772 | 4 | 44.4 | 251 | 2 | H90568 | conserved hypotet |
| 700 | 4 | 44.4 | 238 | 2 | D49316 | ribosomal protein | 773 | 4 | 44.4 | 252 | 2 | AC2291 | tRNA methyltransfe |
| 701 | 4 | 44.4 | 238 | 2 | B84951 | hypotophical prote | 774 | 4 | 44.4 | 252 | 2 | T35989 | probable translati |
| 702 | 4 | 44.4 | 239 | 2 | B89967 | serine proteinase | 775 | 4 | 44.4 | 252 | 2 | H69491 | cell division initi |
| 703 | 4 | 44.4 | 239 | 2 | E64961 | probable transcrip | 776 | 4 | 44.4 | 252 | 2 | E83747 | transcription anti |
| 704 | 4 | 44.4 | 239 | 2 | B85815 | probable 2-compone | 777 | 4 | 44.4 | 252 | 2 | A64492 | toxin sensitivity |
| 705 | 4 | 44.4 | 239 | 2 | C09607 | probable 2-compone | 778 | 4 | 44.4 | 253 | 2 | AF0916 | uridine phosphoryl |
| 706 | 4 | 44.4 | 239 | 2 | F96908 | uncharacterized co | 779 | 4 | 44.4 | 253 | 2 | T46830 | uridine phosphoryl |
| 707 | 4 | 44.4 | 239 | 2 | A75164 | hypotophical prote | 780 | 4 | 44.4 | 253 | 2 | S05491 | uridine phosphoryl |
| 708 | 4 | 44.4 | 239 | 2 | G89867 | hypotophical prote | 781 | 4 | 44.4 | 253 | 2 | G86070 | uridine phosphoryl |
| 709 | 4 | 44.4 | 239 | 2 | E84232 | hypotophical prote | 782 | 4 | 44.4 | 253 | 2 | A98224 | uridine phosphoryl |
| 710 | 4 | 44.4 | 239 | 2 | F86738 | hypotophical prote | 783 | 4 | 44.4 | 253 | 2 | A10460 | uridine phosphoryl |
| 711 | 4 | 44.4 | 239 | 2 | F97542 | hypotophical prote | 784 | 4 | 44.4 | 253 | 2 | T36867 | hypotophical prote |
| 712 | 4 | 44.4 | 239 | 2 | T16829 | hypotophical prote | 785 | 4 | 44.4 | 254 | 2 | B72366 | conserved hypotet |
| 713 | 4 | 44.4 | 241 | 1 | BVFCPU | peripheral membran | 786 | 4 | 44.4 | 254 | 2 | E90054 | hypotophical prote |
| 714 | 4 | 44.4 | 241 | 2 | AH3270 | tRNA (guanine-N1) | 787 | 4 | 44.4 | 255 | 2 | I54307 | MHC H1A-A30JS heav |
| 715 | 4 | 44.4 | 241 | 2 | B82879 | pseudouridylate sy | 788 | 4 | 44.4 | 255 | 2 | F89769 | hypotophical prote |
| 716 | 4 | 44.4 | 241 | 2 | D86057 | hypotophical prote | 789 | 4 | 44.4 | 255 | 2 | T46946 | phosphonoacetaldeh |
| 717 | 4 | 44.4 | 241 | 2 | D91211 | hypotophical prote | 790 | 4 | 44.4 | 255 | 2 | AH2479 | transcription regu |
| 718 | 4 | 44.4 | 241 | 2 | PQ0624 | envelope protein - | 791 | 4 | 44.4 | 256 | 2 | T12396 | NADH2 dehydrogenas |
| 719 | 4 | 44.4 | 241 | 2 | PQ0623 | envelope protein - | 792 | 4 | 44.4 | 256 | 2 | T16661 | hypotophical prote |
| 720 | 4 | 44.4 | 241 | 2 | PQ0620 | envelope protein - | 793 | 4 | 44.4 | 256 | 2 | F84612 | hypotophical prote |
| 721 | 4 | 44.4 | 241 | 2 | H81327 | hypotophical prote | 794 | 4 | 44.4 | 257 | 2 | G64402 | hypotophical prote |
| 722 | 4 | 44.4 | 242 | 1 | BVFCRO | DNA repair protein | 795 | 4 | 44.4 | 257 | 2 | T40880 | hypotophical prote |
| 723 | 4 | 44.4 | 242 | 2 | AI0828 | DNA repair protein | 796 | 4 | 44.4 | 258 | 1 | SNBY3 | proteasome endopep |
| 724 | 4 | 44.4 | 242 | 2 | D85902 | DNA repair protein | 797 | 4 | 44.4 | 258 | 2 | A43692 | T1 protein - rabbi |
| 725 | 4 | 44.4 | 242 | 2 | G91057 | DNA repair protein | 798 | 4 | 44.4 | 258 | 2 | AG0459 | Sec-independent pr |
| 726 | 4 | 44.4 | 242 | 2 | PQ0625 | envelope protein - | 799 | 4 | 44.4 | 258 | 2 | B82249 | uridine phosphoryl |
| 727 | 4 | 44.4 | 242 | 2 | PQ0626 | envelope protein - | 800 | 4 | 44.4 | 259 | 1 | PMWBM | bisphosphoglycerat |
| 728 | 4 | 44.4 | 242 | 2 | H83829 | hypotophical prote | 801 | 4 | 44.4 | 259 | 2 | T12386 | NADH2 dehydrogenas |
| 729 | 4 | 44.4 | 242 | 2 | AB1091 | autolysin, N-acety | 802 | 4 | 44.4 | 259 | 2 | C64059 | uridine phosphoryl |
| 730 | 4 | 44.4 | 242 | 2 | AI1454 | autolysin (N-acety | 803 | 4 | 44.4 | 259 | 2 | G83966 | dihydroxotrate deh |
| 731 | 4 | 44.4 | 242 | 2 | PQ0621 | envelope protein - | 804 | 4 | 44.4 | 259 | 2 | C81168 | conserved hypotet |
| 732 | 4 | 44.4 | 243 | 2 | T26432 | hypotophical prote | 805 | 4 | 44.4 | 259 | 2 | F81937 | hypotophical prote |
| 733 | 4 | 44.4 | 243 | 2 | I54459 | MHC H-2K1-k - mous | 806 | 4 | 44.4 | 260 | 1 | KLBOB | calcium-binding pr |
| 734 | 4 | 44.4 | 244 | 2 | T29079 | hypotophical prote | 807 | 4 | 44.4 | 260 | 2 | T12395 | NADH2 dehydrogenas |
| 735 | 4 | 44.4 | 244 | 2 | T41594 | conserved hypotet | 808 | 4 | 44.4 | 260 | 2 | T12387 | NADH2 dehydrogenas |
| 736 | 4 | 44.4 | 244 | 2 | E64490 | hypotophical prote | 809 | 4 | 44.4 | 260 | 2 | T12394 | NADH2 dehydrogenas |
| 737 | 4 | 44.4 | 244 | 2 | A39365 | cyanamide hydrat | 810 | 4 | 44.4 | 260 | 2 | T12390 | NADH2 dehydrogenas |
| 738 | 4 | 44.4 | 244 | 2 | E97085 | hypotophical prote | 811 | 4 | 44.4 | 260 | 2 | T12397 | NADH2 dehydrogenas |
| 739 | 4 | 44.4 | 245 | 2 | A83856 | 2-heptaprenyl-1,4- | 812 | 4 | 44.4 | 260 | 2 | T12393 | NADH2 dehydrogenas |
| 740 | 4 | 44.4 | 245 | 2 | E69511 | hypotophical prote | 813 | 4 | 44.4 | 260 | 2 | T14435 | NADH2 dehydrogenas |
| 741 | 4 | 44.4 | 246 | 2 | G83959 | tRNA methyltransfe | 814 | 4 | 44.4 | 260 | 2 | T12392 | NADH2 dehydrogenas |
| 742 | 4 | 44.4 | 246 | 2 | B69311 | proteasome, subuni | 815 | 4 | 44.4 | 260 | 2 | I52551 | carbonate dehydrat |
| 743 | 4 | 44.4 | 246 | 2 | S47805 | hypotophical 27.4K | 816 | 4 | 44.4 | 260 | 2 | H97357 | stage 0 sporulatio |
| 744 | 4 | 44.4 | 246 | 2 | F72769 | hypotophical prote | 817 | 4 | 44.4 | 260 | 2 | A70329 | hypotophical prote |
| 745 | 4 | 44.4 | 246 | 2 | T25532 | hypotophical prote | 818 | 4 | 44.4 | 260 | 2 | G75301 | hypotophical prote |
| 746 | 4 | 44.4 | 247 | 2 | A57112 | carbonate dehydrat | 819 | 4 | 44.4 | 260 | 2 | E90984 | probable glycosyl |
| 747 | 4 | 44.4 | 247 | 2 | AF2182 | hypotophical prote | 820 | 4 | 44.4 | 260 | 2 | T28182 | hypotophical prote |
| 748 | 4 | 44.4 | 247 | 2 | T33288 | hypotophical prote | 821 | 4 | 44.4 | 260 | 2 | H85829 | glycosyl transfe |
| 749 | 4 | 44.4 | 247 | 2 | B86157 | hypotophical prote | 822 | 4 | 44.4 | 260 | 2 | T12398 | NADH2 dehydrogenas |
| 750 | 4 | 44.4 | 248 | 2 | ACO630 | response regulator | 823 | 4 | 44.4 | 260 | 2 | T12391 | NADH2 dehydrogenas |
| 751 | 4 | 44.4 | 248 | 2 | D69460 | COH nickel-insert | 824 | 4 | 44.4 | 261 | 1 | A34955 | calcium-binding pr |
| 752 | 4 | 44.4 | 248 | 2 | B81077 | stationary-phase s | 825 | 4 | 44.4 | 261 | 1 | KLRTB | calcium-binding pr |
| 753 | 4 | 44.4 | 248 | 2 | H81864 | SurE protein NMA16 | 826 | 4 | 44.4 | 261 | 1 | S00234 | calcium-binding pr |
| 754 | 4 | 44.4 | 248 | 2 | S75632 | hypotophical prote | 827 | 4 | 44.4 | 262 | 2 | A33470 | fibroin light chai |
| 755 | 4 | 44.4 | 248 | 2 | T18315 | hypotophical prote | 828 | 4 | 44.4 | 263 | 2 | H85376 | hypotophical prote |
| 756 | 4 | 44.4 | 248 | 2 | E64898 | H-repeat-associat | 829 | 4 | 44.4 | 263 | 2 | T04634 | hypotophical prote |
| 757 | 4 | 44.4 | 248 | 2 | A86213 | glycerophosphoryl | 830 | 4 | 44.4 | 264 | 2 | E83923 | hypotophical prote |
| 758 | 4 | 44.4 | 248 | 2 | AH3073 | glycerophosphodie | 831 | 4 | 44.4 | 265 | 2 | T40259 | hypotophical prote |
| 759 | 4 | 44.4 | 249 | 2 | D64310 | nucleotide-binding | 832 | 4 | 44.4 | 265 | 2 | T28102 | hypotophical prote |

| | | | | | | | | | | | | | |
|-----|---|------|-----|---|--------|----------------------|-----|---|------|-----|---|--------|--------------------|
| 833 | 4 | 44.4 | 266 | 2 | T09281 | embryonic abundant | 906 | 4 | 44.4 | 282 | 2 | B71601 | probable integral |
| 834 | 4 | 44.4 | 266 | 2 | E71230 | hypothetical prote | 907 | 4 | 44.4 | 282 | 2 | H97226 | protein containing |
| 835 | 4 | 44.4 | 267 | 2 | B84213 | hypothetical prote | 908 | 4 | 44.4 | 283 | 2 | T24646 | hypothetical prote |
| 836 | 4 | 44.4 | 267 | 2 | T46202 | endoxylglucan tra | 909 | 4 | 44.4 | 283 | 2 | H65154 | probable transpos |
| 837 | 4 | 44.4 | 268 | 2 | C81325 | probable periplasm | 910 | 4 | 44.4 | 283 | 2 | D64448 | hypothetical prote |
| 838 | 4 | 44.4 | 269 | 1 | R5BYL3 | ribosomal protein | 911 | 4 | 44.4 | 283 | 2 | B98040 | pyridoxal/pyridoxi |
| 839 | 4 | 44.4 | 269 | 2 | S61555 | xyloglucan endo-1, | 912 | 4 | 44.4 | 283 | 2 | E85884 | pyridoxal/pyridoxi |
| 840 | 4 | 44.4 | 269 | 2 | S73816 | MG374 homolog G12, | 913 | 4 | 44.4 | 283 | 2 | A65016 | pyridoxal kinase (|
| 841 | 4 | 44.4 | 269 | 2 | AH0555 | phosphonacetaldeh | 914 | 4 | 44.4 | 284 | 2 | S77554 | hypothetical prote |
| 842 | 4 | 44.4 | 269 | 2 | A82240 | conserved hypoteth | 915 | 4 | 44.4 | 284 | 2 | T39813 | hypothetical prote |
| 843 | 4 | 44.4 | 269 | 2 | T36910 | hypothetical prote | 916 | 4 | 44.4 | 284 | 2 | S08385 | hypothetical prote |
| 844 | 4 | 44.4 | 270 | 1 | HLR028 | MHC class I histoc | 917 | 4 | 44.4 | 284 | 2 | A43721 | nodO protein - Rhi |
| 845 | 4 | 44.4 | 270 | 2 | AD1409 | hydrolase (esteras | 918 | 4 | 44.4 | 285 | 2 | T20237 | module formation p |
| 846 | 4 | 44.4 | 270 | 2 | G83418 | probable enoyl-CoA | 919 | 4 | 44.4 | 285 | 2 | G87298 | hypothetical prote |
| 847 | 4 | 44.4 | 270 | 2 | AF2159 | hypothetical prote | 920 | 4 | 44.4 | 285 | 2 | A69748 | short chain dehydr |
| 848 | 4 | 44.4 | 270 | 2 | F64460 | hypothetical prote | 921 | 4 | 44.4 | 285 | 2 | T23183 | hypothetical prote |
| 849 | 4 | 44.4 | 270 | 2 | T22213 | hypothetical prote | 922 | 4 | 44.4 | 286 | 2 | G75407 | transaldolase - De |
| 850 | 4 | 44.4 | 270 | 2 | AE1127 | conserved hypoteth | 923 | 4 | 44.4 | 286 | 2 | G85230 | hypothetical prote |
| 851 | 4 | 44.4 | 270 | 2 | AI1487 | conserved hypoteth | 924 | 4 | 44.4 | 286 | 2 | F84403 | hypothetical prote |
| 852 | 4 | 44.4 | 271 | 2 | E84138 | biotin synthetasis B | 925 | 4 | 44.4 | 286 | 2 | B71663 | hypothetical prote |
| 853 | 4 | 44.4 | 271 | 2 | AB2956 | cell division inhi | 926 | 4 | 44.4 | 286 | 2 | T39404 | hypothetical prote |
| 854 | 4 | 44.4 | 271 | 2 | C98327 | cell division inhi | 927 | 4 | 44.4 | 286 | 2 | A90281 | ABC transporter, A |
| 855 | 4 | 44.4 | 271 | 2 | A96011 | probable cell divi | 928 | 4 | 44.4 | 287 | 2 | D83856 | hypothetical prote |
| 856 | 4 | 44.4 | 271 | 2 | H84337 | spermidine/purasc | 929 | 4 | 44.4 | 287 | 2 | AF3372 | hypothetical prote |
| 857 | 4 | 44.4 | 271 | 2 | B82438 | phosphonacetaldeh | 930 | 4 | 44.4 | 288 | 2 | D97113 | ABC transporter AT |
| 858 | 4 | 44.4 | 271 | 2 | C96010 | conserved hypoteth | 931 | 4 | 44.4 | 288 | 2 | F84042 | probable Grpase (Y |
| 859 | 4 | 44.4 | 272 | 2 | AB1458 | dipeptide ABC tran | 932 | 4 | 44.4 | 288 | 2 | T21770 | hypothetical prote |
| 860 | 4 | 44.4 | 272 | 2 | C86539 | CT041 hypothetical | 933 | 4 | 44.4 | 289 | 2 | H84205 | hypothetical prote |
| 861 | 4 | 44.4 | 272 | 2 | C72084 | conserved hypoteth | 934 | 4 | 44.4 | 289 | 2 | E81259 | hypothetical prote |
| 862 | 4 | 44.4 | 273 | 1 | HLR04W | MHC class I histoc | 935 | 4 | 44.4 | 290 | 2 | F89952 | hypothetical prote |
| 863 | 4 | 44.4 | 273 | 1 | HLR069 | MHC class I histoc | 936 | 4 | 44.4 | 290 | 2 | C72259 | hypothetical prote |
| 864 | 4 | 44.4 | 273 | 2 | I38509 | MHC class I histoc | 937 | 4 | 44.4 | 290 | 2 | AF1133 | hypothetical prote |
| 865 | 4 | 44.4 | 273 | 2 | T34740 | MHC class I histoc | 938 | 4 | 44.4 | 291 | 2 | AC1302 | hypothetical prote |
| 866 | 4 | 44.4 | 273 | 2 | D90516 | esterase/lipase 1 | 939 | 4 | 44.4 | 291 | 2 | AC1674 | hypothetical prote |
| 867 | 4 | 44.4 | 273 | 2 | T39446 | conserved hypoteth | 940 | 4 | 44.4 | 291 | 2 | S67672 | hypothetical prote |
| 868 | 4 | 44.4 | 274 | 1 | HLR032 | MHC class I histoc | 941 | 4 | 44.4 | 291 | 2 | S48990 | hypothetical prote |
| 869 | 4 | 44.4 | 274 | 2 | I68774 | MHC HLA-B39 chain | 942 | 4 | 44.4 | 291 | 2 | T00855 | hypothetical prote |
| 870 | 4 | 44.4 | 274 | 2 | I54463 | MHC HLA-B38 chain | 943 | 4 | 44.4 | 292 | 2 | D98096 | conserved hypoteth |
| 871 | 4 | 44.4 | 274 | 2 | SI6647 | sporulation dipept | 944 | 4 | 44.4 | 292 | 2 | B95232 | conserved hypoteth |
| 872 | 4 | 44.4 | 274 | 2 | JC4294 | ammonia monooxyge | 945 | 4 | 44.4 | 292 | 2 | T02737 | probable ubiquitin |
| 873 | 4 | 44.4 | 274 | 2 | G84353 | hypothetical prote | 946 | 4 | 44.4 | 292 | 2 | B90501 | conserved hypoteth |
| 874 | 4 | 44.4 | 274 | 2 | D97653 | hypothetical prote | 947 | 4 | 44.4 | 292 | 2 | S64361 | hypothetical prote |
| 875 | 4 | 44.4 | 274 | 2 | AB2877 | conserved hypoteth | 948 | 4 | 44.4 | 293 | 2 | E49539 | xyloglucan endo-1, |
| 876 | 4 | 44.4 | 274 | 2 | T22214 | hypothetical prote | 949 | 4 | 44.4 | 294 | 1 | DNCHFM | hypothetical prote |
| 877 | 4 | 44.4 | 274 | 2 | S24439 | class I histocompa | 950 | 4 | 44.4 | 294 | 2 | G83962 | hypothetical prote |
| 878 | 4 | 44.4 | 275 | 1 | LNPM | lectin precursor - | 951 | 4 | 44.4 | 295 | 1 | S29399 | homeotic protein m |
| 879 | 4 | 44.4 | 275 | 2 | S05299 | hypothetical prote | 952 | 4 | 44.4 | 295 | 2 | D69534 | conserved hypoteth |
| 880 | 4 | 44.4 | 276 | 2 | T18742 | hypothetical prote | 953 | 4 | 44.4 | 296 | 2 | A41730 | nucleophosmin NO38 |
| 881 | 4 | 44.4 | 276 | 2 | A84361 | hypothetical prote | 954 | 4 | 44.4 | 296 | 2 | PC1085 | coat protein homol |
| 882 | 4 | 44.4 | 276 | 2 | F95936 | conserved hypoteth | 955 | 4 | 44.4 | 296 | 2 | B40257 | N-acetylglucosyl-L |
| 883 | 4 | 44.4 | 277 | 2 | T34779 | tRNA (guanine-N1) - | 956 | 4 | 44.4 | 297 | 1 | I39938 | RNA15 protein - Ye |
| 884 | 4 | 44.4 | 277 | 2 | T51975 | proteasome endopep | 957 | 4 | 44.4 | 297 | 2 | G69950 | 6-phosphogluconate |
| 885 | 4 | 44.4 | 277 | 2 | C84463 | hypothetical prote | 958 | 4 | 44.4 | 297 | 2 | S33927 | interphotoreceptor |
| 886 | 4 | 44.4 | 277 | 2 | C90574 | ABC transporter pe | 959 | 4 | 44.4 | 297 | 2 | A69968 | phage-related lyti |
| 887 | 4 | 44.4 | 277 | 2 | B88397 | protein H04J21.2 [| 960 | 4 | 44.4 | 297 | 2 | D83825 | hypothetical prote |
| 888 | 4 | 44.4 | 277 | 2 | T17911 | hypothetical prote | 961 | 4 | 44.4 | 297 | 2 | AH2358 | hypothetical prote |
| 889 | 4 | 44.4 | 278 | 1 | S39900 | multicatalytic end | 962 | 4 | 44.4 | 298 | 1 | A69879 | conserved hypoteth |
| 890 | 4 | 44.4 | 278 | 2 | T51974 | proteasome endopep | 963 | 4 | 44.4 | 298 | 2 | S44994 | class I histocompa |
| 891 | 4 | 44.4 | 278 | 2 | G89827 | conserved hypoteth | 964 | 4 | 44.4 | 298 | 2 | T24029 | hypothetical prote |
| 892 | 4 | 44.4 | 279 | 2 | C81381 | orotidine 5'-phosp | 965 | 4 | 44.4 | 298 | 2 | H83863 | modulation of CheA |
| 893 | 4 | 44.4 | 279 | 2 | T09620 | probable lectin 2 | 966 | 4 | 44.4 | 298 | 2 | B75096 | glycosyl transfera |
| 894 | 4 | 44.4 | 279 | 2 | JC4327 | uridine phosphoryl | 967 | 4 | 44.4 | 298 | 2 | B83984 | 6-phosphogluconate |
| 895 | 4 | 44.4 | 280 | 2 | E75216 | hypothetical prote | 968 | 4 | 44.4 | 298 | 2 | B35272 | osteoinductive fac |
| 896 | 4 | 44.4 | 280 | 2 | C71453 | hypothetical prote | 969 | 4 | 44.4 | 298 | 2 | JC4130 | osteoglycin precur |
| 897 | 4 | 44.4 | 280 | 2 | E75216 | NADH2 dehydrogenas | 970 | 4 | 44.4 | 298 | 2 | C55223 | minor tail protein |
| 898 | 4 | 44.4 | 281 | 1 | S26018 | outer membrane pro | 971 | 4 | 44.4 | 298 | 2 | E90172 | hypothetical prote |
| 899 | 4 | 44.4 | 281 | 2 | D70213 | protoporphyrinogen | 972 | 4 | 44.4 | 298 | 2 | AD2715 | ABC transporter, m |
| 900 | 4 | 44.4 | 282 | 2 | G70309 | probable membrane | 973 | 4 | 44.4 | 299 | 2 | D97403 | rbsK protein (AJ00 |
| 901 | 4 | 44.4 | 282 | 2 | AC2294 | hypothetical prote | 974 | 4 | 44.4 | 299 | 2 | AD2621 | ribokinase [import |
| 902 | 4 | 44.4 | 282 | 2 | S61663 | hypothetical prote | 975 | 4 | 44.4 | 299 | 2 | C97030 | arginase [imported |
| 903 | 4 | 44.4 | 282 | 2 | T39471 | hypothetical prote | 976 | 4 | 44.4 | 299 | 2 | I46937 | tissue factor path |
| 904 | 4 | 44.4 | 282 | 2 | T03250 | calmodulin-binding | 977 | 4 | 44.4 | 299 | 2 | A35272 | osteoinductive fac |
| 905 | 4 | 44.4 | 282 | 2 | F82867 | conserved hypoteth | 978 | 4 | 44.4 | 300 | 2 | S12143 | lipoprotein-associ |

979 4 44.4 300 2 B49238 gamma-hemolysin ga
980 4 44.4 301 2 AD0660 probable transcrip
981 4 44.4 301 2 H69508 formylmethanofuran
982 4 44.4 301 2 C69524 deoxyhypusine synt
983 4 44.4 301 2 T24651 hypothetical prote
984 4 44.4 302 1 PAF1A phosphoprotein pho
985 4 44.4 302 2 B35961 hypothetical 21K p
986 4 44.4 302 2 H90717 hypothetical prote
987 4 44.4 302 2 A71709 hypothetical prote
988 4 44.4 302 2 T21843 hypothetical prote
989 4 44.4 303 2 B45067 laminin B1 chain -
990 4 44.4 304 2 A49185 interphotoreceptor
991 4 44.4 304 2 T28891 hypothetical prote
992 4 44.4 304 2 D59100 hypothetical prote
993 4 44.4 304 2 A86842 conserved hypothet
994 4 44.4 304 2 B86641 hypothetical prote
995 4 44.4 305 2 T08836 probable metallopr
996 4 44.4 305 2 D75306 purine nucleoside
997 4 44.4 305 2 F69748 hypothetical prote
998 4 44.4 305 2 B82873 conserved hypothet
999 4 44.4 305 2 T23929 hypothetical prote
1000 4 44.4 306 2 S47906 PAD synthetase - y

ALIGNMENTS

RESULT 1
WZVZB1
vaccinia virus 18K HindIII-C protein - vaccinia virus (strain Ankara and WR)
N:Alternate names: C7L protein; host range protein
C:Species: vaccinia virus
A:Variety: strain Ankara
C:Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A33348; G42503; T30771
R:Kotwal, G.J.; Moss, B.
Virology 167, 524-537, 1988
A:Title: Analysis of a large cluster of nonessential genes deleted from a vaccinia virus
A:Reference number: A94385; MUID:89073756; PMID:2849238
A:Accession: A33348
A:Molecule type: DNA
A:Residues: 1-150 <KOT>
A:Cross-references: UNIPROT:P17363; UNIPARC:UPI00000001F9; GB:M22812; NID:G335691; PIDN:
A:Experimental source: strain WR
R:Johnson, G.P.
submitted to GenBank, June 1990
A:Reference number: A33172
A:Accession: G42503
A:Molecule type: DNA
A:Residues: 1-150 <JOH>
A:Cross-references: UNIPARC:UPI00000001F9
A:Experimental source: strain Copenhagen
R:Antoine, G.; Scheiflinger, P.; Falkner, F.G.; Dorner, F.
submitted to the EMBL Data Library, March 1997
A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain
A:Reference number: Z20877
A:Accession: T30771
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-150 <ANT>
A:Cross-references: UNIPARC:UPI00000001F9; EMBL:U94848; PIDN:AAB96405.1
A:Experimental source: strain Ankara
C:Genetics:
A>Note: MVA018L
C:Superfamily: host range protein, vaccinia C7L type
C:Keywords: early protein

Query Match 100.0%; Score 9; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDTFYV 9
|||||

Db 74 KVDDTFYV 82
RESULT 2
H36837
D8L protein - variola virus (strain India-1967)
C:Species: variola virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: H36837
R:Shinov, V.M.
submitted to GenBank, November 1992
A:Reference number: A36859
A:Accession: H36837
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-150 <BLI>
A:Cross-references: UNIPROT:P33860; UNIPARC:UPI00000000732; GB:X69198; NID:G456758; PIDN:
C:Superfamily: host range protein, vaccinia C7L type

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
|||||
Db 74 KVDDTFYV 82

RESULT 3
T28446
hypothetical protein D111 - variola major virus
C:Species: variola major virus
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28446
R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
A:Reference number: Z20488; MUID:94088747; PMID:8264798
A:Accession: T28446
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-150 <MAS>
A:Cross-references: UNIPROT:P33860; UNIPARC:UPI00000000732; EMBL:L22579; NID:G623595; PID
A:Experimental source: strain "Bangladesh-1975"
C:Superfamily: host range protein, vaccinia C7L type

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
|||||
Db 74 KVDDTFYV 82

RESULT 4
F72151
B14L protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
C:Accession: F72151
R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A:Reference number: A72150
A:Accession: F72151
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-150 <SHC>
A:Cross-references: UNIPROT:P33860; UNIPARC:UPI00000000732; GB:Y16780; NID:G5830555; PIDN:
A:Experimental source: strain Garcia-1966
C:Genetics:
A:Gene: B14L

C;Superfamily: host range protein, vaccinia C7L type

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDPTFYV 9
|||||
Db 74 KVDPTFYV 82

RESULT 5

S75042
Hypothetical protein sl11608 - *Synechocystis* sp. (strain PCC 6803)
C;Species: *Synechocystis* sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75042
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75042
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-770 <KAN>
A;Cross-references: UNIPROT:P73845; UNIPARC:UPI00000C0DCB; EMBL:D90910; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 77.8%; Score 7; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFYX 8
|||||
Db 286 VDDTFYX 292

RESULT 6

C36365
transforming protein homolog MRAS3 - *Rhizomucor racemosus*
C;Species: *Rhizomucor racemosus*
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Accession: C36365
R;Casale, W.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
Mol. Cell. Biol. 10, 6654-6663, 1990
A;Title: Expression of a gene family in the dimorphic fungus *Mucor racemosus* which exhib
A;Reference number: A36365; MUID:91061774; PMID:1701021
A;Accession: C36365
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <CAS>
A;Cross-references: UNIPROT:P22280; UNIPARC:UPI000017642D; GB:M55177
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; nucleotide binding; P-loop
F;11-126/Domain: translation elongation factor Tu homology <ETU>
F;17-24/Region: nucleotide-binding motif A (P-loop)
F;123-126/Region: nucleotide-binding motif A (P-loop)
F;153-155/Region: GTP-binding NKAD motif
F;23,24,42,123,124,126,153/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #sta

Query Match 66.7%; Score 6; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFYX 7
|||||
Db 160 VDDTFYX 165

RESULT 7

B81169

tryptophan synthase, beta chain NMB0699 [imported] - *Neisseria meningitidis* (strain MCS
C;Species: *Neisseria meningitidis*
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81169
R;Rettelein, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MCS8.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: B81169
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-400 <TET>
A;Cross-references: UNIPROT:Q9K0B5; UNIPARC:UPI000013751E; GB:AE002424; GB:AE002098; NI
A;Experimental source: serogroup B, strain MCS8
C;Genetics:
A;Gene: NMB0699
C;Superfamily: tryptophan synthase beta chain; tryptophan synthase beta chain homology

Query Match 66.7%; Score 6; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
|||||
Db 186 VDDTFY 191

RESULT 8

H81936
probable tryptophan synthase (EC 4.2.1.20) beta chain NMA0904 [imported] - *Neisseria me*
C;Species: *Neisseria meningitidis*
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: H81936
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrea
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: H81936
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-400 <PAR>
A;Cross-references: UNIPROT:Q9JVC0; UNIPARC:UPI000013751D; GB:AL162754; GB:AL157959; NI
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: trpB; NMA0904
C;Superfamily: tryptophan synthase beta chain; tryptophan synthase beta chain homology
C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 66.7%; Score 6; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
|||||
Db 186 VDDTFY 191

RESULT 9

S31478
alpha-amylase (EC 3.2.1.1) - *Thermoactinomyces vulgaris*
C;Species: *Thermoactinomyces vulgaris*
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
C;Accession: S31478
R;Hofemeister, B.; Koenig, S.; Hoang, V.; Engel, J.; Mayer, G.; Heese, O.; Hansen, G.; I
submitted to the EMBL Data Library, December 1992
A;Description: The gene amyTV coding for a non-glucogenic alpha-amylase from *Thermoacti*
A;Reference number: S31478
A;Accession: S31478

A;Molecule type: DNA
A;Residues: 1-482 <HOF>
A;Cross-references: UNIPROT:Q60051; UNIPARC:UPI00000B6F58; EMBL:X69807; NID:g48289; PIDN
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
C;Superfamily: cyclomaltohextrin glucanotransferase/alpha-amylase; alpha-amylase core ho
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;194-319/Domain: alpha-amylase core homology <AMY>

Query Match 66.7%; Score 6; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
|||||
Db 409 VDDTFY 414

RESULT 10
C86143
hypothetical protein F6F3.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86143
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C86143
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-485 <STO>
A;Cross-references: UNIPROT:Q9LNU3; UNIPARC:UPI000009E0P7; GB:AE005172; NID:g9665144; PI
C;Genetics:
A;Map position: 1

Query Match 66.7%; Score 6; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
|||||
Db 327 DTFYV 332

RESULT 11
T47790
hypothetical protein F17J16.130 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47790
R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; I
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24476
A;Accession: T47790
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-535 <DAN>
A;Cross-references: UNIPROT:Q9LXS8; UNIPARC:UPI00000AC14B; EMBL:AL163527
A;Experimental source: Cultivar Columbia; BAC clone F17J16
C;Genetics:
A;Map position: 3
A;Note: F17J16.130

Query Match 66.7%; Score 6; DB 2; Length 535;

Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
|||||
Db 374 DTFYV 379

RESULT 12
T26101
hypothetical protein W02B8.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26101
R;Sims, M.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z20151
A;Accession: T26101
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-1256 <WIL>
A;Cross-references: UNIPROT:Q9XVH4; UNIPARC:UPI0000081416; EMBL:Z81136; PIDN:CAB03458.1;
A;Experimental source: clone W02B8
C;Genetics:
A;Gene: CESP:W02B8.2
A;Map position: 2
A;Introns: 27/3; 327/3; 670/3; 949/3; 1073/3

Query Match 66.7%; Score 6; DB 2; Length 1256;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
|||||
Db 1096 DTFYV 1101

RESULT 13
T16507
hypothetical protein F59A6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16507
R;Nhan, M.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid F59A6.
A;Reference number: Z18526
A;Accession: T16507
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-1286 <NHA>
A;Cross-references: UNIPROT:Q21025; UNIPARC:UPI000008155B; EMBL:U41994; NID:g1123047; PI
C;Genetics:
A;Gene: CESP:F59A6.5
A;Introns: 35/3; 335/3; 685/3; 973/3; 1097/3

Query Match 66.7%; Score 6; DB 2; Length 1286;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
|||||
Db 1120 DTFYV 1125

RESULT 14
SS3874
endonuclease precursor - human
C;Species: Homo sapiens (man)
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: SS3874
R;Gerschenon, M.; Houmiel, K.L.; Low, R.L.
Nucleic Acids Res. 23, 88-97, 1995

A;Title: Endonuclease G from mammalian nuclei is identical to the major endonuclease of
 A;Reference number: S53874; MUID:95175374; PMID:7870594
 A;Accession: S53874

A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-72 <GER>
 A;Cross-references: UNIPARC:UPI000017C100

Query Match 55.6%; Score 5; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7
 |||||
 Db 20 DDTFY 24

RESULT 15

D97355

hypothetical protein CAC3711 [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum
 C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C;Accession: D97355

R;Nolling, J.; Berton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4836, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
 A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: D97355

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-90 <KUR>

A;Cross-references: UNIPROT:Q04353; UNIPARC:UPI0000139447; GB:AE001437; PIDN:AAK81631.1;

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC3711

Query Match

Best Local Similarity 55.6%; Score 5; DB 2; Length 90;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
 |||||
 Db 56 KVDDT 60

RESULT 16

S25001

ubiquitin/ribosomal protein S27a fusion protein - garden asparagus
 C;Species: Asparagus officinalis (garden asparagus)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S25001

R;Davies, K.M.; King, G.A.

submitted to the EMBL Data Library, June 1992

A;Description: Isolation and characterization of asparagus officinalis L. cDNA clones en

A;Reference number: S25001

A;Accession: S25001

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-118 <DAV>

A;Cross-references: UNIPROT:P31753; UNIPROT:P03993; UNIPARC:UPI00001699FA; EMBL:X66875;
 A;Superfamily: ubiquitin / rat ribosomal protein S27a; ribosomal protein S27a homology;

C;Keywords: nucleus

F;1-40/Domain: ubiquitin homology (fragment) <UBH>

F;1-40/Product: ubiquitin (fragment) #status predicted <UBI>

F;41-118/Product: ribosomal protein S27a #status predicted <RIBP>

F;65-115/Domain: ribosomal protein S27a homology <RIB>

Query Match

Best Local Similarity 55.6%; Score 5; DB 2; Length 118;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5

Db 71 KVDDT 75
 |||||

RESULT 17

G85757

hypothetical protein Z2511 [imported] - Escherichia coli (strain O157:H7, substrain EDL

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: G85757

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimantanta, E.; Potamousis, K.; Apodaca

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: G85757

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-128 <STO>

A;Cross-references: UNIPROT:Q8X3T8; UNIPARC:UPI00000D0EB0; GB:AE005174; NID:g12515499;

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: Z2511

Query Match

Best Local Similarity 55.6%; Score 5; DB 2; Length 128;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
 |||||
 Db 14 KVDDT 18

RESULT 18

A59055

Phospholipase A2 (EC 3.1.1.4), venom - Indian honeybee

N;Alternate names: allergen api cl

C;Species: Apis mellifera cerana (Indian honeybee)

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 16-Aug-2004

C;Accession: A59055

R;Hoffman, D.R.; Schmidt, J.O.

submitted to the Protein Sequence Database, July 1999

A;Description: Venom phospholipase A2.

A;Reference number: A59055

A;Accession: A59055

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-134 <HOF>

A;Cross-references: UNIPARC:UPI0000050AE5

A;Experimental source: venom

C;Function:

A;Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl

C;Superfamily: Phospholipase A2

C;Keywords: calcium; carboxylic ester hydrolase; glycoprotein; lipid degradation; metal

F;1-134/Product: phospholipase A2 #status experimental <MAT>

F;6,10,12,35/Binding site: calcium (Trp, Gly, Gly, Asp) #status predicted

F;9-31,30-70,37-63,61-95,105-113/Disulfide bonds: #status predicted

F;13/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;34,64/Active site: His, Asp #status predicted

Query Match

Best Local Similarity 55.6%; Score 5; DB 2; Length 134;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7
 |||||
 Db 64 DDTFY 68

RESULT 19

AC0079

hypothetical protein.YP00641 [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

CjDate: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 CjAccession: AC0079
 RjParkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, Nature 413, 523-527, 2001
 A>Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A|Reference number: AB0001; MUID:21470413; PMID:11586360
 A|Accession: AC0079
 A|Status: preliminary
 A|Molecule type: DNA
 A|Residues: 1-134 <KUR>
 A|Cross-references: UNIPROT:Q8ZI74; UNIPARC:UPI00000CD6PF; GB:AL590842; PIDN:CAC89494.1;
 C|Genetics:
 A|Gene: YPO0641

Query Match 55.6%; Score 5; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
 Db 91 DTFY 95

RESULT 20
 I53298
 cellular retinoic acid-binding protein II - rat
 C|Species: *Rattus norvegicus* (Norway rat)
 CjDate: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 CjAccession: I53298
 RjBucco, R.A.; Melner, M.H.; Gordon, D.S.; Leers-Sucheta, S.; Ong, D.E. Endocrinology 136, 2730-2740, 1995
 A>Title: Inducible expression of cellular retinoic acid-binding protein II in rat ovary.
 A|Reference number: I53298; MUID:95269720; PMID:7750498
 A|Accession: I53298
 A|Status: preliminary;
 A|Molecule type: mRNA
 A|Residues: 1-139 <RES>
 A|Cross-references: UNIPROT:P51673; UNIPARC:UPI0000167AAC; EMBL:U23407; NID:g727432; PID
 C|Genetics:
 A|Gene: CRABP II
 C|Superfamily: myelin P2 protein

Query Match 55.6%; Score 5; DB 2; Length 139;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DTFY 7
 Db 49 DTFY 53

RESULT 21
 shk1 kinase-binding protein 5. [imported] - fission yeast (*Schizosaccharomyces pombe*)
 C|Species: *Schizosaccharomyces pombe*
 CjDate: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
 CjAccession: T50420
 RjSeeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrrell, B.G. submitted to the EMBL Data Library, February 2000
 A|Reference number: Z25039
 A|Accession: T50420
 A|Status: preliminary; translated from GB/EMBL/DBJ
 A|Molecule type: DNA
 A|Residues: 1-140 <SEE>
 A|Cross-references: UNIPROT:Q9US59; UNIPARC:UPI000006A970; EMBL:AL157991; PIDN:CAB76222.
 A|Experimental source: strain 972h(-); cosmid c24B10
 C|Genetics:
 A|Gene: SPDB:SPCC24B10.13
 A|Map position: 3

Query Match 55.6%; Score 5; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 Db 41 VDDTF 45

RESULT 22
 UQ0707A
 ubiquitin / ribosomal protein S27a - tomato
 N|Alternate names: ubiquitin fusion protein ubi3
 N|Contains: ribosomal protein S27a; ubiquitin
 C|Species: *Lycopersicon esculentum* (tomato)
 CjDate: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
 CjAccession: S18351; S27280; S14656
 RjHoffman, N.E.; Ko, K.; Milkowski, E. Plant Mol. Biol. 17, 1189-1201, 1991
 A>Title: Isolation and characterization of tomato cDNA and genomic clones encoding the
 A|Reference number: S18351; MUID:92032784; PMID:1657246
 A|Accession: S18351
 A|Molecule type: DNA
 A|Residues: 1-156 <HOF1>
 A|Cross-references: UNIPROT:P27083; UNIPROT:P03993; UNIPARC:UPI000016DE25; EMBL:X58253;
 A|Accession: S27280
 A|Molecule type: mRNA
 A|Residues: 1-156 <HOF2>
 A|Cross-references: UNIPARC:UPI000016DE25; GB:X58253; NID:gl9396; PIDN:CAA41207.1; PID:Q
 C|Genetics:
 A|Gene: UBI3
 A|Map position: 1
 C|Superfamily: ubiquitin / rat ribosomal protein S27a; ribosomal protein S27a homology;
 C|Keywords: protein biosynthesis; protein degradation; ribosome
 F|1-76/Product: ubiquitin #status predicted <MAT1>
 F|1-76/Domain: ubiquitin homology <UBH>
 F|77-156/Product: ribosomal protein S27a #status predicted <MAT2>
 F|101-151/Domain: ribosomal protein S27a homology <RIB>

Query Match 55.6%; Score 5; DB 1; Length 156;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 107 KVDDT 111

RESULT 23
 S25305
 ubiquitin / ribosomal protein S27a - potato
 N|Contains: ribosomal protein S27a; ubiquitin
 C|Species: *Solanum tuberosum* (potato)
 CjDate: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
 CjAccession: S25305; S19798
 RjGarbarino, J.E.; Rockhold, D.R.; Belknap, W.R. Plant Mol. Biol. 20, 235-244, 1992
 A>Title: Expression of stress-responsive ubiquitin genes in potato tubers.
 A|Reference number: S25305; MUID:93004476; PMID:1327270
 A|Accession: S25305
 A|Molecule type: mRNA
 A|Residues: 1-156 <GAR>
 A|Cross-references: UNIPARC:UPI000016DE25; EMBL:Z11669; NID:g21600; PIDN:CAA77735.1; PID
 C|Superfamily: ubiquitin / rat ribosomal protein S27a; ribosomal protein S27a homology;
 C|Keywords: protein biosynthesis; ribosome
 F|1-76/Product: ubiquitin #status predicted <UBI>
 F|1-76/Domain: ubiquitin homology <UBH>
 F|77-156/Product: ribosomal protein S27a #status predicted <MAT>
 F|101-151/Domain: ribosomal protein S27a homology <RIB>

Query Match 55.6%; Score 5; DB 2; Length 156;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 107 KVDDT 111

RESULT 24
 A75176
 dolichyl-phosphate mannose synthase related protein PAB1981 - *Pyrococcus abyssi* (strain C/Species: *Pyrococcus abyssi*)
 C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C/Accession: A75176
 R:anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A/Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome structure
 A/Reference number: A75001
 A/Accession: A75176
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-211 <KAW>
 A/Cross-references: UNIPROT:Q9V162; UNIPARC:UPI0000034682; GB:AJ248284; GB:AL096836; NID
 A/Experimental source: strain Orsay
 C/Genetics:
 A/Gene: PAB1981
 C/Superfamily: Methanobacterium thermoautotrophicum dolichyl-phosphate mannose synthase

Query Match 55.6%; Score 5; DB 2; Length 211;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 139 KVDDT 143

RESULT 25
 A83956
 flagellar hook protein flgE [imported] - *Bacillus halodurans* (strain C-125)
 C/Species: *Bacillus halodurans*
 C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C/Accession: A83956
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
 Nucleic Acids Res. 28, 4317-4331, 2000
 A/Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A/Reference number: A83650; MUID:20512582; PMID:11058132
 A/Accession: A83956
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-263 <STO>
 A/Cross-references: UNIPROT:Q9KA41; UNIPARC:UPI00000C3EF4; GB:AP001515; GB:BA0000004; NID
 A/Experimental source: strain C-125
 C/Genetics:
 A/Gene: flgE
 C/Superfamily: rod protein flgF

Query Match 55.6%; Score 5; DB 2; Length 263;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
 Db 108 DTFY 112

RESULT 26
 B96612
 hypothetical protein F12K22.17 [imported] - *Arabidopsis thaliana*
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: B96612
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: B96612
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-264 <STO>
 A/Cross-references: UNIPROT:Q9FVSO; UNIPARC:UPI00000A44DB; GB:AE005173; NID:gl1079522;
 C/Genetics:
 A/Gene: F12K22.17
 A/Map position: 1

Query Match 55.6%; Score 5; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 107 KVDDT 111

RESULT 27
 C83482
 2-phosphonoacetaldehyde hydrolase PA1311 [imported] - *Pseudomonas aeruginosa* (strain PA
 C/Species: *Pseudomonas aeruginosa*
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C/Accession: C83482
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic path
 A/Reference number: A82950; MUID:20437337; PMID:10984043
 A/Accession: C83482
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-275 <STO>
 A/Cross-references: UNIPROT:Q9I433; UNIPARC:UPI00000C5306; GB:AE004560; GB:AE004091; NID
 A/Experimental source: strain PA01
 C/Genetics:
 A/Gene: phnX; PA1311

Query Match 55.6%; Score 5; DB 2; Length 275;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 186 KVDDT 190

RESULT 28
 H75326
 tRNA (guanine-N1)-methyltransferase - *Deinococcus radiodurans* (strain R1)
 C/Species: *Deinococcus radiodurans*
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
 C/Accession: H75326
 R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A/Reference number: A75250; MUID:20036896; PMID:10567266
 A/Accession: H75326
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-279 <WHI>
 A/Cross-references: UNIPROT:Q9RSW0; UNIPARC:UPI0000137411; GB:AE002038; GB:AE000513; NID
 A/Experimental source: strain R1

C;Genetics:
A;Gene: DR2011
A;Map position: 1
C;Superfamily: tRNA-(mIG37) methyltransferase

Query Match 55.6%; Score 5; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDUT 5
DB 49 KVDUT 53

RESULT 29
T21974
hypothetical protein F38H4.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004
C;Accession: T21974
R;Lennard, N.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19496
A;Accession: T21974
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-284 <WIL>
A;Cross-references: UNIPROT:Q20180; UNIPARC:UPI0000074C84; EMBL:Z77660; PIDN:CAB01173.1;
A;Experimental source: clone F38H4
C;Genetics:
A;Gene: CBSP:F38H4.5
A;Map position: 4
A;Introns: 25/3; 221/3
C;Superfamily: scyllo-inosamine-4-phosphate amidinotransferase

Query Match 55.6%; Score 5; DB 2; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
DB 168 DDTFY 172

RESULT 30
AG3556
heat resistant agglutinin 1 precursor [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AG3556
R;DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letese
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688
A;Accession: AG3556
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-284 <KUR>
A;Cross-references: UNIPROT:Q8YD01; UNIPARC:UPI000058467; GB:AE008918; PIDN:AAL53618.1;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI10376
A;Map position: 11

Query Match 55.6%; Score 5; DB 2; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
DB 75 VDDTF 79

RESULT 31
T09542
endonuclease G (EC 3.1.30.-) precursor - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 12-Jul-2004
C;Accession: T09542
R;Zeviani, M.
submitted to the EMBL Data Library, August 1998
A;Reference number: Z16729
A;Accession: T09542
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-297 <ZEV>
A;Cross-references: UNIPROT:Q14249; UNIPARC:UPI0000161B77; EMBL:X79444; NID:el315166; P;
C;Genetics:
A;Map position: 9q34.1
A;Genome: nuclear
C;Function:
A;Description: involved in the replication and transcription of the mitochondrial genome
C;Superfamily: nuclease NUC1
C;Keywords: endonuclease; hydrolase; mitochondrion

Query Match 55.6%; Score 5; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
DB 156 DDTFY 160

RESULT 32
BS6118
vetispiradiene synthase 2 - Hyoscyamus muticus (fragment)
C;Species: Hyoscyamus muticus
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: BS6118
R;Back, K.; Chappell, J.
J. Biol. Chem. 270, 7375-7381, 1995
A;Title: Cloning and bacterial expression of a sesquiterpene cyclase from Hyoscyamus mut
A;Reference number: A56118; MUID:95221394; PMID:7706281
A;Accession: BS6118
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-300 <BAC>
A;Cross-references: UNIPROT:Q39979; UNIPARC:UPI00000A5CCF; GB:U20189; NID:g763424; PIDN:
C;Superfamily: vetispiradiene synthase 1

Query Match 55.6%; Score 5; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
DB 53 VDDTF 57

RESULT 33
AH0763
probable transcription regulator STY2278 [imported] - Salmonella enterica subsp. enteric
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0763
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0763

```
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-304 <PAR>
C;Cross-references: UNIPARC:UPI0000059C58; GB:AL513382; PIDN:CAD02430.1; PID:g16503297;
C;Genetics:
A;Gene: STY2278
C;Superfamily: probable transcription regulator ybbs

Query Match      55.6%; Score 5; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VDDTF 6
      |||||
Db      99 VDDTF 103

RESULT 34
G97132
uncharacterized phage related protein [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97132
R;Molling, J.; Berton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97132
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-306 <KUR>
A;Cross-references: UNIPROT:Q97HX0; UNIPARC:UPI000000CA33F; GB:AE001437; PIDN:AAK79850.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1886

Query Match      55.6%; Score 5; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVDDT 5
      |||||
Db     111 KVDDT 115

RESULT 35
T49912
hypothetical protein T24H18.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49912
R;Bevan, M.; Robben, J.; Gymnompres, B.; Volckaert, G.; Bancroft, I.; Mewes, H.W.; Rudd,
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25024
A;Accession: T49912
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-311 <BEV>
A;Cross-references: UNIPROT:Q9LXU1; UNIPARC:UPI0000005377; EMBL:AL353013; GSPDB:GN000063;
A;Experimental source: cultivar Columbia; BAC clone T24H18
C;Genetics:
A;Gene: ATSP:T24H18.150
A;Map position: 5
A;Introns: 56/3; 80/3; 110/3; 125/1; 160/3; 192/3; 256/2; 279/3

Query Match      55.6%; Score 5; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVDDT 5
      |||||
Db     160 KVDDT 164
```

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RESULT 36
AD1285
glycerate dehydrogenases homolog lml684 [imported] - Listeria monocytogenes (strain EG
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C;Accession: AD1285
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Faihi, H
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Title: Comparative Genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1285
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-313 <GLA>
A;Cross-references: UNIPROT:Q8Y6K0; UNIPARC:UPI00000553E0; GB:NC_003210; PIDN:CAC99762.
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lml684
C;Superfamily: Phosphoglycerate dehydrogenase

Query Match      55.6%; Score 5; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 DTFY 8
      |||||
Db      24 DTFY 28

RESULT 37
AG1656
glycerate dehydrogenases homolog lin1792 [imported] - Listeria innocua (strain Clp1126
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C;Accession: AG1656
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Faihi, H
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Title: Comparative Genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1656
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-313 <GLA>
A;Cross-references: UNIPROT:Q92AX6; UNIPARC:UPI000000CC675; GB:AL592022; PIDN:CAC97023.1
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: lin1792
C;Superfamily: Phosphoglycerate dehydrogenase

Query Match      55.6%; Score 5; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 DDTFY 7
      |||||
Db      23 DDTFY 27

RESULT 38
SS1729
NSP3 protein - human rotavirus (strain S2)
N;Alternate names: NS34 protein
C;Species: human rotavirus
```

A:Variety: strain S2
 C:Date: 07-May-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S51729
 R:Rao, C.D.; Das, M.; Rao, B.S.; Gowda, K.
 Submitted to the EMBL Data Library, September 1994
 A:Reference number: S51709
 A:Accession: S51729
 A:Molecule type: mRNA
 A:Residues: 1-313 <RAO>
 A:Cross-references: UNIPROT:Q82052; UNIPARC:UPI00000EC0A9; EMBL:X81428; NID:G607093; PID:
 C:Superfamily: rotavirus nonstructural protein

Query Match 55.6%; Score 5; DB 2; Length 313;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 154 VDDTF 158

RESULT 39
 AG0503
 probable regulatory protein STY0014 [imported] - Salmonella enterica subsp. enterica ser
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AG0503
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connerthon, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AG0503
 A:Molecule type: DNA
 A:Status: preliminary
 A:Residues: 1-315 <PAR>
 A:Cross-references: UNIPARC:UPI000005996F; GB:AL513382; PIDN:CAD01167.1; PID:g16501297;
 C:Genetics:
 A:Gene: STY0014

Query Match 55.6%; Score 5; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 84 VDDTF 88

RESULT 40
 F64966
 probable transcription regulator yeeY - Escherichia coli (strain K-12)
 C:Species: Escherichia coli
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
 C:Accession: F64966
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 .A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: F64966
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-316 <BLAT>
 A:Cross-references: UNIPARC:UPI00001680FE; GB:AE000293; GB:U00096; NID:G2367127; PIDN:AP
 A:Experimental source: strain K-12, substrain MG1655
 C:Genetics:
 A:Gene: yeeY
 C:Superfamily: probable transcription regulator ybbS

C:Keywords: DNA binding; nucleotide binding; P-loop; transcription regulation
 F:307-314/Region: nucleotide-binding motif A (P-loop)

Query Match 55.6%; Score 5; DB 1; Length 316;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 106 VDDTF 110

RESULT 41
 A99981
 probable transcription regulator LYSR-type [imported] - Escherichia coli (strain O157:H7
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C:Accession: A99981
 R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: A99981
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-316 <HAY>
 A:Cross-references: UNIPROT:Q8X4U0; UNIPARC:UPI00000D0D78; GB:BA000007; PIDN:BA836240.1;
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: ECs2817
 C:Superfamily: probable transcription regulator ybbS

Query Match 55.6%; Score 5; DB 2; Length 316;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 106 VDDTF 110

RESULT 42
 F85826
 probable transcription regulator LYSR-type yeeY [imported] - Escherichia coli (strain O1
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: F85826
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: F85826
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-316 <STO>
 A:Cross-references: UNIPROT:Q8X4U0; UNIPARC:UPI00000D0D78; GB:AE005174; NID:G12516196;
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: yeeY
 C:Superfamily: probable transcription regulator ybbS

Query Match 55.6%; Score 5; DB 2; Length 316;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 106 VDDTF 110

RESULT 43

T29624

Hypothetical protein K09E3.5 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T29624
 R;Johnson, D.; Gattung, S.
 submitted to the EMBL Data Library, November 1995
 A;Description: The sequence of *C. elegans* cosmid K09E3.
 A;Reference number: Z20655
 A;Accession: T29624
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-317 <JOH>
 A;Cross-references: UNIPROT:Q21395; UNIPARC:UPI0000079763; EMBL:U41033; PIDN:AAA82372.1;
 C;Genetics:
 A;Gene: CESP:K09E3.5
 A;Introns: 75/1; 238/3
 C;Superfamily: *Caenorhabditis elegans* hypothetical protein C08A9.6

Query Match 55.6%; Score 5; DB 2; Length 317;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 148 VDDTF 152

RESULT 44

NCBYN1
 nuclease NUC1 (EC 3.1.1.30.-) precursor, mitochondrial - yeast (*Saccharomyces cerevisiae*)
 N;Alternate names: protein HR329; protein J0310; protein YUL208c
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 C;Accession: S05888; S50777; S46621; S56995; S56998; S45165
 R;Vincent, R.D.; Hofmann, T.J.; Zassenhaus, H.P.
 Nucleic Acids Res. 16, 3297-3312, 1988
 A;Title: Sequence and expression of NUC1, the gene encoding the mitochondrial nuclease
 A;Reference number: S05885; MUID:88233924; PMID:2836792
 A;Accession: S05888
 A;Molecule type: DNA
 A;Residues: 1-329 <VIN>
 A;Cross-references: UNIPROT:P08466; UNIPARC:UPI0000052ED4; EMBL:X06670; NID:G4062; PIDN:
 R;Vandenbol, M.; Durand, P.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.
 Yeast 10, 1657-1662, 1994
 A;Title: Sequence analysis of a 40.2 kb DNA fragment located near the left telomere of Y
 A;Reference number: S50701; MUID:95242842; PMID:7725802
 A;Accession: S50777

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
 A;Residues: 1-329 <VAV>
 A;Cross-references: UNIPARC:UPI0000052ED4; EMBL:X06670; NID:G496934; PIDN:CAA84003.1; PI
 A;Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1994
 R;Purnelle, B.; Coster, F.; Goffeau, A.
 Yeast 10, 1235-1249, 1994
 A;Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies
 a gene ACO1 and two homologues to chromosome III genes.
 A;Reference number: S46621; MUID:95274326; PMID:7754713

A;Accession: S46621
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-329 <PUR>
 A;Cross-references: UNIPARC:UPI0000052ED4; EMBL:X77688; NID:G1183992; PIDN:CAA54748.1; P
 R;Purnelle, B.; Coster, F.; Goffeau, A.
 submitted to the Protein Sequence Database, September 1995
 A;Reference number: S56977

A;Accession: S56995
 A;Molecule type: DNA
 A;Residues: 1-329 <PUW>
 A;Cross-references: UNIPARC:UPI0000052ED4; EMBL:Z49483; NID:G1015588; PIDN:CAA89505.1; P
 R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
 submitted to the Protein Sequence Database, September 1995
 A;Reference number: S56835

A;Accession: S56998

A;Molecule type: DNA

A;Residues: 1-329 <VAN>

A;Cross-references: UNIPARC:UPI0000052ED4; EMBL:Z49483; NID:G1015588; PIDN:CAA89505.1;

C;Genetics:

A;Gene: SGD:NUC1; MIPS:YJL208C

A;Cross-references: SGD:S0003744; MIPS:YJL208C

A;Map position: 10L

A;Genome: nuclear

C;Complex: homodimer

C;Function:

A;Description: nuclease

A;Note: the protein has both RNase and DNase activity

C;Superfamily: nuclease NUC1

C;Keywords: homodimer; hydrolase; membrane protein; mitochondrion

F;138/Active site: His #status predicted

Query Match 55.6%; Score 5; DB 1; Length 329;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 Db 153 DDTFY 157

RESULT 45

T33944

Hypothetical protein C01B4.6 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T33944

R;Smith, A.; Wamsley, P.; Fronick, W.

submitted to the EMBL Data Library, February 1999

A;Description: The sequence of *C. elegans* cosmid C01B4.

A;Reference number: Z21443

A;Accession: T33944

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-330 <SMI>

A;Cross-references: UNIPROT:Q9UAT6; UNIPARC:UPI000007A31B; EMBL:AF125952; PIDN:AAD14698

A;Experimental source: strain Bristol N2; clone C01B4

C;Genetics:

A;Gene: CESP:C01B4.6

A;Map position: 5

A;Introns: 49/1; 100/3; 133/3; 304/3

C;Superfamily: aldose 1-epimerase

Query Match 55.6%; Score 5; DB 2; Length 330;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 189 VDDTF 193

RESULT 46

A10491

probable membrane protein YPO4045 [imported] - *Yersinia pestis* (strain CO92)

C;Species: *Yersinia pestis*

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: A10491

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;

Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: A10491

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-330 <KUR>

A;Cross-references: UNIPROT:Q829Y6; UNIPARC:UPI00000DCDAD; GB:AL590842; PIDN:CAC93501.1;
C;Gene: YPO4045

Query Match 55.6%; Score 5; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
|||
Db 179 DTFYY 183

RESULT 47

D91184
hypothetical protein ECs4444 [imported] - Escherichia coli (strain O157:H7, substrain R1)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: D91184

R;Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gagawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: D91184
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-331 <HAY>

A;Cross-references: UNIPROT:Q8XDM7; UNIPARC:UPI00000D033C; GB:BA000007; PIDN:BA837867.1;

A;Experimental source: strain O157:H7, substrain R1MD 0509952

C;Genetics:

A;Gene: ECs4444

Query Match 55.6%; Score 5; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
|||
Db 179 DTFYY 183

RESULT 48

B86031
hypothetical protein yiaH [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: B86031

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: B86031

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-331 <STO>

A;Cross-references: UNIPROT:Q8XDM7; UNIPARC:UPI00000D033C; GB:AE005174; NID:gl2518299; F

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: yiaH

Query Match 55.6%; Score 5; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
|||
Db 179 DTFYY 183

RESULT 49

S47782

hypothetical 37.6K protein (glyO-xyLB intergenic region) - Escherichia coli (strain K-1-
N)Alternate names: hypothetical protein o331

C;Species: Escherichia coli

C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004

C;Accession: S47782; C65155

R;Plunkett, G.

submitted to the EMBL Data Library, March 1994

A;Reference number: S47666

A;Accession: S47782

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-331 <PLU>

A;Cross-references: UNIPROT:P37669; UNIPARC:UPI000013B368; EMBL:U00039; NID:g466582; PID

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: C65155

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-331 <BLAT>

A;Cross-references: UNIPARC:UPI000013B368; GB:AE000433; GB:U00096; NID:gl789977; PIDN:AA

A;Experimental source: strain K-12, substrain MGI655

C;Genetics:

A;Gene: yiaH

Query Match 55.6%; Score 5; DB 2; Length 331;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
|||
Db 179 DTFYY 183

RESULT 50

C56118

vetispiradiene synthase 2 - Hyoscyamus muticus (fragment)

C;Species: Hyoscyamus muticus

C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C;Accession: C56118

R;Back, K.; Chappell, J.

J. Biol. Chem. 270, 7375-7381, 1995

A;Title: Cloning and bacterial expression of a sesquiterpene cyclase from Hyoscyamus mut

A;Reference number: A56118; MUID:95221394; PMID:7706281

A;Accession: C56118

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-350 <BAC>

A;Cross-references: UNIPROT:Q39980; UNIPARC:UPI00000A5281; GB:U20190; NID:g763426; PIDN:

A;Note: authors translated the codon GAA for residue 181 as Val, and GCA for residue 182

C;Superfamily: vetispiradiene synthase 1

Query Match 55.6%; Score 5; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 102 VDDTF 106

RESULT 51

AC2367

glucose-1-phosphate thymidyltransferase [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AC2367

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: JN0319; PU0032
R:Haas, H.; Redl, B.; Friedlin, E.; Stoeffler, G.
Gene 113, 129-133, 1992
A:Title: Isolation and analysis of the *Penicillium chrysogenum* *phoA* gene encoding a secreted phosphatase
A:Reference number: JN0319; MUID:92225342; PMID:1563629
A:Accession: JN0319
A:Molecule type: DNA
A:Residues: 1-412 <HAA>
A:Cross-references: UNIPROT:P37274; UNIPARC:UPI00001319B2; GB:M80366; NID:g169175; PIDN:PI00032
A:Accession: PU0032
A:Molecule type: protein
A:Residues: 49-75;132-150;185-202;240-273;316-344;368-396 <HAA1>
A:Cross-references: UNIPARC:UPI0000179849; UNIPARC:UPI000017984A; UNIPARC:UPI000017984B;
C:Genetics:
A:Gene: *phoA*
A:Introns: 64/3
C:Keywords: glycoprotein; phosphoric monoester hydrolase
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-411/Product: acid phosphatase #status predicted <MAT>
F:74,121,186,217,332,343/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.6%; Score 5; DB 2; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 278 DDTFY 282

RESULT 57
JC2389
acid phosphatase (EC 3.1.3.2) - *Aspergillus ficuum*
C:Species: *Aspergillus ficuum*
C>Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 12-Sep-1997
C:Accession: JC2389; PC2243
R:Ehrlich, K.C.; Montalbano, B.G.; Mullaney, E.J.; Dischinger Jr., H.C.; Ullah, A.H.J.
Biochem. Biophys. Res. Commun. 204, 63-68, 1994
A:Title: An acid phosphatase from *Aspergillus ficuum* has homology to *Penicillium chrysogenum*
A:Reference number: JC2389; MUID:95032134; PMID:7945393
A:Accession: JC2389
A:Molecule type: DNA
A:Residues: 1-417 <EHR1>
A:Cross-references: UNIPARC:UPI00001319B1; GB:L20566; NID:g304094; PID:g304095
A:Accession: PC2243
A:Molecule type: protein
A:Residues: 32-180;204-220;252-297;325-413 <EHR2>
A:Cross-references: UNIPARC:UPI0000179845; UNIPARC:UPI0000179846; UNIPARC:UPI0000179847;
C:Genetics:
A:Gene: *APPhoA*
A:Introns: 64/3
C:Keywords: glycoprotein; phosphoric monoester hydrolase
F:215-216/Region: catalytic #status predicted
F:122,187,209,218,333,383/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.6%; Score 5; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 279 DDTFY 283

RESULT 58
B31776
hypothetical protein (LAC12 3' region) - yeast (*Kluyveromyces marxianus* var. *lactis*)
C:Species: *Kluyveromyces marxianus* var. *lactis*, *Candida sphaerica*
C>Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
A:Accession: B31776
R:Chang, Y.D.; Dickson, R.C.
J. Biol. Chem. 263, 16696-16703, 1988

A:Title: Primary structure of the lactose permease gene from the yeast *Kluyveromyces fragilis*
A:Reference number: A92683; MUID:89034156; PMID:3053697
A:Accession: B31776
A:Molecule type: DNA
A:Residues: 1-422 <CHA>
A:Cross-references: UNIPROT:P08540; UNIPARC:UPI0000168907; GB:X06997; NID:g2856; PIDN:PI00032

Query Match 55.6%; Score 5; DB 2; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 293 DDTFY 297

RESULT 59
T36585
probable membrane protein - *Streptomyces coelicolor*
C:Species: *Streptomyces coelicolor*
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
A:Accession: T36585
R:Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z21575
A:Accession: T36585
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-425 <OLI>
A:Cross-references: UNIPROT:Q9X8T4; UNIPARC:UPI00000DB069; EMBL:AL049826; PIDN:CAB42736.
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: *SCOREDB:SCH24.20C*

Query Match 55.6%; Score 5; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 359 VDDTF 363

RESULT 60
E86575
phosphate permease [imported] - *Chlamydomonas reinhardtii* (strain J138)
C:Species: *Chlamydomonas reinhardtii*, *Chlamydia pneumoniae*
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
A:Accession: E86575
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishiguro, M.
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of *Chlamydia pneumoniae* J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: E86575
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <STO>
A:Cross-references: UNIPROT:Q9Z7M4; UNIPARC:UPI00001656B5; GB:BA000008; NID:g8979052; PI00032
A:Experimental source: strain J138
C:Genetics:
A:Gene: *Ygo4*

Query Match 55.6%; Score 5; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYIV 9
|||||
Db 223 TFYIV 227

RESULT 61
D72049

phosphate permease - Chlamydophila pneumoniae (strain CWL029)
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: D72049
R;Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
A:Title: Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: D72049
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <ARN>
A:Cross-references: UNIPROT:Q9Z7M4; UNIPARC:UPI00000139BC5; GB:AE001363; NID: A:Experimental source: strain CWL029
C:Genetics:
A:Gene: Y9o4

Query Match 55.6%; Score 5; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFFYV 9
|||||
Db 223 TFFYV 227

RESULT 62
G87334
acyl-CoA dehydrogenase family protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: G87334
R;Nierman, W.C.; Feidblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: G87334
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-435 <STO>
A:Cross-references: UNIPROT:Q9AAB4; UNIPARC:UPI000000C712A; GB:AE005673; NID:g13421911; H C:Genetics:
A:Gene: CC0690
C:Superfamily: acyl-CoA dehydrogenase

Query Match 55.6%; Score 5; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 75 VDDTF 79

RESULT 63
JS0374
hypothetical 51.6K protein - soybean chlorotic mottle virus
C:Species: soybean chlorotic mottle virus
A:Note: host Glycine max (soybean)
C:Accession: JS0374
R;Hasegawa, A.; Verver, J.; Shimada, A.; Saito, M.; Goldbach, R.; van Kammen, A.; Miki, Nucleic Acids Res. 17, 9993-10013, 1989
A:Title: The complete sequence of soybean chlorotic mottle virus DNA and the identification
A:Reference number: JS0372; MUID:90098857; PMID:2602148
A:Accession: JS0374
A:Molecule type: DNA
A:Residues: 1-440 <HAS>
A:Cross-references: UNIPARC:UPI000017A805; GB:X15828; NID:g58833; PIDN:CAA33828.1; PID:9 C:Keywords: DNA binding; zinc finger

Query Match 55.6%; Score 5; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 8
|||||
Db 147 DTFYV 151

RESULT 64
H81777
UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diamino-pimelate-D-alanyl-D-alanine ligase (E C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-Oct-2004
C:Accession: H81777
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More ; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: H81777
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-452 <PAR>
A:Cross-references: UNIPROT:Q9JSZ1; UNIPARC:UPI000000C4D1F; GB:AL162758; GB:AL157959; NID: A:Experimental source: serogroup A, strain 22491
C:Genetics:
A:Gene: murF; NMA2068
C:Superfamily: UDP-N-acetylmuramate-alanine ligase
C:Keywords: ligase

Query Match 55.6%; Score 5; DB 2; Length 452;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
Db 80 KVDDT 84

RESULT 65
D81202
UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase NMB C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C:Accession: D81202
R;Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; V A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: D81202
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-455 <TET>
A:Cross-references: UNIPROT:Q9K0Y8; UNIPARC:UPI000000C449F; GB:AE002397; GB:AE002098; NID: A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0416
C:Superfamily: UDP-N-acetylmuramate-alanine ligase

Query Match 55.6%; Score 5; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
Db 80 KVDDT 84

RESULT 66

T00090
glycosyltransferase rgpEc - Streptococcus mutans
C:Species: Streptococcus mutans
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C:Accession: T00090
R:Yamashita, Y.; Teukioka, Y.; Tomihisa, K.; Nakano, Y.; Koga, T.
J. Bacteriol. 181, 5803-5807, 1998
A:Title: Genes involved in cell wall localization and side chain formation of rhamnose-9
A:Reference number: Z14108
A:Accession: T00090
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-465 <YAM>
A:Cross-references: UNIPROT:O82877; UNIPARC:UPI00000BAC49; EMBL:AB010970; NID:dl224517;
A:Experimental source: strain Xc
C:Genetics:
A:Gene: rgpEc

Query Match 55.6%; Score 5; DB 2; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
DB 183 VDDTF 187

RESULT 67
T24724
hypothetical protein T09A5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T24724
R:Lightning, J.
submitted to the EMBL Data Library, August 1994
A:Reference number: Z19928
A:Accession: T24724
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-468 <WIL>
A:Cross-references: UNIPARC:UPI00001779A5; EMBL:Z36753; PIDN:CAA85338.1; GSPDB:GN000020;
A:Experimental source: clone T09A5
C:Genetics:
A:Gene: CESP:T09A5.3
A:Map position: 2
A:Introns: 35/2; 84/3; 126/2; 156/3; 198/1; 237/2; 282/1; 348/3; 391/1; 429/3
C:Superfamily: acetylcholine receptor

Query Match 55.6%; Score 5; DB 2; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TPYYV 9
DB 246 TPYYV 250

RESULT 68
T01260
probable ammonium transport protein F16M14.22 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01260; T02516; B84803
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, July 1998
A:Description: Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence.
A:Reference number: Z14213
A:Accession: T01260
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-475 <ROU>
A:Cross-references: UNIPROT:Q9M6N7; UNIPARC:UPI0000048613; EMBL:AC003028; NID:g3335356;
A:Experimental source: cultivar Columbia

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, August 1998
A:Description: Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence.
A:Reference number: Z14676
A:Accession: T02516
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-434 <RO2>
A:Cross-references: UNIPARC:UPI0000178E16; EMBL:AC004683; NID:g33395441; PID:g33395443
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: B84803
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-475 <STO>
A:Cross-references: UNIPARC:UPI0000048613; GB:AE002093; NID:g6598436; PIDN:AAC28754.2; C
C:Genetics:
A:Gene: At2g38290
A:Map position: 2
A:Introns: 104/3; 201/3; 297/1; 331/3
C:Superfamily: ammonium transporter nrgA

Query Match 55.6%; Score 5; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
DB 331 KVDDT 335

RESULT 69
JC7179
acid phosphatase (EC 3.1.3.2) Pho610 - Yeast (Kluyveromyces marxianus)
N:Alternate names: Pho610 protein
C:Species: Kluyveromyces marxianus
C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
C:Accession: JC7179
R:Yoda, K.; Ko, J.H.; Nagamatsu, T.; Lin, Y.; Kaibara, C.; Kawada, T.; Tomishige, N.; Ha
Biosci. Biotechnol. Biochem. 64, 142-148, 2000
A:Title: Molecular characterization of a novel yeast cell-wall acid phosphatase cloned f
A:Reference number: JC7179; MUID:20169637; PMID:10705459
A:Accession: JC7179
A:Molecule type: DNA
A:Residues: 1-483 <YOB>
A:Cross-references: UNIPROT:Q7M4U8; UNIPARC:UPI000017984F; GB:E02615
A:Experimental source: strain Y-610
C:Comment: This enzyme, highly glycosylated, is a covalently-linked cell-wall protein ha
rganic compounds.
C:Genetics:
A:Gene: pho610
C:Keywords: cell wall; endoplasmic reticulum; glycoprotein; phosphoric monoester hydrola

Query Match 55.6%; Score 5; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
DB 294 DDTFY 298

RESULT 70
T47974
hypothetical protein F15G16.210 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47974

R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Queb
 A;Reference number: 224480
 A;Accession: T47974
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-483 <DEH>
 A;Cross-references: UNIPROT:Q9M356; UNIPARC:UPI000009E4DF; EMBL:AL132959
 A;Experimental source: cultivar Columbia; BAC clone F15G16
 C;Genetics:
 A;Map position: 3
 A;Note: F15G16.210

Query Match 55.6%; Score 5; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
 |||||
 Db 326 DTFY 330

RESULT 71
 D86385
 hypothetical protein F2J7.6 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: D86385
 R;Theologas, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.P.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: D86385
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-483 <STO>
 A;Cross-references: UNIPROT:Q9C6M0; UNIPARC:UPI00000AC338; GB:AB005172; NID:g10092330; F
 C;Genetics:
 A;Map position: 1

Query Match 55.6%; Score 5; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
 |||||
 Db 326 DTFY 330

RESULT 72
 S40051
 starch synthase (EC 2.4.1.21) glgA - Bacillus subtilis
 N;Alternate names: starch (bacterial glycogen) synthase glgA
 C;Species: Bacillus subtilis
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S40051; E69632; S36627
 R;Kiel, J.A.K.W.; Boels, J.M.; Beldman, G.; Venema, G.
 Mol. Microbiol. 11, 203-218, 1994
 A;Title: Glycogen in Bacillus subtilis: molecular characterization of an operon encoding
 A;Reference number: S40048; MUID:94195107; PMID:8145641
 A;Accession: S40051
 A;Molecule type: DNA
 A;Residues: 1-484 <KIE>
 A;Cross-references: UNIPROT:P39125; UNIPARC:UPI000006096A; EMBL:Z25795; NID:g397487; PID
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertex
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.;
 Nature 390, 249-256, 1997
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galie
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
 Koetex, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
 A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
 A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Sero
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
 A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A;Reference number: A69580; MUID:98044033; PMID:9384377
 A;Accession: E69632
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-484 <KUN>
 A;Cross-references: UNIPARC:UPI000006096A; GB:Z99119; GB:AL009126; NID:g2635411; PIDN:C
 A;Experimental source: strain 168
 C;Genetics:
 A;Gene: glgA
 A;Start codon: TTG
 C;Superfamily: starch synthase
 C;Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 55.6%; Score 5; DB 2; Length 484;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DTFY 7
 |||||
 Db 250 DTFY 254

RESULT 73
 AB1584
 hypothetical protein lin1211 [imported] - Listeria innocua (strain Clip11262)
 C;Species: Listeria innocua
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AB1584
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsihi, H.
 Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
 A;Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AB1584
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-486 <GLA>
 A;Cross-references: UNIPROT:Q92CG1; UNIPARC:UPI00000CC4D0; GB:AL592022; PIDN:CAC96442.1
 A;Experimental source: strain Clip11262
 C;Genetics:
 A;Gene: lin1211

Query Match 55.6%; Score 5; DB 2; Length 486;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
 |||||
 Db 251 DTFY 255

RESULT 74
 A82632
 ammonium transporter Xfl844 [imported] - Xylella fastidiosa (strain 9a5c)
 C;Species: Xylella fastidiosa
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: A82632

R; anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequences Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: A82632
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-492 <SIM>
A:Cross-references: UNIPROT:Q9PCD7; UNIPARC:UPI00000C2857; GB:AE004005; GB:AE003849; NID: A82632
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canargo, L.E.A.; Carraro, D.M.; Carrier, H. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm, J.D.; Junqueira, M.B.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigh, Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, B.C.; Miyaki, C.Y.; , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak, A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1844
C:Superfamily: ammonium transporter nrgA

Query Match 55.6%; Score 5; DB 2; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 393 KVDDT 397

RESULT 75
G90430
conserved hypothetical protein [imported] - *Sulfolobus solfataricus*
C:Species: *Sulfolobus solfataricus*
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 28-Jul-2003
C:Accession: G90430
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arret, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: *Sulfolobus solfataricus* complete genome.
A:Reference number: A99139
A:Accession: G90430
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-506 <KUR>
A:Cross-references: UNIPARC:UPI00000647AB; GB:AE006641; NID:G13815879; PIDN:AAK42702.1;
C:Genetics:
A:Gene: SS02575
C:Superfamily: glycyI monoaminopeptidase

Query Match 55.6%; Score 5; DB 2; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 272 KVDDT 276

RESULT 76
T22836
hypothetical protein F57B7.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T22836
R:Lennard, N.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19623
A:Accession: T22836
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-508 <WIL>
A:Cross-references: UNIPROT:Q20930; UNIPARC:UPI000017BA38; EMBL:Z74037; PIDN:CAA98493.1
A:Experimental source: clone F57B7
C:Genetics:
A:Gene: CBSP:F57B7.4
A:Map position: 5
A:Introns: 45/3; 137/2; 221/2; 256/2; 306/2; 409/3; 451/3

Query Match 55.6%; Score 5; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 175 VDDTF 179

RESULT 77
S49620
phytoene dehydrogenase (EC 1.3.-.-) - *Rhodobacter sphaeroides*
N:Alternate names: phytoene desaturase
C:Species: *Rhodobacter sphaeroides*
C:Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S49620
R:Lang, H.P.; Cogdell, R.J.; Takaichi, S.; Hunter, C.N.
submitted to the EMBL Data Library, November 1994
A:Description: The complete DNA sequence, specific TMS insertion map and gene assignment
A:Reference number: S49619
A:Accession: S49620
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-518 <LAN>
A:Cross-references: UNIPROT:P54980; UNIPARC:UPI00001284C3; EMBL:X82458; NID:G575405; PIJ
C:Genetics:
A:Gene: ctri
C:Superfamily: phytoene dehydrogenase
C:Keywords: oxidoreductase

Query Match 55.6%; Score 5; DB 2; Length 518;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
Db 379 DDTFY 383

RESULT 78
TS0745
phytoene dehydrogenase (EC 1.3.-.-) [imported] - *Rhodobacter sphaeroides*
C:Species: *Rhodobacter sphaeroides*
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C:Accession: TS0745
R:Choudhary, M.; Kaplan, S.
Nucleic Acids Res. 28, 862-867, 2000
A:Title: DNA sequence analysis of the photosynthesis region of *Rhodobacter sphaeroides*
A:Reference number: Z25222; MUID:20115911; PMID:10648776
A:Accession: TS0745
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-518 <CHO>
A:Cross-references: UNIPROT:P54980; UNIPARC:UPI000016E416; EMBL:AF195122; PIDN:AAF24289
A:Experimental source: strain 2.4.1
C:Genetics:
A:Gene: ctri
C:Superfamily: phytoene dehydrogenase

C;Keywords: oxidoreductase

Query Match 55.6%; Score 5; DB 2; Length 518;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 379 DDTFY 383

RESULT 79

A56118
vetispiradiene synthase 1 - Hyoscyamus muticus (fragment)
C;Species: Hyoscyamus muticus
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56118
R;Back, K.; Chappell, J.
J. Biol. Chem. 270, 7375-7381, 1995
A;Title: Cloning and bacterial expression of a sesquiterpene cyclase from Hyoscyamus muticus
A;Reference number: A56118; MUID:95221394; PMID:7706281
A;Accession: A56118
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-520 <BAC>
A;Cross-references: UNIPROT:Q39978; UNIPARC:UPI00000A1DF5; GB:U20188; NID:G763422; PIDN:
C;Superfamily: vetispiradiene synthase 1

Query Match 55.6%; Score 5; DB 2; Length 520;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 272 VDDTF 276

RESULT 80

A32617
phytoene dehydrogenase (EC 1.3.-.-) - Rhodobacter capsulatus
N;Alternate names: phytoene desaturase
C;Species: Rhodobacter capsulatus
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
C;Accession: A32617; S04402
R;Bartley, G.B.; Scolnik, P.A.
J. Biol. Chem. 264, 13109-13113, 1989
A;Title: Carotenoid biosynthesis in photosynthetic bacteria. Genetic characterization of
A;Reference number: A32617; MUID:89327279; PMID:2546948
A;Accession: A32617
A;Molecule type: DNA
A;Residues: 1-524 <BAR>
A;Cross-references: UNIPROT:P17054; UNIPARC:UPI00001284C2; GB:J04969; NID:G340554; PIDN:
R;Armstrong, G.A.; Alberti, M.; Leach, F.; Hearst, J.E.
Mol. Gen. Genet. 216, 254-268, 1989
A;Title: Nucleotide sequence, organization, and nature of the protein products of the ca
A;Reference number: S04401; MUID:89313663; PMID:2747617
A;Accession: S04402
A;Molecule type: DNA
A;Residues: 1-524 <ARM>
A;Cross-references: UNIPARC:UPI00001284C2; EMBL:X52291; NID:G45996; PIDN:CAA36533.1; PID
A;Note: translation of codons 1-33 is not given
A;Note: the authors translated the codon GTG for residue 34 as Met
C;Genetics:
A;Gene: crtI
C;Superfamily: phytoene dehydrogenase
C;Keywords: carotenoid biosynthesis; oxidoreductase

Query Match 55.6%; Score 5; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||

Db 378 DDTFY 382

RESULT 81

T34417
delayed rectifier channel protein homolog exp-2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34417
R;Fulton, B.; Wohldmann, P.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of C. elegans cosmid F12F3.
A;Reference number: Z21521
A;Accession: T34417
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-528 <FUL>
A;Cross-references: UNIPROT:P91256; UNIPARC:UPI0000164218; EMBL:U80022; PIDN:AAC25887.1
A;Experimental source: strain Bristol N2; clone F12F3
C;Genetics:
A;Gene: exp-2; CESP:F12F3.1
A;Map position: 5
A;Introns: 42/2; 135/3; 173/3; 213/3; 271/3; 469/1

Query Match 55.6%; Score 5; DB 2; Length 528;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
Db 213 KVDDT 217

RESULT 82

F90418
ABC transporter, probable SSO2468 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: F90418
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: F90418
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-535 <KUR>
A;Cross-references: UNIPROT:Q97VY5; UNIPARC:UPI000006475A; GB:AE006641; NID:G13815769;
C;Genetics:
A;Gene: SSO2468

Query Match 55.6%; Score 5; DB 2; Length 535;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYVY 9
|||||
Db 399 TFYVY 403

RESULT 83

S54586
probable membrane protein YMR279c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YMR279c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S54586
R;Pearson, D.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54582
A;Accession: S54586

A:Molecule type: DNA
A:Residues: 1-540 <PEA>
A:Cross-references: UNIPROT:Q03263; UNIPARC:UPI000013B942; EMBL:Z49704; NID:G825540; PID
A:Experimental source: strain AB972
C:Genetics:
A:Gene: MIPS:YMR279C
A:Cross-references: SGD:S0004892
A:Map position: 13R
C:Superfamily: aminotriazole resistance protein YML116w
C:Keywords: transmembrane protein
F:109-125/Domain: transmembrane #status predicted <TM1>
F:139-155/Domain: transmembrane #status predicted <TM2>
F:174-190/Domain: transmembrane #status predicted <TM3>
F:233-249/Domain: transmembrane #status predicted <TM4>
F:268-284/Domain: transmembrane #status predicted <TM5>
F:298-314/Domain: transmembrane #status predicted <TM6>
F:335-351/Domain: transmembrane #status predicted <TM7>
F:377-393/Domain: transmembrane #status predicted <TM8>
F:400-416/Domain: transmembrane #status predicted <TM9>
F:435-451/Domain: transmembrane #status predicted <TM10>
F:503-519/Domain: transmembrane #status predicted <TM11>
Query Match 55.6%; Score 5; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TFYYV 9
Db 353 TFYYV 357
RESULT 84
T06264
3-dehydroquininate dehydratase (EC 4.2.1.10) / shikimate 5-dehydrogenase (EC 1.1.1.25) - b
N:Contains: 3-dehydroquininate dehydratase (EC 4.2.1.10); shikimate 5-dehydrogenase (EC 1.
C:Species: Lycopersicon esculentum (tomato)
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T06264
R:Bischoff, M.
submitted to the EMBL Data Library, November 1997
A:Description: Lycopersicon esculentum dehydroquininate dehydratase/shikimate:NADP oxidore
A:Reference number: Z15575
A:Accession: T06264
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-545 <BIS>
A:Cross-references: UNIPROT:Q65917; UNIPARC:UPI00000A2F9F; EMBL:AF033194; NID:G3169882;
A:Experimental source: strain UC82b
C:Superfamily: 3-dehydroquininate dehydratase / shikimate dehydrogenase; 3-dehydroquininate
C:Keywords: carbon-oxygen lyase; hydro-lyase; oxidoreductase
F:24-254/Domain: 3-dehydroquininate dehydratase homology <DQ>
F:324-529/Domain: shikimate dehydrogenase homology <SKD>
Query Match 55.6%; Score 5; DB 2; Length 545;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDT 5
Db 470 KVDDT 474
RESULT 85
I39593
exeA protein - Aeromonas hydrophila
C:Species: Aeromonas hydrophila
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: I39593
R:Jahagirdar, R.; Howard, S.P.
J. Bacteriol. 176, 6819-6826, 1994
A:Title: Isolation and characterization of a second exe operon required for extracellular
A:Reference number: I39593; MUID:95050248; PMID:7961440
A:Accession: I39593

A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-547 <RES>
A:Cross-references: UNIPROT:P45754; UNIPARC:UPI000012BC18; EMBL:X81473; NID:G551215; PTI
C:Superfamily: Aeromonas hydrophila exeA protein
Query Match 55.6%; Score 5; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDT 5
Db 314 KVDDT 318
RESULT 86
TS1035
hypothetical protein B15120.50 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C:Accession: TS1035
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, July 2000
A:Reference number: Z25286
A:Accession: TS1035
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-548 <SCH>
A:Cross-references: UNIPROT:Q9P3K6; UNIPARC:UPI000006AF57; EMBL:AL389900; GSPDB:GN00116,
A:Experimental source: BAC clone B15120; strain OR74A
C:Genetics:
A:Gene: NCSP:B15120.50
A:Map position: 6
Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TFYYV 9
Db 252 TFYYV 256
RESULT 87
T03714
5-epi-aristolochene synthase - common tobacco
N:Alternate names: sesquiterpene cyclase
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03714
R:Facchini, P.J.; Chappell, J.
Proc. Natl. Acad. Sci. U.S.A. 89, 11088-11092, 1992
A:Title: Gene family for an elicitor-induced sesquiterpene cyclase in tobacco.
A:Reference number: Z15024; MUID:93066390; PMID:1438319
A:Accession: T03714
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-550 <FAC>
A:Cross-references: UNIPROT:Q40577; UNIPARC:UPI000014C8BF; EMBL:L04680; NID:gl70342; PTD
A:Experimental source: strain NK326
C:Genetics:
A:Introns: 37/3; 126/1; 251/2; 324/2; 370/3; 452/3
C:Function:
A:Description: mediates the conversion of the isoprenoid intermediate farnesyl diphosphat
C:Superfamily: vetispiradiene synthase 1
Query Match 55.6%; Score 5; DB 2; Length 550;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
Db 302 VDDTF 306


```
RESULT 88
D90250
glycogen synthase [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: D90250
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sensesen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: D90250
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-566 <KUR>
A:Cross-references: UNIPROT:Q97ZD3; UNIPARC:UPI0000064308; GB:AE006641; NID:gl3814171; F
C:Genetics:
A:Gene: SSO0987

Query Match 55.6%; Score 5; DB 2; Length 566;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 516 KVDDT 520

RESULT 89
ERBP22
DNA-directed DNA polymerase (EC 2.7.7.7) - phage PZA
N:Alternate names: gene 2 protein (gp2)
C:Species: phage PZA
A:Note: host Bacillus subtilis
C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 31-Dec-2004
C:Accession: D24528
R:Paces, V.; Vilek, C.; Urbanek, P.; Hostomsky, Z.
Gene 38, 45-56, 1985
A:Title: Nucleotide sequence of the major early region of Bacillus subtilis phage PZA, a
A:Reference number: A91538; MUID:86056991; PMID:3334048
A:Accession: D24528
A:Molecule type: DNA
A:Residues: 1-572 <PAC>
A:Cross-references: UNIPROT:P06950; UNIPARC:UPI00001297E3; GB:M11813; GB:M13904; GB:M139
C:Genetics:
A:Gene: 2
C:Superfamily: DNA polymerase, Bacillus phage type
C:Keywords: DNA binding; early protein; nucleotidyltransferase

Query Match 55.6%; Score 5; DB 1; Length 572;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 565 VDDTF 569

RESULT 90
T37452
68K ankryrin-like protein - vaccinia virus (strain Ankara)
C:Species: vaccinia virus
A:Variety: strain Ankara
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T37452
R:Antoine, G.; Scheifflinger, F.; Falkner, F.G.; Dörner, F.
submitted to the EMBL Data Library, March 1997
A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain
A:Reference number: Z20877
A:Accession: T37452

A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-574 <ANT>
A:Cross-references: UNIPROT:O57263; UNIPARC:UPI000007EC4; EMBL:U94848; PIDN:ANB96556.1
A:Experimental source: strain Ankara
C:Genetics:
A:Note: MVA186R

Query Match 55.6%; Score 5; DB 2; Length 574;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
Db 424 DDTFY 428

RESULT 91
JQ1811
B17R protein - vaccinia virus (strain WR)
C:Species: vaccinia virus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JQ1811
R:Smith, G.L.; Chan, Y.S.; Howard, S.T.
J. Gen. Virol. 72, 1349-1376, 1991
A:Title: Nucleotide sequence of 42kbp of vaccinia virus strain WR from near the right i
A:Reference number: JQ1767; MUID:91259063; PMID:2045793
A:Accession: JQ1811
A:Molecule type: DNA
A:Residues: 1-574 <SMI>
A:Cross-references: UNIPROT:Q01222; UNIPARC:UPI000013822A; DDBJ:D11079; NID:g222717; PI

Query Match 55.6%; Score 5; DB 2; Length 574;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
Db 424 DDTFY 428

RESULT 92
H42527
B18R protein - vaccinia virus (strain Copenhagen)
C:Species: vaccinia virus
A:Note: host Homo sapiens (man)
C>Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C:Accession: H42527
R:Johnson, G.P.
submitted to GenBank, June 1990
A:Reference number: A33172
A:Accession: H42527
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-574 <JOH>
A:Cross-references: UNIPROT:P21076; UNIPARC:UPI0000138229

Query Match 55.6%; Score 5; DB 2; Length 574;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
Db 424 DDTFY 428

RESULT 93
A36857
B19R protein - variola virus
N:Alternate names: B18R protein (COP)
C:Species: variola virus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A36857; S46876
```

R;Blinov, V.M.
 submitted to GenBank, November 1992
 A:Reference number: A36859
 A:Accession: A36857
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-574 <BLI>
 A:Cross-references: UNIPROT:P33824; UNIPARC:UPI000013822B; GB:X69198; NID:g456758; PIDN:
 A:Experimental source: strain India-1967, ssp. major, isolate Ind3
 R;Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Froil
 submitted to the EMBL Data Library, April 1992
 A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
 A:Reference number: S46868
 A:Accession: S46876
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-574 <COL>
 A:Cross-references: UNIPARC:UPI000013822B; EMBL:X67117; NID:G516428; PIDN:CAA47528.1; PI
 A:Experimental source: strain India-1967, isolate Ind3

Query Match 55.6%; Score 5; DB 2; Length 574;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 Db 424 DDTFY 428

RESULT 94

T28615
 hypothetical protein B16R - variola major virus
 C:Species: variola major virus
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T28615
 R;Massung, R.F.; Eposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
 Nature 366, 748-751, 1993
 A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
 A:Reference number: Z20488; MUID:94088747; PMID:8264798
 A:Accession: T28615
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-574 <MAS>
 A:Cross-references: UNIPROT:P33824; UNIPARC:UPI000013822B; EMBL:L22579; NID:g623595; PID
 A:Experimental source: strain Bangladesh 1975

Query Match 55.6%; Score 5; DB 2; Length 574;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 Db 424 DDTFY 428

RESULT 95

C72174
 DBR protein - variola minor virus (strain Garcia-1966)
 C:Species: variola minor virus
 C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
 C:Accession: C72174
 R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopaz
 submitted to GenBank, March 1998
 A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
 A:Reference number: A72150
 A:Accession: C72174
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-574 <SHC>
 A:Cross-references: UNIPROT:Q89523; UNIPARC:UPI0000061DB3; GB:Y16780; NID:G5830555; PIDN
 A:Experimental source: strain Garcia-1966
 C:Genetics:
 A:Gene: DBR

Query Match 55.6%; Score 5; DB 2; Length 574;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 Db 424 DDTFY 428

RESULT 96

ERBP29
 DNA-directed DNA polymerase (EC 2.7.7.7) - phage phi-29
 N:Alternate names: early protein gp2
 C:Species: phage phi-29
 A:Note: host Bacillus subtilis
 C:Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 31-Dec-2004
 C:Accession: A04282; B93439; S11668; S11669
 R;Yoshikawa, H.; Ito, J.
 Gene 17, 323-335, 1982

A:Title: Nucleotide sequence of the major early region of bacteriophage phi29.
 A:Reference number: A91493; MUID:82262795; PMID:6809534
 A:Accession: A04282
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-575 <YOS>
 A:Cross-references: UNIPROT:P03680; UNIPARC:UPI00001297E1; GB:J02478; NID:g15
 A:Note: the authors report the amino acid composition of the translated protein; the ref
 R;Escarmis, C.; Salas, M.
 Nucleic Acids Res. 10, 5785-5798, 1982
 A:Title: Nucleotide sequence of the early genes 3 and 4 of bacteriophage psi29.
 A:Reference number: A93439; MUID:83064518; PMID:6292852
 A:Accession: B93439
 A:Molecule type: DNA
 A:Residues: 1-85 <ESC>
 A:Cross-references: UNIPARC:UPI0000174B74
 C:Genetics:
 A:Gene: 2
 A:Map position: 16-6
 C:Superfamily: DNA polymerase, Bacillus phage type
 C:Keywords: DNA binding; DNA replication; early protein; nucleotidyltransferase

Query Match 55.6%; Score 5; DB 1; Length 575;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 568 VDDTF 572

RESULT 97

S46210
 3-dehydroquinase dehydratase (EC 4.2.1.10) / shikimate 5-dehydrogenase (EC 1.1.1.25) pre
 N:Contains: 3-dehydroquinase dehydratase (EC 4.2.1.10); shikimate 5-dehydrogenase (EC 1.
 C:Species: Nicotiana tabacum, (common tobacco)
 C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
 C:Accession: S46210; S77973
 R;Bonner, C.A.; Jensen, R.A.
 Biochem. J. 302, 11-14, 1994
 A:Title: Cloning of cDNA encoding the bifunctional dehydroquinase shikimate dehydrogenase
 A:Reference number: S46210; MUID:94347087; PMID:8067995
 A:Accession: S46210
 A:Molecule type: mRNA
 A:Residues: 1-579 <BON>
 A:Cross-references: UNIPROT:Q42947; UNIPARC:UPI00000A5896; GB:L32794; NID:G535770; PIDN:
 A:Experimental source: strain SR1
 A:Accession: S77973
 A:Molecule type: protein
 A:Residues: 24-30 <JEN>
 A:Cross-references: UNIPARC:UPI00000176055
 C:Genetics:
 A:Genome: nuclear

C;Superfamily: 3-dehydroquininate dehydratase / shikimate dehydrogenase; 3-dehydroquininate
 C;Keywords: carbon-oxygen lyase; hydro-lyase; oxidoreductase; plastid
 F;1-23/Domain: transit peptide (plastid) (fragment) #status predicted <TNP>
 F;24-579/Product: 3-dehydroquininate dehydratase / shikimate 5-dehydrogenase #status expected
 F;34-245/Domain: 3-dehydroquininate dehydratase homology <DQD>
 F;315-520/Domain: shikimate dehydrogenase homology <SKD>

Query Match 55.6%; Score 5; DB 2; Length 579;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
 |||||
 Db 461 KVDDT 465

RESULT 98
 JC5721
 vacuolar protein sorting protein 13b - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004
 C;Accession: JC5721
 R;Pevsner, J.; Heu, S.C.; Hyde, P.S.; Scheller, R.H.
 Gene 183, 7-14, 1996
 A;Title: Mammalian homologues of yeast vacuolar protein sorting (vps) genes implicated in
 A;Reference number: JC5720; MUID:97149272; PMID:8996080
 A;Accession: JC5721
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-617 <PRV>
 A;Cross-references: UNIPROT:Q63616; UNIPARC:UPI00001388FF; GB:U35245; NID:g1477469; PIDN
 A;Experimental source: brain
 C;Comment: This protein is involved in vasicular trafficking between the Golgi and lysos

Query Match 55.6%; Score 5; DB 2; Length 617;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
 |||||
 Db 251 VDDTF 255

RESULT 99
 T45864
 probable tyrosine phosphatase - Arabidopsis thaliana
 N;Alternate names: protein F3A4.190
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 C;Accession: T45864
 R;Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May
 submitted to the Protein Sequence Database, December 1999
 A;Reference number: 223007
 A;Accession: T45864
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-628 <BAR>
 A;Cross-references: UNIPROT:Q58N07; UNIPARC:UPI000000A6A3; EMBL:AL132978
 A;Experimental source: cultivar Columbia; BAC clone F3A4
 C;Genetics:
 A;Map position: 3
 A;Introns: 192/3; 226/3; 245/3; 267/3; 326/3; 355/3; 377/2; 399/1; 414/3; 458/2; 481/3
 A;Note: F3A4.190

Query Match 55.6%; Score 5; DB 2; Length 628;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
 |||||
 Db 57 KVDDT 61

RESULT 100

AC0741
 oligopeptidase B (EC 3.4.21.83) [imported] - Salmonella enterica subsp. enterica serovar
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AC0741
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
 th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
 S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AC0741
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-683 <PAR>
 A;Cross-references: UNIPARC:UPI000059D05; GB:AL513382; PIDN:CAD05630.1; PID:g16503127;
 C;Genetics:
 A;Gene: STY2085
 C;Superfamily: prolyl oligopeptidase
 C;Keywords: hydrolase; serine proteinase

Query Match 55.6%; Score 5; DB 2; Length 683;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7

|||||
 Db 221 DDTFY 225

RESULT 101

AB0217
 oligopeptidase B (EC 3.4.21.83) [imported] - Yersinia pestis (strain CO92)
 C;Species: Yersinia pestis
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AB0217
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AB0217
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-683 <KUR>
 A;Cross-references: UNIPROT:Q8ZFD4; UNIPARC:UPI00000CD849; GB:AL590842; PIDN:CAC90598.1
 C;Genetics:
 A;Gene: ptrB
 C;Superfamily: prolyl oligopeptidase
 C;Keywords: hydrolase; serine proteinase

Query Match 55.6%; Score 5; DB 2; Length 683;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7

|||||
 Db 221 DDTFY 225

RESULT 102

C90948
 proteinase II [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
 C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C;Accession: C90948
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
 Gaeawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
 DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
 A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: C90948
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-686 <HAY>
 A:Cross-references: UNIPROT:Q8XCK4; UNIPARC:UPI00000D0477; GB:BA000007; PIDN:BA035978.1;
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: ECs2555
 C:Superfamily: prolyl oligopeptidase

Query Match 55.6%; Score 5; DB 2; Length 686;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYVV 9
 |||||
 Db 185 TFYVV 189

RESULT 103

G85796
 proteinase II [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: G85796
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: G85796
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-686 <STO>
 A:Cross-references: UNIPROT:Q8XCK4; UNIPARC:UPI00000D0477; GB:AE005174; NID:gl2515898; H
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: pfr8
 C:Superfamily: prolyl oligopeptidase

Query Match 55.6%; Score 5; DB 2; Length 686;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYVV 9
 |||||
 Db 185 TFYVV 189

RESULT 104

AI2849
 GDEF family protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004
 C:Accession: AI2849
 R:Wood, D.W.; Scubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
 erage, G.; Gilllet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AI2849
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-696 <KUR>
 A:Cross-references: UNIPROT:Q8UDAI; UNIPARC:UPI00000D1E16; GB:AE008688; PIDN:AAL43215.1;
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu2226

A:Map position: circular chromosome
 C:Superfamily: Sensor diguanylate cyclase/c-di-GMP phosphodiesterase with MHYT sensor do

Query Match 55.6%; Score 5; DB 2; Length 696;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 672 VDDTF 676

RESULT 105

G97626
 hypothetical protein AGR_C_4046 [imported] - Agrobacterium tumefaciens (strain C58, Cere
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 05-Oct-2004
 C:Accession: G97626
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: G97626
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-696 <KUR>
 A:Cross-references: UNIPROT:Q8UDAI; UNIPARC:UPI00000D1E16; GB:AE007869; PIDN:AAK87968.1;
 C:Genetics:
 A:Gene: AGR_C_4046
 A:Map position: circular chromosome
 C:Superfamily: Sensor diguanylate cyclase/c-di-GMP phosphodiesterase with MHYT sensor do

Query Match 55.6%; Score 5; DB 2; Length 696;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 672 VDDTF 676

RESULT 106

TS1034
 hypothetical protein B15I20.40 [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 31-Dec-2004
 C:Accession: TS1034
 R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, July 2000
 A:Reference number: 225286
 A:Accession: TS1034
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-705 <SCH>
 A:Cross-references: UNIPROT:Q96U83; UNIPARC:UPI0000179F6E; EMBL:AL388900; GSPDB:GN00116;
 A:Experimental source: BAC clone B15I20; strain OR74A
 C:Genetics:
 A:Gene: NCSP:B15I20.40
 A:Map position: 6
 A:Introns: 287/3

Query Match 55.6%; Score 5; DB 2; Length 705;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 Db 379 DDTFY 383

RESULT 107

B32571

ribosomal protein S6 kinase II (EC 2.7.1.-) alpha chain homolog (clone Mu6A) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: B32571
 R:Alcorta, D.A.; Crews, C.M.; Sweet, L.J.; Bankston, L.; Jones, S.W.; Erikson, R.L.
 Mol. Cell. Biol. 9, 3850-3859, 1989
 A:Title: Sequence and expression of chicken and mouse rsk: homologs of Xenopus laevis r1
 A:Reference number: A93113; MUID:89384612; PMID:2779569
 A:Accession: B32571
 A:Molecule type: mRNA
 A:Residues: 1-724 <ALC>
 A:CROSS-references: UNIPROT:P18653; UNIPARC:UPI0000020D74; GB:M23489
 C:Superfamily: ribosomal protein S6 kinase II; protein kinase homology
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:60-321/Domain: protein kinase homology <KIN1>
 F:68-76/Region: protein kinase homology <KIN2>
 F:416-675/Domain: protein kinase ATP-binding motif
 F:405-664/Domain: protein kinase homology <KIN2>

Query Match 55.6%; Score 5; DB 1; Length 724;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFFY 7
 |||||
 Db 335 DDTFFY 339

RESULT 108
 I51901
 ribosomal protein S6 kinase 2 (EC 2.7.1.-) 1 - human
 N:Alternate names: MAP kinase-activated PK1; p90 S6 kinase; ribosomal protein S6 kinase
 C:Species: Homo sapiens (man)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I51901
 R:Moller, D.E.; Xia, C.H.; Tang, W.; Zhu, A.X.; Jakubowski, M.
 Am. J. Physiol. 266, 351-359, 1994
 A:Title: Human rsk isoforms: cloning and characterization of tissue-specific expression.
 A:Reference number: I51901
 A:Accession: I51901
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-735 <MOL>
 A:CROSS-references: UNIPROT:Q15418; UNIPARC:UPI0000035BE4; GB:I07597; NID:g292456; PIDN:
 C:Comment: Although ribosomal protein S6 (see PIR:R3HU6) is phosphorylated by this enzyme
 C:Genetics:
 A:Gene: GDB:RPS6KAL; RSK; HU-1; RSK1
 A:CROSS-references: GDB:365638; OMIM:601684
 A:Map position: 3pter-3qter
 C:Superfamily: ribosomal protein S6 kinase II; protein kinase homology
 C:Keywords: ATP; monomer; phosphoprotein; phosphotransferase; serine/threonine-specific
 F:60-321/Domain: protein kinase homology <KIN1>
 F:68-76/Region: protein kinase ATP-binding motif
 F:416-675/Domain: protein kinase homology <KIN2>
 F:424-432/Region: protein kinase ATP-binding motif

Query Match 55.6%; Score 5; DB 2; Length 735;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFFY 7
 |||||
 Db 346 DDTFFY 350

RESULT 109
 A53300
 ribosomal protein S6 kinase (EC 2.7.-) II - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: A53300
 R:Grove, J.R.; Price, D.J.; Banerjee, P.; Balasubramanyam, A.; Ahmad, M.F.; Avruch, J.
 Biochemistry 32, 7727-7738, 1993
 A:Title: Regulation of an epitope-tagged recombinant Rsk-1 S6 kinase by phorbol ester an

A:Reference number: A53300; MUID:93349850; PMID:7688567
 A:Accession: A53300
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-735 <RES>
 A:CROSS-references: UNIPROT:Q63531; UNIPARC:UPI000012DB2D; GB:M99169; NID:g206771; PIDN:
 C:Genetics:
 A:Gene: Rsk-1
 C:Superfamily: ribosomal protein S6 kinase II; protein kinase homology
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:60-321/Domain: protein kinase homology <KIN1>
 F:68-76/Region: protein kinase ATP-binding motif
 F:416-675/Domain: protein kinase homology <KIN2>
 F:424-432/Region: protein kinase ATP-binding motif #status atypical

Query Match 55.6%; Score 5; DB 2; Length 735;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFFY 7
 |||||
 Db 346 DDTFFY 350

RESULT 110
 A81430
 outer membrane protein Cj0129c [imported] - Campylobacter jejuni (strain NCTC 11168)
 C:Species: Campylobacter jejuni
 C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C:Accession: A81430
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
 Nature 403, 665-668, 2000
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals, hy:
 A:Reference number: A81250; MUID:20150912; PMID:10688204
 A:Accession: A81430
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-739 <PAR>
 A:CROSS-references: UNIPROT:Q9PI28; UNIPARC:UPI00000C2051; GB:AL1139074; GB:AL111168; NI:
 A:Experimental source: serotype O2, strain NCTC 11168
 C:Genetics:
 A:Gene: Cj0129c

Query Match 55.6%; Score 5; DB 2; Length 739;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 |||||
 Db 400 KVDDT 404

RESULT 111
 A32571
 ribosomal protein S6 kinase II (EC 2.7.1.-) alpha chain homolog - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A32571
 R:Alcorta, D.A.; Crews, C.M.; Sweet, L.J.; Bankston, L.; Jones, S.W.; Erikson, R.L.
 Mol. Cell. Biol. 9, 3850-3859, 1989
 A:Title: Sequence and expression of chicken and mouse rsk: homologs of Xenopus laevis r1
 A:Reference number: A93113; MUID:89384612; PMID:2779569
 A:Accession: A32571
 A:Molecule type: mRNA
 A:Residues: 1-752 <ALC>
 A:CROSS-references: UNIPROT:P18652; UNIPARC:UPI000012DB30; GB:M28488; NID:g551555; PIDN:
 C:Superfamily: ribosomal protein S6 kinase II; protein kinase homology
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:78-339/Domain: protein kinase homology <KIN1>
 F:86-94/Region: protein kinase ATP-binding motif
 F:433-692/Domain: protein kinase homology <KIN2>

Query Match 55.6%; Score 5; DB 1; Length 752;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DTFY 7
 |||||
 DB 364 DTFY 368

RESULT 112

T27276
 hypothetical protein Y63D3A.6b - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T27276
 R:White, S.
 submitted to the EMBL Data Library, October 1998
 A:Reference number: Z20335
 A:Accession: T27276
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-752 <WIL>
 A:Cross-references: UNIPROT:Q9UIV9; UNIPARC:UPI000007E517; EMBL:AL032652; PIDN:CAA21710.
 C:Experimental source: clone Y63D3A
 C:Genetics:
 A:Gene: CBSP:Y63D3A.6b
 A:Map position: 1
 A:Introns: 42/1, 80/3; 132/3; 211/3; 248/1, 329/2; 400/3; 564/3; 676/3; 711/3

Query Match 55.6%; Score 5; DB 2; Length 752;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYV 9
 |||||
 DB 14 TFYV 18

RESULT 113

D87965
 protein Y63D3A.6b [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: D87965
 R:anonymous, The C. elegans Sequencing Consortium.
 Science 282, 202-208, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
 A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: D87965
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-778 <STO>
 A:Cross-references: UNIPROT:Q9UIV9; UNIPARC:UPI000017A561; GB:chr_I; PIDN:CAA21710.1; PI
 C:Genetics:
 A:Gene: Y63D3A.6b
 A:Map position: 1

Query Match 55.6%; Score 5; DB 2; Length 778;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYV 9
 |||||
 DB 14 TFYV 18

RESULT 114

T00990
 hypothetical protein At2g26570 [imported] - Arabidopsis thaliana
 N:Alternate names: hypothetical protein T9J22.24
 C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 C:Accession: T00990; B84662
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, R.
 submitted to the EMBL Data Library, April 1998
 A:Description: Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence.
 A:Reference number: Z14161
 A:Accession: T00990
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-807 <ROU>
 A:Cross-references: UNIPROT:O48724; UNIPARC:UPI00000A832E; EMBL:AC002505; NID:g2739359;
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: B84662
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-807 <STO>
 A:Cross-references: UNIPARC:UPI00000A832E; GB:AE002093; NID:g2739382; PIDN:AAC14505.1; C
 C:Genetics:
 A:Gene: At2g26570; T9J22.24
 A:Map position: 2
 A:Introns: 196/3

Query Match 55.6%; Score 5; DB 2; Length 807;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 DB 80 VDDTF 84

RESULT 115

S69563
 suppressor protein PSp1 - Yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YDR505c
 C:Species: Saccharomyces cerevisiae
 C>Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C:Accession: S69563; S59357
 R:Dietrich, F.S.
 submitted to the EMBL Data Library, August 1995
 A:Description: The sequence of S. cerevisiae cosmids 8166, 9787, 9717, and lambda 3073.
 A:Reference number: S69553
 A:Accession: S69563
 A:Molecule type: DNA
 A:Residues: 1-841 <DIE>
 A:Cross-references: UNIPROT:P50896; UNIPARC:UPI00001327E3; EMBL:U33057; NID:g927764; PID
 R:Formosa, T.; Nittis, T.
 submitted to the EMBL Data Library, August 1995
 A:Description: High copy suppressors of the temperature sensitivity of DNA polymerase al
 A:Reference number: S59357
 A:Accession: S59357
 A:Molecule type: DNA
 A:Residues: 1-115, 'C', 117-121, 'KCLRLIQSCVP', 134-197, 'RAILLPHHTVLAT', 211-731, 'K', 733-841
 A:Cross-references: UNIPARC:UPI0000168A3B; EMBL:U33115; NID:g992653; PID:g992654
 C:Genetics:
 A:Gene: SGD:PSP1; GIN5
 A:Cross-references: SGD:S0002913; MIPS:YDR505c
 A:Map position: 4R
 C:Function:
 A:Description: high copy suppressor of polymerase mutations

Query Match 55.6%; Score 5; DB 2; Length 841;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYV 9
 |||||

Db 734 TFFYV 738

RESULT 116

T01809
hypothetical protein A.TM021B04.3 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01809
R;Dante, M.; Wamsley, P.; Gibson, A.
submitted to the EMBL Data Library, June 1997
A;Description: The sequence of A. thaliana TM021B04.
A;Reference number: Z1440
A;Accession: T01809
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-938 <DAN>
A;Cross-references: UNIPROT:O04660; UNIPARC:UPI00000A24EC; EMBL:AF007271; NID:g2191181;
C;Genetics:
A;Gene: ATSP:A.TM021B04.3
A;Map position: 5
A;Introns: 125/1; 559/3; 664/1; 798/3

Query Match 55.6%; Score 5; DB 2; Length 938;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 209 VDDTF 213

RESULT 117

S44622
C50C3.3 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 30-Jun-2001
C;Accession: S44622
R;Favell, A.D.
submitted to the EMBL Data Library, May 1993
A;Description: Sequence of the C. elegans cosmid C50C3.
A;Reference number: S44627
A;Accession: S44622
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-955 <FAV>
A;Cross-references: UNIPARC:UPI000017B6B2; EMBL:L14433; NID:g289649; PID:g289655
C;Genetics:
A;Introns: 203/3; 461/3; 599/3; 702/1

Query Match 55.6%; Score 5; DB 2; Length 955;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
Db 533 KVDDT 537

RESULT 118

B71468
probable insulinase family/proteinase III - Chlamydia trachomatis (serotype D, strain UW)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 31-Dec-2004
C;Accession: B71468
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: B71468
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-956 <ARN>

A;Cross-references: UNIPROT:O84812; UNIPARC:UPI00000D33B0; GB:AE001353; GB:AE001273; NI;
A;Experimental source: serotype D, strain UW-3/Cx

C;Genetics:

A;Gene: ptr

C;Superfamily: insulin-degrading enzyme (IDE)/zinc protease

Query Match 55.6%; Score 5; DB 2; Length 956;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 491 DDTFY 495

RESULT 119

T39912
conserved hypothetical protein SPBC216.06c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39912
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21890
A;Accession: T39912
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-971 <LYN>
A;Cross-references: UNIPROT:Q9UUM2; UNIPARC:UPI000006C882; EMBL:AL049558; PIDN:CAB40166
A;Experimental source: strain 972h; cosmid c216
C;Genetics:
A;Gene: SPDB:SPBC216.06c
A;Map position: 2
A;Introns: 316/3

Query Match 55.6%; Score 5; DB 2; Length 971;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
|||||
Db 670 DTFY 674

RESULT 120

T43656
mating-type switching protein swil - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43656
R;Schmidt, H.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z22605
A;Accession: T43656
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-971 <SCH>
A;Cross-references: UNIPROT:Q9UUM2; UNIPARC:UPI000016916E; EMBL:Y19036; PIDN:CAB44362.1

C;Genetics:

A;Gene: swil

A;Introns: 316/3

Query Match 55.6%; Score 5; DB 2; Length 971;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
|||||
Db 670 DTFY 674

RESULT 121

B89009
Protein T27C4.4 [imported] - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: B89009
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biological processes
A:Reference number: A75000; PMID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999
A:Accession: B89009
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-973 <STO>
A:Cross-references: UNIPROT:O61907; UNIPARC:UPI000017A66C; GB:chr_V; PIDN:AAC17700.1; PIR:17700.1
C:Genetics:
A:Gene: T27C4.4
A:Map position: 5

Query Match
Best Local Similarity 55.6%; Score 5; DB 2; Length 973;
Matches 100.0%; Pred.No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 258 DDTFY 262

RESULT 122
D83393
RND multidrug efflux transporter PA2018 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C;Species: *Pseudomonas aeruginosa*
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83393
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A;Reference number: AB2950; MUID:20437337; PMID:10984043
A;Accession: D83393
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1045 <STO>
A;Cross-references: UNIPROT:Q9RG59; UNIPARC:UPI00000D420B; CB:AE004628; CB:AE004091; NID
A;Experimental source: strain PA01
C;Genetics:
C;Superfamily: acriflavin resistance protein

| | | | | | |
|-----------------------|--------|--------------|---------|-------------|---|
| Query Match | 55.6% | Score 5 | DB 2 | Length 1045 | |
| Best Local Similarity | 100.0% | Pred. No. | 2.9e+02 | | |
| Matches | 5 | Conservative | 0 | Mismatches | 0 |
| | | | | Indels | 0 |
| Gaps | 0 | | | | |

| | | | |
|----|-----|-----------|--|
| Qy | 1 | KVDDT 5 | |
| | | | |
| Db | 234 | KVDDT 238 | |

| | |
|---|--------------------------------|
| RESULT 123 | |
| AE1852 | |
| hypothetical protein alr0366 [imported] - Nostoc sp. (strain PCC 7120) | |
| C:Species: Nostoc sp. PCC 7120 | |
| A:Name: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 | |
| C:Date: 14-Dec-2001 | #sequence_revision 14-Dec-2001 |
| A:Reference number: AB1807 | #PMID:11759840 |
| C:Accession: AE1852 | |
| R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. | |
| Nakaazaki, N.; Shimpo, S. | 2001 |
| DNA Res. | 8, 205-213, 2001 |
| A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena | |
| A:Reference number: AB1807 | #PMID:11759840 |
| A:Accession: AE1852 | |

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1152 <KUR>
A:Cross-references: UNIPROT:08YZU1; UNIPARC:UPI000000CDD0F; GB:BA000019; PIDN:BA072324.1
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr0366

```
Query Match      55.6%; Score 5; DB 2; Length 1152;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 KVDDT 5
|||
Db 370 KVDDT 374

RESULT 124
AG2457

transcription-repair coupling factor all5215 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AG2457
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; PMID:11759840; PMID:11759845

A;Accession:On: RefSeq
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1185 <KUR>
A;Cross-references: UNIPROT:Q8YLTL; UNIPARC:UPI00000CEDD4; GB:BA000019; PIDN:BA076914.1;
A;Experimental source: strain PCC 7120
C;Genetics:
C;Gene: all5215
C;Superfamily: transcription-repair coupling protein

| | | | | |
|-----------------------|-----------------|--------------------|-----------|--------------|
| Query Match | 55.6% | Score 5; | DB 2; | Length 1185; |
| Best Local Similarity | 100.0%; | Pred. No. 3.2e+02; | | |
| Matches 5; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | |
|----|------|-------|------|
| Qy | 1 | KVDDT | 5 |
| | | | |
| Db | 1028 | KVDDT | 1032 |

RESULT 125
GAF domain protein (cyclic nt signal transduct.) PFB0510w - malaria parasite (Plasmodium falciparum)
C/Species: Plasmodium falciparum
C/Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C/Accession: D71613
R/Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Perleac, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998

A>Title: Chromosome 2 sequence of the human malaria parasite *Plasmodium falciparum*.
A/Reference number: A71600; MUID:95021743; PMID:9804551
A/Accession: D71613
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-1245 <AR>
A/Cross-references: UNIPROT:O96195; UNIPARC:UPI00000761C9; GB:AE001399; GB:AE001362; NID
A/Experimental source: clone 3D7
A/Genetics: C:Genetics:
A/Gene: PFB0510w

```

Query Match      55.6%; Score 5; DB 2; Length 1245;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 DDTFY 7

```


Db 759 DDTFY 763
|||||
RESULT 126
T14476
pela protein - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14476
R;Yasukawa, H.; Mohanty, S.; Firtel, R.A.
submitted to the EMBL Data Library, December 1997
A:Reference number: Z18117
A:Accession: T14476
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1269 <YAS>
A:Cross-references: UNIPROT:O43993; UNIPARC:UPI000007CA48; EMBL:AF038919; NID:g2766695;
A:Experimental source: strain Kax3
C:Genetics:
A:Gene: pela
Query Match 55.6%; Score 5; DB 2; Length 1369;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDT 5
|||||
Db 395 KVDDT 399
RESULT 127
S58307
hypothetical 149.2K protein SPAC1F5.01 c18b11.11 - fission yeast (Schizosaccharomyces po
C:Species: Schizosaccharomyces pombe
C>Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: T37903; T38094; S58307
R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z21753
A:Accession: T37903
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1294 <DE2>
A:Cross-references: UNIPROT:Q09716; UNIPARC:UPI0000139F4B; EMBL:Z50728; NID:g929886; PID
A:Experimental source: strain 972h-; cosmid c18B11
R;Gentles, S.; Odell, C.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z21768
A:Accession: T38094
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1143-1294 <GEN>
A:Cross-references: UNIPARC:UPI0000162011; EMBL:Z68136; PIDN:CAA92229.1; GSPDB:GN000066;
A:Experimental source: strain 972h-; cosmid c1F5
C:Genetics:
A:Gene: SPAC1F5.01; SPAC18B11.11
A:Map position: 1L
Query Match 55.6%; Score 5; DB 2; Length 1294;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TFYIV 9
|||||
Db 560 TFYIV 564
RESULT 128
E71622
probable membrane associated protein PFB0125c - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004

C:Accession: E71622
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Azavind, L.; Koonin, E.V.
; Perteu, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: E71622
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1308 <GAR>
A:Cross-references: UNIPROT:O96129; UNIPARC:UPI000017B62A; GB:AE001374; GB:AE001362; NI
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0125c
Query Match 55.6%; Score 5; DB 2; Length 1308;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 DDTFY 7
|||||
Db 321 DDTFY 325
RESULT 129
T40993
protein kinase cekl - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40993
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
submitted to the EMBL Data Library, March 1999
A:Reference number: Z21962
A:Accession: T40993
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1338 <LYN>
A:Cross-references: UNIPROT:P38938; UNIPARC:UPI00001274D0; EMBL:AL049559; PIDN:CAB40178
A:Experimental source: strain 972h-; cosmid c1450
C:Genetics:
A:Gene: SPDB:SPCC1450.11c
A:Map position: 3
Query Match 55.6%; Score 5; DB 2; Length 1338;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
|||||
Db 1078 VDDTF 1082
RESULT 130
S50943
hypothetical protein YML049c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YM9827.03c
C:Species: Saccharomyces cerevisiae
C>Date: 10-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S50943
R;Odell, C.; Bowman, S.
submitted to the EMBL Data Library, January 1995
A:Reference number: S50941
A:Accession: S50943
A:Molecule type: DNA
A:Residues: 1-1361 <ODE>
A:Cross-references: UNIPROT:Q04693; UNIPARC:UPI00000530F0; EMBL:Z47816; NID:g642303; PI
C:Genetics:
A:Gene: SGD:RSE1
A:Cross-references: SGD:S0004513; MIPS:YML049c
A:Map position: 13L
Query Match 55.6%; Score 5; DB 2; Length 1361;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db 1251 DDTFY 1255

RESULT 131
 T22111.2 protein - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: G86344
 R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: G86344
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1552 <STO>
 A:Cross-references: UNIPROT:Q9LPV0; UNIPARC:UPI00000A17A2; GB:AE005172; NID:g9886986; PI
 C:Genetics:
 A:Map position: 1

Query Match 55.6%; Score 5; DB 2; Length 1552;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 465 KVDDT 469

RESULT 132
 T29861
 hypothetical protein F10G2.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T29861
 R:Murray, J.; Wohldmann, P.
 submitted to the EMBL Data Library, July 1996
 A:Description: The sequence of C. elegans cosmid F10G2.
 A:Reference number: Z20701
 A:Accession: T29861
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1614 <MUR>
 A:Cross-references: UNIPARC:UPI000017B8DA; EMBL:U64836; PIDN:AAB04826.1; GSPDB:GN000023;
 A:Experimental source: strain Bristol N2; clone F10G2
 C:Genetics:
 A:Gene: CESP:F10G2.5
 A:Map position: 5
 A:Introns: 62/2; 738/1; 778/3; 951/3; 1040/3; 1108/2; 1152/2; 1294/3; 1401/3

Query Match 55.6%; Score 5; DB 2; Length 1614;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFIYV 9
 Db 1453 TFIYV 1457

RESULT 133
 S48385

hypothetical protein YIL149c - yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C>Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
 C:Accession: S48385
 R:Churcher, C.
 submitted to the EMBL Data Library, September 1994
 A:Reference number: S48310
 A:Accession: S48385
 A:Molecule type: DNA
 A:Residues: 1-1679 <CHU>
 A:Cross-references: UNIPROT:P40457; UNIPARC:UPI000013B453; GB:Z47047; EMBL:Z38059; NID:g
 C:Genetics:
 A:Gene: SGD:MLP2; MIPS:YIL149c
 A:Cross-references: SGD:S0001411
 A:Map position: 9L

Query Match 55.6%; Score 5; DB 2; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 1084 KVDDT 1088

RESULT 134
 T17485
 peptidase synthetase homolog PCZA363.5 - Amycolatopsis orientalis
 C:Species: Amycolatopsis orientalis
 C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
 C:Accession: T17485
 R:Van Wageningen, A.; Kirkpatrick, P.; Williams, D.; Harris, B.; Kershaw, J.; Lennard, N
 Chem. Biol. 3, 155-162, 1998
 A>Title: Sequencing and analysis of genes involved in the biosynthesis of a vancomycin
 A:Reference number: Z18804
 A:Accession: T17485
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1860 <VAN>
 A:Cross-references: UNIPROT:O52821; UNIPARC:UPI00000B1899; EMBL:AJ223999; NID:e1251240;
 C:Keywords: carrier protein
 F:512-953/Domain: acetate-CoA ligase homology <ACL>
 F:969-1037/Domain: acyl carrier protein homology <ACP>

Query Match 55.6%; Score 5; DB 2; Length 1860;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 Db 990 VDDTF 994

RESULT 135
 T03884
 hypothetical protein F07G11.9 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T03884
 R:Sammons, L.; Wohldmann, P.; Sansone, J.
 submitted to the EMBL Data Library, July 1997
 A:Description: The sequence of C. elegans cosmid F07G11.
 A:Reference number: Z15127
 A:Accession: T03884
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2025 <SAM>
 A:Cross-references: UNIPROT:O16237; UNIPARC:UPI0000077F90; EMBL:AF016419; NID:g2291159;
 C:Genetics:
 A:Map position: V
 A:Introns: 62/2; 703/1; 743/3; 930/3; 1019/3; 1087/2; 1131/2; 1273/3; 1380/3; 1593/2; 19
 A>Note: F07G11.9

Query Match 55.6%; Score 5; DB 2; Length 2025;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TFFYV 9
 |||||
 Db 1432 TFFYV 1436

RESULT 136
 T00327
 polypeptide - infectious flacherie virus
 C;Species: infectious flacherie virus
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T00327
 R;Isawa, H.; Asano, S.; Sahara, K.; Iizuka, T.; Bando, H.
 Arch. Virol. 143, 127-143, 1998
 A;Title: Analysis of genetic information of an insect picorna-like virus, infectious flacherie virus.
 A;Reference number: Z14139; MUID:98166871; PMID:9505971
 A;Accession: T00327
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: genomic RNA
 A;Residues: 1-3085 <ISA>
 A;Cross-references: UNIPROT:O70710; UNIPARC:UPI000000F1097; EMBL:AB000906; NID:g3025414;
 C;Keywords: polyprotein

Query Match 55.6%; Score 5; DB 2; Length 3085;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
 |||||
 Db 1175 VDDTF 1179

RESULT 137
 T22812
 hypothetical protein ZC116.3 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T22812; T27494
 R;Burton, J.
 submitted to the EMBL Data Library, June 1996
 A;Reference number: Z19618
 A;Accession: T22812
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-3871 <WIL>
 A;Cross-references: UNIPROT:Q20911; UNIPARC:UPI00000821EA; EMBL:Z74473; PIDN:CAA98952.1;
 A;Experimental source: clone F56H9
 R;Smye, R.
 submitted to the EMBL Data Library, June 1996
 A;Reference number: Z20376
 A;Accession: T27494
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-3871 <W12>
 A;Cross-references: UNIPARC:UPI00000821EA; EMBL:Z74046; PIDN:CAA98557.1; GSPDB:GN000023;
 A;Experimental source: clone ZC116
 C;Genetics:
 A;Gene: CRSP:ZC116.3
 A;Map position: 5
 A;Introns: 29/3; 66/2; 244/1; 359/3; 422/1; 549/1; 572/1; 728/1; 820/1; 889/3; 1189/1; 1276/1; 2809/1; 2906/3; 3051/3; 3176/1; 3254/1; 3341/2; 3536/1; 3565/2; 3582/3; 3609/1;
 C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology

Query Match 55.6%; Score 5; DB 2; Length 3871;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
 |||||

Db 1380 KVDDT 1384

RESULT 138
 T30192
 Probable peptide synthetase - Aureobasidium pullulans
 C;Species: Aureobasidium pullulans
 C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
 C;Accession: T30192
 R;Peery, R.B.; Thornevell, S.J.; Tobin, M.B.; Skatrud, P.L.
 submitted to the EMBL Data Library, January 1997
 A;Description: Discovery of an MDR-like gene adjacent to a peptide synthetase in Aureobasidium pullulans.
 A;Reference number: Z20767
 A;Accession: T30192
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-10797 <PSE>
 A;Cross-references: UNIPROT:O94116; UNIPARC:UPI000017CF3F; EMBL:U85909; NID:g4099310; P
 C;Genetics:
 A;Introns: 2078/3; 4142/3; 6075/3; 7963/3; 7985/2
 C;Keywords: carrier protein
 F;1618-1688/Domain: acyl carrier protein homology <ACP1>
 F;3682-3752/Domain: acyl carrier protein homology <ACP2>
 F;5615-5685/Domain: acyl carrier protein homology <ACP3>
 F;7503-7573/Domain: acyl carrier protein homology <ACP4>
 F;9683-9752/Domain: acyl carrier protein homology <ACP5>

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 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
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 Db 10462 KVDDT 10466

RESULT 139
 B53415
 lectin chain B - Iris hollandica (Dutch Iris) (fragment)
 C;Species: Iris hollandica (Dutch Iris)
 C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999
 C;Accession: B53415
 R;Mo, H.; Van Damme, E.J.M.; Peumans, W.J.; Goldstein, I.J.
 J. Biol. Chem. 269, 7666-7673, 1994
 A;Title: Isolation and characterization of an N-acetyl-D-galactosamine-binding lectin
 A;Reference number: A53415; MUID:94171801; PMID:8125593
 A;Accession: B53415
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-25 <MOA>
 A;Cross-references: UNIPARC:UPI000017CAD0

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 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDT 5
 |||||
 Db 1 VDDT 4

RESULT 140
 C64536
 hypothetical protein HP0131 - Helicobacter pylori (strain 26695)
 C;Species: Helicobacter pylori
 C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C;Accession: C64536
 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
 Nature 388, 539-547, 1997
 A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
 A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: C64536
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-33 <TOM>
A:Cross-references: UNIPROT:O24945; UNIPARC:UPI00000C07A2; GB:AE000535; GB:AE000511; NID

Query Match 44.4%; Score 4; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFFY 8
Db 11 TFFY 14

RESULT 141
I56058
cell surface glycoprotein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56058
R:Nakayama, K.; Tokito, S.; Jaulin, C.; Delarbre, C.; Kourilsky, P.; Nakauchi, H.; Gache
J. Immunol. 144, 2400-2408, 1990
A:Title: Comparative structure of two duplicated T1a class I genes (T10c and 37) of the
A:Reference number: I56058; MUID:90187889; PMID:1968929
A:Accession: I56058
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-37 <RES>
A:Cross-references: UNIPROT:Q31130; UNIPARC:UPI000008A63F; GB:M34072; NID:G623439; PIDN
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein

Query Match 44.4%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 18 VDDT 21

RESULT 142
S21665
S-layer protein - Acetogenium kivui
C:Species: Acetogenium kivui
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S21665
R:Peters, J.; Rudolf, S.; Oschkinat, H.; Mengelle, R.; Sumper, M.; Kellermann, J.; Lottsp
Biol. Chem. Hoppe-Seyler 373, 171-176, 1992
A:Title: Evidence for tyrosine-linked glycosaminoglycan in a bacterial surface protein.
A:Reference number: S21665; MUID:92281680; PMID:1596358
A:Accession: S21665
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-37 <PET>
A:Cross-references: UNIPARC:UPI000017A8BF

Query Match 44.4%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDD 4
Db 26 KVDD 29

RESULT 143
E72269
hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: E72269
R:Nelson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: E72269
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-37 <ARN>
A:Cross-references: UNIPROT:O9X125; UNIPARC:UPI00000C12B9; GB:AE001785; GB:AE000512; NID
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1299

Query Match 44.4%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDD 4
Db 5 KVDD 8

RESULT 144
S71381
lebetin 2 isoform alpha - Vipera lebetina
C:Species: Vipera lebetina
C>Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C:Accession: S71381; S71382; S71379
R:Barbouche, R.; Marrakchi, N.; Mansuelle, P.; Krifi, M.; Fenouillet, E.; Rochat, H.; El
FEBS Lett. 392, 6-10, 1996
A:Title: Novel anti-platelet aggregation polypeptides from Vipera lebetina venom: isolat
A:Reference number: S71379; MUID:96354866; PMID:8769304
A:Accession: S71381
A:Molecule type: protein
A:Residues: 1-38 <BAR>
A:Cross-references: UNIPROT:Q7LZ09; UNIPARC:UPI00000030733
A:Experimental source: venom
A:Accession: S71382
A:Molecule type: protein
A:Residues: 2-38 <BA2>
A:Cross-references: UNIPARC:UPI00000030734
A:Experimental source: venom
A:Accession: S71379
A:Molecule type: protein
A:Residues: 1-13 <BA3>
A:Cross-references: UNIPARC:UPI0000003072F
A:Experimental source: venom
C:Keywords: anticoagulant; venom
F:14-30/Disulfide bonds: #status predicted

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Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDD 4
Db 32 KVDD 35

RESULT 145
B81717
hypothetical protein TC0307 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81717
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: B81717
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-46 <TET>
A;Cross-references: UNIPROT:Q9PL01; UNIPARC:UPI0000057893; GB:AE002298; GB:AE002160; NID:10580362;
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0307

Query Match 44.4%; Score 4; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFFY 8
|||
Db 27 TFFY 30

RESULT 146
JH0643
GTP-binding protein rab13 - mouse (fragment)
N;Alternate names: rab protein Rab13
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JH0643
R;Chavrier, P.; Simons, K.; Zerial, M.
Gene 112, 261-264, 1992
A;Title: The complexity of the Rab and Rho GTP-binding protein subfamilies revealed by a
A;Reference number: JH0639; MUID:92210010; PMID:1555775
A;Accession: JH0643
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-49 <CHA>
A;Cross-references: UNIPROT:P35283; UNIPARC:UPI0000027C50; GB:W79303
A;Experimental source: kidney
C;Genetics:
A;Gene: rab13
A;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; membrane trafficking; P-loop

Query Match 44.4%; Score 4; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTF 6
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Db 11 DDTF 14

RESULT 147
A60718
phospholipase A2 homolog, non-pancreatic - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Aug-2004
C;Accession: A60718
R;Seilhamer, J.J.; Randall, T.L.; Johnson, L.K.; Heinzmann, C.; Klisak, I.; Sparkes, R.S.
J. Cell. Biochem. 39, 327-337, 1989
A;Title: Novel gene exon homologous to pancreatic phospholipase A-2: sequence and chromo
A;Reference number: A60718; MUID:89214375; PMID:2708461
A;Accession: A60718
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-50 <SEI>
A;Cross-references: UNIPROT:Q7M4M6; UNIPARC:UPI0000142253
C;Comment: This genomic fragment is homologous to exon 2 of pancreatic phospholipase A2.
C;Genetics:
A;Map position: 1
C;Superfamily: Phospholipase A2

Query Match 44.4%; Score 4; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
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Db 45 VDDT 48

RESULT 148
B60718
phospholipase A2 homolog, non-pancreatic - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 16-Aug-2004
C;Accession: B60718
R;Seilhamer, J.J.; Randall, T.L.; Johnson, L.K.; Heinzmann, C.; Klisak, I.; Sparkes, R.
J. Cell. Biochem. 39, 327-337, 1989
A;Title: Novel gene exon homologous to pancreatic phospholipase A-2: sequence and chrom
A;Reference number: A60718; MUID:89214375; PMID:2708461
A;Accession: B60718
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <SEI>
A;Cross-references: UNIPROT:Q7M333; UNIPARC:UPI0000175895
C;Superfamily: Phospholipase A2

Query Match 44.4%; Score 4; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
|||
Db 45 VDDT 48

RESULT 149
B84236
hypothetical protein Vng0788h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84236
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,
; Leitchauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabb
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: B84160; MUID:20504483; PMID:11016950
A;Accession: B84236
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-53 <STO>
A;Cross-references: UNIPROT:Q9HRA4; UNIPARC:UPI000006371D; GB:AE004437; NID:10580362;
C;Genetics:
A;Gene: VNG0788H

Query Match 44.4%; Score 4; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
|||
Db 5 VDDT 8

RESULT 150
S05489
alpha-amylase (EC 3.2.1.1) 2.54 precursor - wheat (fragment)
C;Species: Triticum aestivum (common wheat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Dec-2004
C;Accession: S05489
R;Huttly, A.K.; Martienssen, R.A.; Baulcombe, D.C.
Mol. Gen. Genet. 214, 232-240, 1988
A;Title: Sequence heterogeneity and differential expression of the alpha--Amy-2 gene fa
A;Reference number: S05486; MUID:89181522; PMID:2467183
A;Accession: S05489
A;Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-58 <HUT>
A:Cross-references: UNIPROT:P11786; UNIPARC:UPI0000175A39; EMBL:X13580
C:Genetics:
A:Gene: amy2
A:Map position: 7A
A:Introns: 29/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, plant type; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDD 4
Db 49 KVDD 52

Search completed: May 17, 2006, 06:28:04
Job time : 59.5 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 17, 2006, 06:28:51 ; Search time 37 Seconds
(without alignments)
21.291 Million cell updates/sec

Title: US-10-764-985-2

Perfect score: 9

Sequence: 1 KVDDTFYV 9

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 1

Total number of hits satisfying chosen parameters: 624216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTRUS COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | | Length | DB | ID | Description |
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| 1 | 6 | 66.7 | 382 | 2 | US-09-489-039A-10751 | | Sequence 10751, A |
| 2 | 5 | 55.6 | 21 | 2 | US-09-962-756-691 | | Sequence 691, App |
| 3 | 5 | 55.6 | 27 | 2 | US-09-962-756-1425 | | Sequence 1425, Ap |
| 4 | 5 | 55.6 | 78 | 2 | US-09-732-210-338 | | Sequence 338, App |
| 5 | 5 | 55.6 | 80 | 2 | US-09-732-210-346 | | Sequence 346, App |
| 6 | 5 | 55.6 | 126 | 2 | US-09-740-002-23 | | Sequence 23, Appl |
| 7 | 5 | 55.6 | 128 | 2 | US-09-270-767-60895 | | Sequence 60895, A |
| 8 | 5 | 55.6 | 143 | 2 | US-09-248-76A-14343 | | Sequence 14343, A |
| 9 | 5 | 55.6 | 157 | 2 | US-09-668-262A-2 | | Sequence 2, Appli |
| 10 | 5 | 55.6 | 157 | 2 | US-10-427-442-2 | | Sequence 2, Appli |
| 11 | 5 | 55.6 | 162 | 2 | US-09-270-767-56930 | | Sequence 56930, A |
| 12 | 5 | 55.6 | 174 | 2 | US-09-270-757-57344 | | Sequence 57344, A |
| 13 | 5 | 55.6 | 177 | 2 | US-09-710-279-2532 | | Sequence 2532, Ap |
| 14 | 5 | 55.6 | 202 | 2 | US-09-107-532A-4432 | | Sequence 4432, Ap |
| 15 | 5 | 55.6 | 235 | 2 | US-09-216-393B-31 | | Sequence 31, Appl |
| 16 | 5 | 55.6 | 230 | 2 | US-10-101-464A-787 | | Sequence 787, App |
| 17 | 5 | 55.6 | 279 | 1 | US-08-326-286-5 | | Sequence 5, Appli |
| 18 | 5 | 55.6 | 285 | 2 | US-09-252-91A-30991 | | Sequence 30991, A |
| 19 | 5 | 55.6 | 301 | 2 | US-09-328-332-6685 | | Sequence 6685, Ap |
| 20 | 5 | 55.6 | 349 | 2 | US-09-940-016-9786 | | Sequence 9786, Ap |
| 21 | 5 | 55.6 | 370 | 2 | US-09-134-000C-5050 | | Sequence 5050, Ap |
| 22 | 5 | 55.6 | 373 | 2 | US-09-914-098-34 | | Sequence 34, Appl |
| 23 | 5 | 55.6 | 378 | 2 | US-10-414-759-2 | | Sequence 2, Appli |
| 24 | 5 | 55.6 | 378 | 2 | US-10-414-759-4 | | Sequence 4, Appli |
| 25 | 5 | 55.6 | 378 | 2 | US-10-123-058-2 | | Sequence 2, Appli |
| 26 | 5 | 55.6 | 378 | 2 | US-10-123-058-4 | | Sequence 4, Appli |

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| 101 | 4 | 44.4 | 6 | 2 | US-09-747-408-22 | Sequence 22, Appl | 174 | 4 | 44.4 | 22 | 2 | US-09-202-161B-28 | Sequence 28, Appl |
| 102 | 4 | 44.4 | 7 | 2 | US-09-966-288-23 | Sequence 23, Appl | 175 | 4 | 44.4 | 23 | 1 | US-08-293-778-5 | Sequence 5, Appl |
| 103 | 4 | 44.4 | 7 | 2 | US-09-996-288-90 | Sequence 90, Appl | 176 | 4 | 44.4 | 23 | 1 | US-08-480-190-101 | Sequence 101, App |
| 104 | 4 | 44.4 | 7 | 2 | US-09-996-288-99 | Sequence 99, Appl | 177 | 4 | 44.4 | 23 | 1 | US-08-480-190-101 | Sequence 101, App |
| 105 | 4 | 44.4 | 7 | 2 | US-09-996-265-23 | Sequence 23, Appl | 178 | 4 | 44.4 | 23 | 1 | US-08-488-379-101 | Sequence 101, App |
| 106 | 4 | 44.4 | 7 | 2 | US-09-996-265-90 | Sequence 90, Appl | 179 | 4 | 44.4 | 23 | 1 | US-08-488-379-195 | Sequence 195, App |
| 107 | 4 | 44.4 | 7 | 2 | US-09-996-265-99 | Sequence 99, Appl | 180 | 4 | 44.4 | 23 | 1 | US-08-475-399A-101 | Sequence 101, App |
| 108 | 4 | 44.4 | 8 | 2 | US-10-092-263-4 | Sequence 4, Appl | 181 | 4 | 44.4 | 23 | 2 | US-08-475-399A-195 | Sequence 195, App |
| 109 | 4 | 44.4 | 10 | 1 | US-08-166-195A-22 | Sequence 22, Appl | 182 | 4 | 44.4 | 23 | 2 | US-08-077-255A-101 | Sequence 101, App |
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| 111 | 4 | 44.4 | 10 | 1 | US-08-436-772-22 | Sequence 22, Appl | 184 | 4 | 44.4 | 23 | 5 | PCT-US93-07545-101 | Sequence 101, App |
| 112 | 4 | 44.4 | 10 | 1 | US-08-436-772-23 | Sequence 23, Appl | 185 | 4 | 44.4 | 23 | 5 | PCT-US93-07545-195 | Sequence 195, App |
| 113 | 4 | 44.4 | 10 | 1 | US-08-436-883B-22 | Sequence 22, Appl | 186 | 4 | 44.4 | 25 | 2 | US-09-200-757-5 | Sequence 5, Appl |
| 114 | 4 | 44.4 | 10 | 1 | US-08-436-883B-23 | Sequence 23, Appl | 187 | 4 | 44.4 | 28 | 1 | US-08-436-772-55 | Sequence 55, Appl |
| 115 | 4 | 44.4 | 10 | 2 | US-09-200-757-3 | Sequence 3, Appl | 188 | 4 | 44.4 | 28 | 1 | US-08-436-883B-55 | Sequence 55, Appl |
| 116 | 4 | 44.4 | 14 | 1 | US-09-200-757-4 | Sequence 4, Appl | 189 | 4 | 44.4 | 34 | 2 | US-09-270-767-59590 | Sequence 59590, A |
| 117 | 4 | 44.4 | 14 | 1 | US-07-712-476A-3 | Sequence 3, Appl | 190 | 4 | 44.4 | 38 | 1 | US-07-712-476A-4 | Sequence 4, Appl |
| 118 | 4 | 44.4 | 14 | 7 | 5204097-4 | Patent No. 5204097 | 191 | 4 | 44.4 | 38 | 2 | US-08-630-916A-35 | Sequence 35, Appl |
| 119 | 4 | 44.4 | 16 | 1 | US-08-480-190-171 | Sequence 171, App | 192 | 4 | 44.4 | 38 | 2 | US-09-270-767-57102 | Sequence 57102, A |
| 120 | 4 | 44.4 | 16 | 1 | US-08-488-379-171 | Sequence 171, App | 193 | 4 | 44.4 | 38 | 2 | US-09-902-540-13720 | Sequence 13720, A |
| 121 | 4 | 44.4 | 16 | 2 | US-08-475-399A-171 | Sequence 171, App | 194 | 4 | 44.4 | 41 | 1 | US-08-229-280-5 | Sequence 5, Appl |
| 122 | 4 | 44.4 | 16 | 2 | US-08-077-255A-171 | Sequence 171, App | 195 | 4 | 44.4 | 41 | 2 | US-10-318-675-153 | Sequence 153, App |
| 123 | 4 | 44.4 | 16 | 5 | PCT-US93-07545-171 | Sequence 171, App | 196 | 4 | 44.4 | 42 | 1 | US-08-745-254A-2 | Sequence 2, Appl |
| 124 | 4 | 44.4 | 17 | 1 | US-08-480-190-97 | Sequence 97, Appl | 197 | 4 | 44.4 | 42 | 2 | US-09-383-667-8 | Sequence 8, Appl |
| 125 | 4 | 44.4 | 17 | 1 | US-08-480-190-108 | Sequence 108, App | 198 | 4 | 44.4 | 44 | 4 | US-08-955-636-1 | Sequence 1, Appl |
| 126 | 4 | 44.4 | 17 | 1 | US-08-488-379-97 | Sequence 97, Appl | 199 | 4 | 44.4 | 44 | 2 | US-08-955-636-19 | Sequence 19, Appl |
| 127 | 4 | 44.4 | 17 | 1 | US-08-488-379-108 | Sequence 108, App | 200 | 4 | 44.4 | 44 | 2 | US-08-955-636-20 | Sequence 20, Appl |
| 128 | 4 | 44.4 | 17 | 1 | US-08-672-345C-65 | Sequence 65, Appl | 201 | 4 | 44.4 | 44 | 2 | US-08-955-636-21 | Sequence 21, Appl |
| 129 | 4 | 44.4 | 17 | 2 | US-09-214-095D-65 | Sequence 65, Appl | 202 | 4 | 44.4 | 44 | 2 | US-08-955-636-22 | Sequence 22, Appl |
| 130 | 4 | 44.4 | 17 | 2 | US-08-475-399A-97 | Sequence 97, Appl | 203 | 4 | 44.4 | 44 | 2 | US-08-955-636-24 | Sequence 24, Appl |
| 131 | 4 | 44.4 | 17 | 2 | US-08-475-399A-108 | Sequence 108, App | 204 | 4 | 44.4 | 44 | 2 | US-08-955-636-25 | Sequence 25, Appl |
| 132 | 4 | 44.4 | 17 | 2 | US-08-077-255A-97 | Sequence 97, Appl | 205 | 4 | 44.4 | 44 | 2 | US-08-955-636-35 | Sequence 35, Appl |
| 133 | 4 | 44.4 | 17 | 2 | US-08-077-255A-108 | Sequence 108, App | 206 | 4 | 44.4 | 44 | 2 | US-09-303-239-1 | Sequence 1, Appl |
| 134 | 4 | 44.4 | 17 | 2 | US-09-940-727B-65 | Sequence 65, Appl | 207 | 4 | 44.4 | 44 | 2 | US-09-497-591-1 | Sequence 1, Appl |
| 135 | 4 | 44.4 | 17 | 5 | PCT-US93-07545-97 | Sequence 97, Appl | 208 | 4 | 44.4 | 44 | 2 | US-08-803-810-1 | Sequence 1, Appl |
| 136 | 4 | 44.4 | 17 | 5 | PCT-US93-07545-108 | Sequence 108, App | 209 | 4 | 44.4 | 45 | 1 | US-08-965-832-2 | Sequence 2, Appl |
| 137 | 4 | 44.4 | 18 | 1 | US-08-480-190-106 | Sequence 106, App | 210 | 4 | 44.4 | 47 | 2 | US-08-930-917A-6 | Sequence 1, Appl |
| 138 | 4 | 44.4 | 18 | 1 | US-08-488-379-106 | Sequence 106, App | 211 | 4 | 44.4 | 47 | 2 | US-08-930-917A-6 | Sequence 6, Appl |
| 139 | 4 | 44.4 | 18 | 2 | US-08-475-399A-106 | Sequence 106, App | 212 | 4 | 44.4 | 47 | 2 | US-10-144-929-121 | Sequence 121, App |
| 140 | 4 | 44.4 | 18 | 2 | US-08-077-255A-106 | Sequence 106, App | 213 | 4 | 44.4 | 47 | 2 | US-09-612-925H-2 | Sequence 2, Appl |
| 141 | 4 | 44.4 | 18 | 2 | US-09-612-925H-4 | Sequence 4, Appl | 214 | 4 | 44.4 | 47 | 2 | US-09-612-925H-10 | Sequence 10, Appl |
| 142 | 4 | 44.4 | 18 | 5 | PCT-US93-07545-106 | Sequence 106, App | 215 | 4 | 44.4 | 48 | 2 | US-08-569-749-9 | Sequence 9, Appl |
| 143 | 4 | 44.4 | 19 | 1 | US-08-480-190-94 | Sequence 94, Appl | 216 | 4 | 44.4 | 48 | 2 | US-08-569-749-10 | Sequence 10, Appl |
| 144 | 4 | 44.4 | 19 | 1 | US-08-480-190-105 | Sequence 105, App | 217 | 4 | 44.4 | 48 | 2 | US-09-689-366-9 | Sequence 9, Appl |
| 145 | 4 | 44.4 | 19 | 1 | US-08-488-379-94 | Sequence 94, Appl | 218 | 4 | 44.4 | 48 | 2 | US-09-689-366-10 | Sequence 10, Appl |
| 146 | 4 | 44.4 | 19 | 1 | US-08-488-379-105 | Sequence 105, App | 219 | 4 | 44.4 | 48 | 2 | US-10-232-286-9 | Sequence 9, Appl |
| 147 | 4 | 44.4 | 19 | 2 | US-08-475-399A-94 | Sequence 94, Appl | 220 | 4 | 44.4 | 48 | 2 | US-10-232-286-10 | Sequence 10, Appl |
| 148 | 4 | 44.4 | 19 | 2 | US-08-475-399A-105 | Sequence 105, App | 221 | 4 | 44.4 | 48 | 2 | US-10-934-717-9 | Sequence 9, Appl |
| 149 | 4 | 44.4 | 19 | 2 | US-08-077-255A-94 | Sequence 94, Appl | 222 | 4 | 44.4 | 48 | 2 | US-10-934-717-10 | Sequence 10, Appl |
| 150 | 4 | 44.4 | 19 | 2 | US-08-077-255A-105 | Sequence 105, App | 223 | 4 | 44.4 | 48 | 5 | PCT-US96-12860-9 | Sequence 9, Appl |
| 151 | 4 | 44.4 | 19 | 5 | PCT-US93-07545-94 | Sequence 94, Appl | 224 | 4 | 44.4 | 48 | 5 | PCT-US96-12860-10 | Sequence 10, Appl |
| 152 | 4 | 44.4 | 20 | 1 | PCT-US93-07545-105 | Sequence 105, App | 225 | 4 | 44.4 | 52 | 2 | US-09-270-767-32185 | Sequence 32185, A |
| 153 | 4 | 44.4 | 20 | 1 | US-08-480-190-93 | Sequence 93, Appl | 226 | 4 | 44.4 | 52 | 2 | US-09-270-767-47402 | Sequence 47402, A |
| 154 | 4 | 44.4 | 20 | 1 | US-08-480-190-104 | Sequence 104, App | 227 | 4 | 44.4 | 53 | 2 | US-09-902-540-13760 | Sequence 12760, A |
| 155 | 4 | 44.4 | 20 | 1 | US-08-488-379-93 | Sequence 93, Appl | 228 | 4 | 44.4 | 56 | 2 | US-09-513-999C-4527 | Sequence 4527, Ap |
| 156 | 4 | 44.4 | 20 | 1 | US-08-488-379-104 | Sequence 104, App | 229 | 4 | 44.4 | 58 | 1 | US-07-664-989B-85 | Sequence 85, Appl |
| 157 | 4 | 44.4 | 20 | 2 | US-08-475-399A-93 | Sequence 93, Appl | 230 | 4 | 44.4 | 58 | 1 | US-08-358-160-62 | Sequence 62, Appl |
| 158 | 4 | 44.4 | 20 | 2 | US-08-475-399A-104 | Sequence 104, App | 231 | 4 | 44.4 | 58 | 1 | US-08-086-630C-70 | Sequence 70, Appl |
| 159 | 4 | 44.4 | 20 | 2 | US-08-077-255A-93 | Sequence 93, Appl | 232 | 4 | 44.4 | 58 | 1 | US-08-086-630C-75 | Sequence 75, Appl |
| 160 | 4 | 44.4 | 20 | 2 | US-08-077-255A-104 | Sequence 104, App | 233 | 4 | 44.4 | 58 | 1 | US-08-086-630C-78 | Sequence 78, Appl |
| 161 | 4 | 44.4 | 20 | 5 | PCT-US93-07545-93 | Sequence 93, Appl | 234 | 4 | 44.4 | 58 | 1 | US-08-086-630C-79 | Sequence 79, Appl |
| 162 | 4 | 44.4 | 20 | 5 | PCT-US93-07545-104 | Sequence 104, App | 235 | 4 | 44.4 | 58 | 1 | US-08-086-630C-83 | Sequence 83, Appl |
| 163 | 4 | 44.4 | 20 | 7 | 5204097-3 | Patent No. 5204097 | 236 | 4 | 44.4 | 58 | 1 | US-08-086-630C-84 | Sequence 84, Appl |
| 164 | 4 | 44.4 | 21 | 1 | US-08-480-190-92 | Sequence 92, Appl | 237 | 4 | 44.4 | 58 | 1 | US-08-086-630C-86 | Sequence 86, Appl |
| 165 | 4 | 44.4 | 21 | 1 | US-08-480-190-103 | Sequence 103, App | 238 | 4 | 44.4 | 58 | 1 | US-08-086-630C-89 | Sequence 89, Appl |
| 166 | 4 | 44.4 | 21 | 1 | US-08-488-379-92 | Sequence 92, Appl | 239 | 4 | 44.4 | 58 | 1 | US-08-086-630C-90 | Sequence 90, Appl |
| 167 | 4 | 44.4 | 21 | 1 | US-08-488-379-103 | Sequence 103, App | 240 | 4 | 44.4 | 58 | 1 | US-08-086-630C-102 | Sequence 102, App |
| 168 | 4 | 44.4 | 21 | 2 | US-08-475-399A-92 | Sequence 92, Appl | 241 | 4 | 44.4 | 58 | 1 | US-08-086-630C-106 | Sequence 106, App |
| 169 | 4 | 44.4 | 21 | 2 | US-08-475-399A-103 | Sequence 103, App | 242 | 4 | 44.4 | 58 | 1 | US-08-086-630C-107 | Sequence 107, App |
| 170 | 4 | 44.4 | 21 | 2 | US-08-077-255A-92 | Sequence 92, Appl | 243 | 4 | 44.4 | 58 | 1 | US-08-086-630C-127 | Sequence 127, App |
| 171 | 4 | 44.4 | 21 | 2 | US-08-077-255A-103 | Sequence 103, App | 244 | 4 | 44.4 | 58 | 1 | US-08-086-630C-128 | Sequence 128, App |
| 172 | 4 | 44.4 | 21 | 5 | PCT-US93-07545-92 | Sequence 92, Appl | 245 | 4 | 44.4 | 58 | 1 | US-08-086-630C-129 | Sequence 129, App |

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| 392 | 4 | 44.4 | 79 | 2 | US-09-732-210-347 | Sequence 347, App | 465 | 4 | 44.4 | 112 | 2 | US-09-134-001C-2968 | Sequence 2968, Ap |
| 393 | 4 | 44.4 | 79 | 2 | US-09-732-210-352 | Sequence 352, App | 466 | 4 | 44.4 | 112 | 2 | US-09-270-767-3828 | Sequence 3828, A |
| 394 | 4 | 44.4 | 79 | 2 | US-09-513-999C-5255 | Sequence 525, App | 466 | 4 | 44.4 | 112 | 2 | US-09-270-767-4883 | Sequence 4883, A |
| 395 | 4 | 44.4 | 80 | 2 | US-09-134-001C-3508 | Sequence 3508, Ap | 467 | 4 | 44.4 | 112 | 2 | US-09-270-767-53545 | Sequence 53545, A |
| 396 | 4 | 44.4 | 82 | 2 | US-09-134-001C-3874 | Sequence 3874, Ap | 469 | 4 | 44.4 | 114 | 2 | US-09-344-587-9 | Sequence 9, Appli |
| 397 | 4 | 44.4 | 82 | 2 | US-09-621-976-7153 | Sequence 7153, Ap | 470 | 4 | 44.4 | 114 | 2 | US-10-104-047-3819 | Sequence 3819, Ap |
| 398 | 4 | 44.4 | 82 | 2 | US-09-248-796A-26326 | Sequence 26326, A | 471 | 4 | 44.4 | 115 | 2 | US-09-134-000C-6275 | Sequence 6275, Ap |
| 399 | 4 | 44.4 | 84 | 2 | US-09-489-039A-9596 | Sequence 9596, Ap | 472 | 4 | 44.4 | 115 | 2 | US-09-248-796A-21440 | Sequence 21440, A |
| 400 | 4 | 44.4 | 87 | 2 | US-09-381-150A-3 | Sequence 3, Appli | 473 | 4 | 44.4 | 115 | 2 | US-09-902-540-15352 | Sequence 15352, A |
| 401 | 4 | 44.4 | 87 | 2 | US-09-248-796A-23163 | Sequence 23163, A | 474 | 4 | 44.4 | 116 | 1 | US-07-988-273-5 | Sequence 5, Appli |
| 402 | 4 | 44.4 | 89 | 2 | US-08-816-977-4 | Sequence 4, Appli | 475 | 4 | 44.4 | 116 | 1 | US-08-672-345C-106 | Sequence 106, App |
| 403 | 4 | 44.4 | 89 | 2 | US-08-816-977-8 | Sequence 8, Appli | 476 | 4 | 44.4 | 116 | 2 | US-09-270-767-48038 | Sequence 48038, A |
| 404 | 4 | 44.4 | 89 | 2 | US-09-334-477-4 | Sequence 4, Appli | 477 | 4 | 44.4 | 116 | 2 | US-09-726-219A-217 | Sequence 217, App |
| 405 | 4 | 44.4 | 89 | 2 | US-09-334-477-8 | Sequence 8, Appli | 478 | 4 | 44.4 | 116 | 2 | US-09-196-522-217 | Sequence 217, App |
| 406 | 4 | 44.4 | 90 | 2 | US-09-673-809-24 | Sequence 24, Appli | 479 | 4 | 44.4 | 116 | 5 | PCT-US933-12019-5 | Sequence 5, Appli |
| 407 | 4 | 44.4 | 90 | 2 | US-09-673-809-103 | Sequence 103, App | 480 | 4 | 44.4 | 117 | 2 | US-08-936-165A-347 | Sequence 347, App |
| 408 | 4 | 44.4 | 90 | 2 | US-09-673-809-105 | Sequence 105, App | 481 | 4 | 44.4 | 118 | 1 | US-08-524-757-4 | Sequence 4, Appli |
| 409 | 4 | 44.4 | 91 | 2 | US-09-248-796A-27490 | Sequence 27490, A | 482 | 4 | 44.4 | 118 | 1 | US-08-524-757-10 | Sequence 10, Appli |
| 410 | 4 | 44.4 | 92 | 2 | US-09-489-039A-11823 | Sequence 11823, A | 483 | 4 | 44.4 | 118 | 2 | US-09-513-999C-8071 | Sequence 8071, Ap |
| 411 | 4 | 44.4 | 92 | 2 | US-09-270-767-31666 | Sequence 31666, A | 484 | 4 | 44.4 | 118 | 2 | US-09-513-999C-8072 | Sequence 8072, Ap |
| 412 | 4 | 44.4 | 93 | 2 | US-09-073-297-12 | Sequence 12, Appli | 485 | 4 | 44.4 | 118 | 2 | US-09-902-540-14833 | Sequence 14833, A |
| 413 | 4 | 44.4 | 93 | 2 | US-09-248-796A-23162 | Sequence 23162, A | 486 | 4 | 44.4 | 119 | 2 | US-09-732-210-660 | Sequence 660, App |
| 414 | 4 | 44.4 | 93 | 2 | US-09-248-796A-24709 | Sequence 24709, A | 487 | 4 | 44.4 | 119 | 2 | US-10-104-047-2840 | Sequence 2840, Ap |
| 415 | 4 | 44.4 | 93 | 2 | US-09-471-276-915 | Sequence 915, App | 488 | 4 | 44.4 | 120 | 2 | US-09-621-976-7484 | Sequence 7484, Ap |
| 416 | 4 | 44.4 | 94 | 2 | US-09-902-540-15017 | Sequence 15017, A | 489 | 4 | 44.4 | 120 | 2 | US-09-270-767-45419 | Sequence 45419, A |
| 417 | 4 | 44.4 | 95 | 2 | US-09-248-796A-21466 | Sequence 21466, A | 490 | 4 | 44.4 | 120 | 2 | US-09-513-999C-4290 | Sequence 4290, Ap |
| 418 | 4 | 44.4 | 95 | 2 | US-09-248-796A-24736 | Sequence 24736, A | 491 | 4 | 44.4 | 121 | 2 | US-09-187-999-35 | Sequence 35, Appli |
| 419 | 4 | 44.4 | 97 | 2 | US-08-816-977-23 | Sequence 23, Appli | 492 | 4 | 44.4 | 122 | 1 | US-08-276-852-80 | Sequence 80, Appli |
| 420 | 4 | 44.4 | 97 | 2 | US-08-816-977-27 | Sequence 27, Appli | 493 | 4 | 44.4 | 122 | 1 | US-08-899-575-80 | Sequence 80, Appli |
| 421 | 4 | 44.4 | 97 | 2 | US-08-818-112-72 | Sequence 72, Appli | 494 | 4 | 44.4 | 122 | 1 | US-08-899-575-80 | Sequence 80, Appli |
| 422 | 4 | 44.4 | 97 | 2 | US-08-818-111-73 | Sequence 73, Appli | 495 | 4 | 44.4 | 122 | 5 | PCP-US95-08743-80 | Sequence 3427, Ap |
| 423 | 4 | 44.4 | 97 | 2 | US-09-056-556-72 | Sequence 72, Appli | 495 | 4 | 44.4 | 122 | 2 | US-09-134-000C-3427 | Sequence 3427, Ap |
| 424 | 4 | 44.4 | 97 | 2 | US-09-072-596-73 | Sequence 73, Appli | 497 | 4 | 44.4 | 123 | 2 | US-09-949-016-6592 | Sequence 80, Appli |
| 425 | 4 | 44.4 | 97 | 2 | US-09-072-967-72 | Sequence 72, Appli | 498 | 4 | 44.4 | 123 | 2 | US-09-550-163-2 | Sequence 5592, Ap |
| 426 | 4 | 44.4 | 97 | 2 | US-09-334-477-23 | Sequence 23, Appli | 499 | 4 | 44.4 | 123 | 2 | US-09-550-163-4 | Sequence 2, Appli |
| 427 | 4 | 44.4 | 97 | 2 | US-09-334-477-27 | Sequence 27, Appli | 500 | 4 | 44.4 | 124 | 2 | US-09-513-999C-4287 | Sequence 4287, Ap |
| 428 | 4 | 44.4 | 97 | 2 | US-10-193-002-73 | Sequence 73, Appli | 501 | 4 | 44.4 | 126 | 2 | US-09-240-274-17 | Sequence 17, Appli |
| 429 | 4 | 44.4 | 98 | 2 | US-10-084-843-72 | Sequence 72, Appli | 502 | 4 | 44.4 | 126 | 2 | US-09-848-798-17 | Sequence 17, Appli |
| 430 | 4 | 44.4 | 98 | 2 | US-09-248-796A-27698 | Sequence 27698, A | 503 | 4 | 44.4 | 127 | 2 | US-09-240-274-145 | Sequence 145, App |
| 431 | 4 | 44.4 | 98 | 2 | US-09-305-243-45 | Sequence 45, Appli | 504 | 4 | 44.4 | 127 | 2 | US-09-270-767-48045 | Sequence 48045, A |
| 432 | 4 | 44.4 | 99 | 2 | US-09-513-999C-4288 | Sequence 4288, Ap | 505 | 4 | 44.4 | 127 | 2 | US-09-248-796A-21342 | Sequence 21342, A |
| 433 | 4 | 44.4 | 100 | 2 | US-09-248-796A-21520 | Sequence 21520, A | 506 | 4 | 44.4 | 127 | 2 | US-09-848-798-145 | Sequence 145, App |
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| 435 | 4 | 44.4 | 101 | 2 | US-09-248-796A-25796 | Sequence 25796, A | 508 | 4 | 44.4 | 130 | 2 | US-08-936-165A-491 | Sequence 491, App |
| 436 | 4 | 44.4 | 101 | 2 | US-09-513-999C-6190 | Sequence 6190, Ap | 509 | 4 | 44.4 | 130 | 2 | US-09-107-433-3668 | Sequence 3068, Ap |
| 437 | 4 | 44.4 | 103 | 2 | US-10-094-749-3258 | Sequence 3258, Ap | 510 | 4 | 44.4 | 130 | 2 | US-09-605-703B-2198 | Sequence 2198, Ap |
| 438 | 4 | 44.4 | 104 | 2 | US-08-858-207A-328 | Sequence 328, App | 511 | 4 | 44.4 | 131 | 2 | US-09-247-155-175 | Sequence 175, App |
| 439 | 4 | 44.4 | 104 | 2 | US-09-248-796A-27204 | Sequence 27204, A | 512 | 4 | 44.4 | 131 | 2 | US-09-839-709-2 | Sequence 2, Appli |
| 440 | 4 | 44.4 | 104 | 2 | US-10-014-012-216 | Sequence 216, App | 513 | 4 | 44.4 | 131 | 2 | US-09-732-210-1340 | Sequence 1340, Ap |
| 441 | 4 | 44.4 | 105 | 2 | US-08-899-330-10 | Sequence 10, Appli | 514 | 4 | 44.4 | 131 | 2 | US-09-732-210-1341 | Sequence 1341, Ap |
| 442 | 4 | 44.4 | 105 | 2 | US-09-107-532A-5070 | Sequence 5070, Ap | 515 | 4 | 44.4 | 131 | 2 | US-09-732-210-1352 | Sequence 1352, Ap |
| 443 | 4 | 44.4 | 106 | 1 | US-09-756-541-10 | Sequence 10, Appli | 516 | 4 | 44.4 | 131 | 2 | US-09-543-681A-5501 | Sequence 5501, Ap |
| 444 | 4 | 44.4 | 106 | 2 | US-08-378-939-44 | Sequence 44, Appli | 517 | 4 | 44.4 | 131 | 2 | US-09-270-767-33577 | Sequence 33577, A |
| 445 | 4 | 44.4 | 106 | 2 | US-10-101-464A-657 | Sequence 657, App | 518 | 4 | 44.4 | 131 | 2 | US-09-270-767-48794 | Sequence 48794, A |
| 446 | 4 | 44.4 | 106 | 2 | US-09-996-288-21 | Sequence 21, Appli | 519 | 4 | 44.4 | 131 | 2 | US-09-513-999C-7397 | Sequence 7397, Ap |
| 447 | 4 | 44.4 | 106 | 2 | US-09-996-265-21 | Sequence 21, Appli | 520 | 4 | 44.4 | 131 | 2 | US-09-991-181-276 | Sequence 276, App |
| 448 | 4 | 44.4 | 107 | 2 | US-09-270-767-37624 | Sequence 37624, A | 521 | 4 | 44.4 | 131 | 2 | US-09-990-444-276 | Sequence 276, App |
| 449 | 4 | 44.4 | 107 | 2 | US-09-270-767-52841 | Sequence 52841, A | 522 | 4 | 44.4 | 131 | 2 | US-09-903-190-175 | Sequence 175, App |
| 450 | 4 | 44.4 | 108 | 1 | US-08-245-511-10 | Sequence 10, Appli | 523 | 4 | 44.4 | 131 | 2 | US-09-997-333-276 | Sequence 276, App |
| 451 | 4 | 44.4 | 108 | 1 | US-08-888-366-6 | Sequence 6, Appli | 524 | 4 | 44.4 | 131 | 2 | US-09-992-598-276 | Sequence 276, App |
| 452 | 4 | 44.4 | 108 | 1 | US-08-600-993A-10 | Sequence 10, Appli | 525 | 4 | 44.4 | 131 | 2 | US-09-989-735-276 | Sequence 276, App |
| 453 | 4 | 44.4 | 108 | 2 | US-09-270-767-43418 | Sequence 43418, A | 526 | 4 | 44.4 | 131 | 3 | US-09-989-726-276 | Sequence 276, App |
| 454 | 4 | 44.4 | 109 | 2 | US-09-252-991A-20785 | Sequence 20785, A | 527 | 4 | 44.4 | 131 | 3 | US-09-997-514-276 | Sequence 276, App |
| 455 | 4 | 44.4 | 109 | 2 | US-09-497-997C-29 | Sequence 29, Appli | 528 | 4 | 44.4 | 131 | 3 | US-09-989-728-276 | Sequence 276, App |
| 456 | 4 | 44.4 | 110 | 2 | US-09-214-095D-86 | Sequence 86, Appli | 529 | 4 | 44.4 | 131 | 3 | US-09-997-349-276 | Sequence 276, App |
| 457 | 4 | 44.4 | 110 | 2 | US-09-270-767-34919 | Sequence 34919, A | 530 | 4 | 44.4 | 131 | 3 | US-09-997-653-276 | Sequence 276, App |
| 458 | 4 | 44.4 | 110 | 2 | US-09-270-767-50136 | Sequence 50136, A | 531 | 4 | 44.4 | 131 | 3 | US-09-989-293A-276 | Sequence 276, App |
| 459 | 4 | 44.4 | 110 | 2 | US-09-248-796A-26406 | Sequence 26406, A | 532 | 4 | 44.4 | 132 | 2 | US-09-673-395A-166 | Sequence 166, App |
| 460 | 4 | 44.4 | 110 | 2 | US-09-513-999C-7843 | Sequence 7843, Ap | 533 | 4 | 44.4 | 133 | 2 | US-09-107-532A-5991 | Sequence 5991, Ap |
| 461 | 4 | 44.4 | 110 | 2 | US-09-940-727B-86 | Sequence 86, Appli | 534 | 4 | 44.4 | 133 | 2 | US-09-270-767-48505 | Sequence 48505, A |
| 462 | 4 | 44.4 | 111 | 1 | US-07-754-918A-11 | Sequence 11, Appli | 535 | 4 | 44.4 | 133 | 2 | US-09-902-540-11050 | Sequence 11050, A |
| 463 | 4 | 44.4 | 111 | 2 | US-09-540-236-2670 | Sequence 2670, Ap | 536 | 4 | 44.4 | 134 | 2 | US-09-134-000C-5312 | Sequence 5312, Ap |
| 464 | 4 | 44.4 | 112 | 2 | US-09-134-001C-2933 | Sequence 2933, Ap | 537 | 4 | 44.4 | 134 | 2 | US-09-540-236-2372 | Sequence 2972, Ap |

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| 538 | 4 | 44.4 | 134 | 2 | US-09-583-110-4917 | Sequence 4917, Ap | 611 | 4 | 44.4 | 162 | 2 | US-09-540-236-2231 | Sequence 2231, Ap |
| 539 | 4 | 44.4 | 134 | 2 | US-09-270-767-32241 | Sequence 32241, A | 612 | 4 | 44.4 | 162 | 2 | US-09-270-767-35276 | Sequence 35276, A |
| 540 | 4 | 44.4 | 134 | 2 | US-09-270-767-47458 | Sequence 47458, A | 613 | 4 | 44.4 | 162 | 2 | US-09-270-767-50493 | Sequence 50493, A |
| 541 | 4 | 44.4 | 134 | 2 | US-09-270-767-57612 | Sequence 57612, A | 614 | 4 | 44.4 | 162 | 2 | US-09-248-796A-15063 | Sequence 15063, A |
| 542 | 4 | 44.4 | 135 | 2 | US-09-489-039A-13003 | Sequence 13003, A | 615 | 4 | 44.4 | 162 | 2 | US-09-612-925H-8 | Sequence 8, Appl |
| 543 | 4 | 44.4 | 136 | 2 | US-09-513-999C-7844 | Sequence 7844, Ap | 616 | 4 | 44.4 | 162 | 2 | US-09-612-925H-26 | Sequence 26, Appl |
| 544 | 4 | 44.4 | 136 | 3 | US-10-162-335-78 | Sequence 78, Appl | 617 | 4 | 44.4 | 164 | 2 | US-09-370-838-203 | Sequence 203, Ap |
| 545 | 4 | 44.4 | 137 | 2 | US-09-270-767-33279 | Sequence 33279, A | 618 | 4 | 44.4 | 164 | 2 | US-09-543-681A-6917 | Sequence 6917, Ap |
| 546 | 4 | 44.4 | 137 | 2 | US-09-270-767-48496 | Sequence 48496, A | 619 | 4 | 44.4 | 164 | 2 | US-09-710-279-2398 | Sequence 2398, Ap |
| 547 | 4 | 44.4 | 137 | 2 | US-09-513-999C-4291 | Sequence 4291, Ap | 620 | 4 | 44.4 | 164 | 2 | US-09-854-133-203 | Sequence 203, Ap |
| 548 | 4 | 44.4 | 138 | 1 | US-08-468-709B-2 | Sequence 2, Appl | 621 | 4 | 44.4 | 164 | 2 | US-09-902-540-15184 | Sequence 15184, A |
| 549 | 4 | 44.4 | 138 | 1 | US-08-468-709B-12 | Sequence 12, Appl | 622 | 4 | 44.4 | 166 | 2 | US-09-107-532A-4035 | Sequence 4035, Ap |
| 550 | 4 | 44.4 | 138 | 1 | US-08-241-664B-2 | Sequence 2, Appl | 623 | 4 | 44.4 | 166 | 2 | US-09-513-999C-8067 | Sequence 8067, Ap |
| 551 | 4 | 44.4 | 138 | 1 | US-08-241-664B-12 | Sequence 12, Appl | 624 | 4 | 44.4 | 167 | 2 | US-09-489-039A-13896 | Sequence 13896, A |
| 552 | 4 | 44.4 | 138 | 2 | US-09-702-705-328 | Sequence 328, Ap | 625 | 4 | 44.4 | 167 | 2 | US-09-248-796A-20740 | Sequence 20740, A |
| 553 | 4 | 44.4 | 138 | 2 | US-09-736-457-328 | Sequence 328, Ap | 626 | 4 | 44.4 | 168 | 2 | US-09-270-767-44166 | Sequence 44166, A |
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| 557 | 4 | 44.4 | 138 | 2 | US-09-658-824-328 | Sequence 328, Ap | 630 | 4 | 44.4 | 169 | 2 | US-10-222-566-24 | Sequence 24, Appl |
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| 559 | 4 | 44.4 | 138 | 2 | US-10-017-754-328 | Sequence 11054, A | 632 | 4 | 44.4 | 169 | 2 | US-10-143-024A-24 | Sequence 24, Appl |
| 560 | 4 | 44.4 | 138 | 2 | US-09-651-563-328 | Sequence 328, Ap | 633 | 4 | 44.4 | 169 | 2 | US-10-222-162-24 | Sequence 24, Appl |
| 561 | 4 | 44.4 | 138 | 2 | US-09-519-642-328 | Sequence 328, Ap | 634 | 4 | 44.4 | 170 | 2 | US-09-439-554-18 | Sequence 18, Appl |
| 562 | 4 | 44.4 | 138 | 5 | PCT-US93-03936-2 | Sequence 2, Appl | 635 | 4 | 44.4 | 170 | 2 | US-09-270-767-45422 | Sequence 45422, A |
| 563 | 4 | 44.4 | 139 | 2 | US-09-465-559-12 | Sequence 12, Appl | 636 | 4 | 44.4 | 170 | 2 | US-09-605-703B-146 | Sequence 146, App |
| 564 | 4 | 44.4 | 140 | 2 | US-09-489-039A-10534 | Sequence 10534, A | 637 | 4 | 44.4 | 170 | 2 | US-09-605-703B-146 | Sequence 146, App |
| 565 | 4 | 44.4 | 140 | 2 | US-09-583-110-3229 | Sequence 3229, Ap | 638 | 4 | 44.4 | 171 | 2 | US-09-248-796A-18942 | Sequence 18942, A |
| 566 | 4 | 44.4 | 141 | 2 | US-09-328-352-6339 | Sequence 6339, Ap | 639 | 4 | 44.4 | 172 | 2 | US-09-621-976-4131 | Sequence 4131, Ap |
| 567 | 4 | 44.4 | 141 | 2 | US-09-710-279-1718 | Sequence 1718, Ap | 640 | 4 | 44.4 | 173 | 2 | US-09-509-744-4 | Sequence 4, Appl |
| 568 | 4 | 44.4 | 142 | 2 | US-09-107-532A-5617 | Sequence 5617, Ap | 641 | 4 | 44.4 | 175 | 2 | US-09-543-681A-6922 | Sequence 6922, Ap |
| 569 | 4 | 44.4 | 142 | 2 | US-09-513-999C-5204 | Sequence 5204, Ap | 642 | 4 | 44.4 | 176 | 2 | US-09-540-236-3395 | Sequence 3395, Ap |
| 570 | 4 | 44.4 | 143 | 2 | US-09-270-767-41137 | Sequence 41137, A | 643 | 4 | 44.4 | 176 | 2 | US-09-605-703B-388 | Sequence 388, App |
| 571 | 4 | 44.4 | 143 | 2 | US-09-270-767-56353 | Sequence 56353, A | 644 | 4 | 44.4 | 176 | 2 | US-09-605-703B-390 | Sequence 390, App |
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| 573 | 4 | 44.4 | 144 | 2 | US-09-583-110-4496 | Sequence 4496, Ap | 646 | 4 | 44.4 | 177 | 2 | US-08-770-544-22 | Sequence 22, Appl |
| 574 | 4 | 44.4 | 144 | 2 | US-09-270-767-46704 | Sequence 46704, A | 647 | 4 | 44.4 | 179 | 2 | US-09-579-259-22 | Sequence 22, Appl |
| 575 | 4 | 44.4 | 145 | 1 | US-08-166-195A-50 | Sequence 50, Appl | 648 | 4 | 44.4 | 179 | 2 | US-09-650-324A-22 | Sequence 22, Appl |
| 576 | 4 | 44.4 | 145 | 2 | US-09-107-532A-5485 | Sequence 5485, Ap | 649 | 4 | 44.4 | 179 | 2 | US-09-248-796A-14684 | Sequence 56764, A |
| 577 | 4 | 44.4 | 145 | 2 | US-09-513-999C-7009 | Sequence 7009, Ap | 650 | 4 | 44.4 | 179 | 2 | Sequence 22, Appl | |
| 578 | 4 | 44.4 | 145 | 2 | US-09-471-276-1287 | Sequence 1287, Ap | 651 | 4 | 44.4 | 179 | 2 | Sequence 13, Appl | |
| 579 | 4 | 44.4 | 146 | 1 | US-08-436-772-50 | Sequence 50, Appl | 652 | 4 | 44.4 | 179 | 2 | Sequence 135, App | |
| 580 | 4 | 44.4 | 146 | 1 | US-08-436-883B-50 | Sequence 50, Appl | 653 | 4 | 44.4 | 181 | 2 | Sequence 136, App | |
| 581 | 4 | 44.4 | 147 | 2 | US-09-270-767-37475 | Sequence 37475, A | 654 | 4 | 44.4 | 181 | 2 | Sequence 137, App | |
| 582 | 4 | 44.4 | 147 | 2 | US-09-270-767-52692 | Sequence 52692, A | 655 | 4 | 44.4 | 182 | 1 | Sequence 138, App | |
| 583 | 4 | 44.4 | 147 | 2 | US-09-902-540-15811 | Sequence 15811, A | 656 | 4 | 44.4 | 182 | 1 | Sequence 139, App | |
| 584 | 4 | 44.4 | 148 | 2 | US-09-270-767-33466 | Sequence 33466, A | 657 | 4 | 44.4 | 182 | 1 | Sequence 138, App | |
| 585 | 4 | 44.4 | 148 | 2 | US-09-270-767-35425 | Sequence 35425, A | 658 | 4 | 44.4 | 182 | 1 | Sequence 139, App | |
| 586 | 4 | 44.4 | 148 | 2 | US-09-270-767-46460 | Sequence 46460, A | 659 | 4 | 44.4 | 182 | 1 | Sequence 140, App | |
| 587 | 4 | 44.4 | 148 | 2 | US-09-270-767-48683 | Sequence 48683, A | 660 | 4 | 44.4 | 182 | 1 | Sequence 141, App | |
| 588 | 4 | 44.4 | 148 | 2 | US-09-270-767-48683 | Sequence 48683, A | 661 | 4 | 44.4 | 182 | 1 | Sequence 142, App | |
| 589 | 4 | 44.4 | 148 | 7 | 5180813-2 | Patent No. 5180813 | 662 | 4 | 44.4 | 182 | 1 | Sequence 143, App | |
| 590 | 4 | 44.4 | 149 | 2 | US-09-252-991A-31934 | Sequence 31934, A | 663 | 4 | 44.4 | 182 | 1 | Sequence 144, App | |
| 591 | 4 | 44.4 | 149 | 2 | US-09-270-767-42544 | Sequence 42544, A | 664 | 4 | 44.4 | 182 | 1 | Sequence 145, App | |
| 592 | 4 | 44.4 | 155 | 2 | US-09-589-287B-23 | Sequence 23, Appl | 665 | 4 | 44.4 | 182 | 1 | Sequence 146, App | |
| 593 | 4 | 44.4 | 155 | 2 | US-09-588-947A-23 | Sequence 23, Appl | 666 | 4 | 44.4 | 182 | 1 | Sequence 147, App | |
| 594 | 4 | 44.4 | 155 | 2 | US-09-589-286A-23 | Sequence 23, Appl | 667 | 4 | 44.4 | 182 | 1 | Sequence 148, App | |
| 595 | 4 | 44.4 | 155 | 2 | US-09-507-968D-23 | Sequence 23, Appl | 668 | 4 | 44.4 | 182 | 1 | Sequence 149, App | |
| 596 | 4 | 44.4 | 155 | 2 | US-09-589-285-23 | Sequence 23, Appl | 669 | 4 | 44.4 | 182 | 1 | Sequence 150, App | |
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| 598 | 4 | 44.4 | 157 | 2 | US-09-489-039A-12693 | Sequence 12693, A | 671 | 4 | 44.4 | 182 | 1 | Sequence 152, App | |
| 599 | 4 | 44.4 | 157 | 2 | US-09-134-000C-5250 | Sequence 5250, Ap | 672 | 4 | 44.4 | 182 | 1 | Sequence 153, App | |
| 600 | 4 | 44.4 | 157 | 5 | PCT-US94-01149-34 | Sequence 34, Appl | 673 | 4 | 44.4 | 182 | 1 | Sequence 154, App | |
| 601 | 4 | 44.4 | 158 | 2 | US-09-107-433-4280 | Sequence 4280, Ap | 674 | 4 | 44.4 | 182 | 1 | Sequence 155, App | |
| 602 | 4 | 44.4 | 159 | 1 | US-08-606-143-45 | Sequence 45, Appl | 675 | 4 | 44.4 | 182 | 1 | Sequence 156, App | |
| 603 | 4 | 44.4 | 159 | 2 | US-09-270-767-33621 | Sequence 33621, A | 676 | 4 | 44.4 | 182 | 1 | Sequence 157, App | |
| 604 | 4 | 44.4 | 159 | 2 | US-09-270-767-48838 | Sequence 48838, A | 677 | 4 | 44.4 | 182 | 1 | Sequence 158, App | |
| 605 | 4 | 44.4 | 160 | 2 | US-09-543-681A-7581 | Sequence 7581, Ap | 678 | 4 | 44.4 | 182 | 1 | Sequence 159, App | |
| 606 | 4 | 44.4 | 160 | 2 | US-09-248-796A-15801 | Sequence 15801, A | 679 | 4 | 44.4 | 182 | 1 | Sequence 160, App | |
| 607 | 4 | 44.4 | 161 | 2 | US-09-605-703B-1830 | Sequence 1830, Ap | 680 | 4 | 44.4 | 182 | 1 | Sequence 161, App | |
| 608 | 4 | 44.4 | 162 | 1 | US-08-244-557-2 | Sequence 2, Appl | 681 | 4 | 44.4 | 182 | 1 | Sequence 162, App | |
| 609 | 4 | 44.4 | 162 | 1 | US-08-606-143-44 | Sequence 44, Appl | 682 | 4 | 44.4 | 182 | 1 | Sequence 163, App | |
| 610 | 4 | 44.4 | 162 | 2 | US-08-930-917A-19 | Sequence 19, Appl | 683 | 4 | 44.4 | 182 | 1 | Sequence 164, App | |

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| 685 | 4 | 44.4 | 182 | 1 | US-08-127-954-166 | Sequence 166, App | 758 | 4 | 44.4 | 197 | 2 | US-09-830-230A-620 | Sequence 620, App |
| 686 | 4 | 44.4 | 182 | 1 | US-08-127-954-167 | Sequence 167, App | 759 | 4 | 44.4 | 199 | 2 | US-09-377-497-69 | Sequence 69, Appl |
| 687 | 4 | 44.4 | 182 | 1 | US-08-127-954-168 | Sequence 168, App | 760 | 4 | 44.4 | 199 | 2 | US-10-090-365-35 | Sequence 35, Appl |
| 688 | 4 | 44.4 | 182 | 1 | US-08-127-954-169 | Sequence 169, App | 761 | 4 | 44.4 | 199 | 2 | US-09-728-911-35 | Sequence 35, Appl |
| 689 | 4 | 44.4 | 182 | 1 | US-08-127-954-170 | Sequence 170, App | 762 | 4 | 44.4 | 200 | 2 | US-09-134-000C-5989 | Sequence 5989, Ap |
| 690 | 4 | 44.4 | 182 | 1 | US-08-127-954-171 | Sequence 171, App | 763 | 4 | 44.4 | 200 | 2 | US-09-248-796A-24082 | Sequence 24082, A |
| 691 | 4 | 44.4 | 182 | 1 | US-08-127-954-172 | Sequence 172, App | 764 | 4 | 44.4 | 201 | 2 | US-09-902-540-16581 | Sequence 16581, A |
| 692 | 4 | 44.4 | 182 | 1 | US-08-127-954-173 | Sequence 173, App | 765 | 4 | 44.4 | 202 | 1 | US-07-807-022A-1 | Sequence 1, Appli |
| 693 | 4 | 44.4 | 182 | 2 | US-09-502-540-14652 | Sequence 14652, A | 766 | 4 | 44.4 | 202 | 2 | US-08-930-917A-20 | Sequence 20, Appl |
| 694 | 4 | 44.4 | 183 | 2 | US-09-270-767-57954 | Sequence 57954, A | 767 | 4 | 44.4 | 202 | 2 | US-09-252-991A-17985 | Sequence 17985, A |
| 695 | 4 | 44.4 | 183 | 2 | US-09-248-796A-21579 | Sequence 21579, A | 768 | 4 | 44.4 | 202 | 2 | US-09-328-352-5176 | Sequence 5176, Ap |
| 696 | 4 | 44.4 | 184 | 1 | US-08-865-336-1 | Sequence 1, Appli | 769 | 4 | 44.4 | 202 | 2 | US-09-602-777A-62 | Sequence 62, Appl |
| 697 | 4 | 44.4 | 184 | 2 | US-09-153-586-21 | Sequence 21, Appl | 770 | 4 | 44.4 | 202 | 2 | US-09-612-925H-27 | Sequence 27, Appl |
| 698 | 4 | 44.4 | 184 | 2 | US-09-858-580-21 | Sequence 21, Appl | 771 | 4 | 44.4 | 203 | 2 | US-09-270-767-32925 | Sequence 32925, A |
| 699 | 4 | 44.4 | 185 | 1 | US-08-333-750C-2 | Sequence 2, Appli | 772 | 4 | 44.4 | 203 | 2 | US-09-270-767-48142 | Sequence 48142, A |
| 700 | 4 | 44.4 | 185 | 2 | US-08-965-689A-1 | Sequence 1, Appli | 773 | 4 | 44.4 | 204 | 2 | US-09-830-230A-318 | Sequence 318, App |
| 701 | 4 | 44.4 | 185 | 2 | US-09-234-613-2 | Sequence 2, Appli | 774 | 4 | 44.4 | 206 | 2 | US-09-248-796A-14212 | Sequence 14212, A |
| 702 | 4 | 44.4 | 185 | 2 | US-09-359-967-1 | Sequence 1, Appli | 775 | 4 | 44.4 | 206 | 2 | US-09-949-016-7005 | Sequence 7005, Ap |
| 703 | 4 | 44.4 | 185 | 2 | US-09-570-856B-8 | Sequence 8, Appli | 776 | 4 | 44.4 | 208 | 2 | US-09-094-103-4 | Sequence 4, Appli |
| 704 | 4 | 44.4 | 185 | 2 | US-09-583-110-5249 | Sequence 5249, Ap | 777 | 4 | 44.4 | 208 | 2 | US-09-198-452A-134 | Sequence 134, App |
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| 706 | 4 | 44.4 | 185 | 2 | US-09-216-430C-6 | Sequence 6, Appli | 779 | 4 | 44.4 | 208 | 2 | US-08-781-986A-5200 | Sequence 5200, Ap |
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| 713 | 4 | 44.4 | 185 | 2 | US-09-989-735-211 | Sequence 211, App | 786 | 4 | 44.4 | 211 | 2 | US-09-445-774-24 | Sequence 24, Appl |
| 714 | 4 | 44.4 | 185 | 3 | US-09-989-726-211 | Sequence 211, App | 787 | 4 | 44.4 | 211 | 2 | US-09-270-767-44160 | Sequence 44160, A |
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| 717 | 4 | 44.4 | 185 | 3 | US-09-997-349-211 | Sequence 211, App | 790 | 4 | 44.4 | 211 | 2 | US-10-222-162-40 | Sequence 40, Appl |
| 718 | 4 | 44.4 | 185 | 3 | US-09-997-653-211 | Sequence 211, App | 791 | 4 | 44.4 | 212 | 2 | US-09-125-619-32 | Sequence 32, Appl |
| 719 | 4 | 44.4 | 185 | 3 | US-09-989-293A-211 | Sequence 211, App | 792 | 4 | 44.4 | 212 | 2 | US-09-125-619-41 | Sequence 41, Appl |
| 720 | 4 | 44.4 | 186 | 2 | US-09-248-796A-28131 | Sequence 28131, A | 793 | 4 | 44.4 | 212 | 2 | US-09-125-619-44 | Sequence 44, Appl |
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| 724 | 4 | 44.4 | 187 | 2 | US-09-248-796A-20621 | Sequence 20621, A | 797 | 4 | 44.4 | 212 | 2 | US-10-222-566-41 | Sequence 41, Appl |
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| 726 | 4 | 44.4 | 189 | 2 | US-09-080-643-4 | Sequence 4, Appli | 799 | 4 | 44.4 | 212 | 2 | US-10-143-024A-32 | Sequence 32, Appl |
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| 728 | 4 | 44.4 | 189 | 2 | US-09-107-433-5147 | Sequence 5147, Ap | 801 | 4 | 44.4 | 212 | 2 | US-10-143-024A-44 | Sequence 44, Appl |
| 729 | 4 | 44.4 | 190 | 2 | US-09-107-433-4319 | Sequence 4319, Ap | 802 | 4 | 44.4 | 212 | 2 | US-10-222-162-32 | Sequence 32, Appl |
| 730 | 4 | 44.4 | 191 | 2 | US-09-183-861-82 | Sequence 82, Appl | 803 | 4 | 44.4 | 212 | 2 | US-10-222-162-41 | Sequence 41, Appl |
| 731 | 4 | 44.4 | 191 | 2 | US-09-022-765-82 | Sequence 82, Appl | 804 | 4 | 44.4 | 212 | 1 | US-08-874-832-7 | Sequence 7, Appli |
| 732 | 4 | 44.4 | 191 | 2 | US-09-551-974A-82 | Sequence 82, Appl | 805 | 4 | 44.4 | 213 | 2 | US-09-097-233-7 | Sequence 7, Appli |
| 733 | 4 | 44.4 | 191 | 2 | US-09-565-501A-82 | Sequence 82, Appl | 806 | 4 | 44.4 | 213 | 2 | US-08-961-083-34 | Sequence 34, Appl |
| 734 | 4 | 44.4 | 191 | 2 | US-09-639-206A-82 | Sequence 82, Appl | 807 | 4 | 44.4 | 213 | 2 | US-09-125-619-39 | Sequence 39, Appl |
| 735 | 4 | 44.4 | 191 | 2 | US-09-874-923-82 | Sequence 82, Appl | 808 | 4 | 44.4 | 213 | 2 | US-09-536-784-34 | Sequence 34, Appl |
| 736 | 4 | 44.4 | 192 | 2 | US-09-107-532A-4015 | Sequence 4015, Ap | 809 | 4 | 44.4 | 213 | 2 | US-09-540-236-3815 | Sequence 3815, Ap |
| 737 | 4 | 44.4 | 192 | 2 | US-09-583-110-5295 | Sequence 5295, Ap | 810 | 4 | 44.4 | 213 | 2 | US-10-222-566-39 | Sequence 39, Appl |
| 738 | 4 | 44.4 | 192 | 2 | US-09-248-796A-20678 | Sequence 20678, A | 811 | 4 | 44.4 | 213 | 2 | US-10-143-024A-39 | Sequence 39, Appl |
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| 740 | 4 | 44.4 | 193 | 2 | US-09-393-627B-20 | Sequence 20, Appl | 813 | 4 | 44.4 | 213 | 2 | US-09-538-092-719 | Sequence 719, App |
| 741 | 4 | 44.4 | 193 | 2 | US-09-393-627B-21 | Sequence 21, Appl | 814 | 4 | 44.4 | 213 | 2 | US-09-996-288-213 | Sequence 213, App |
| 742 | 4 | 44.4 | 193 | 2 | US-09-393-627B-24 | Sequence 24, Appl | 815 | 4 | 44.4 | 213 | 2 | US-09-996-265-213 | Sequence 213, App |
| 743 | 4 | 44.4 | 193 | 2 | US-09-248-796A-24070 | Sequence 24070, A | 816 | 4 | 44.4 | 213 | 2 | US-10-222-162-39 | Sequence 39, Appl |
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| 746 | 4 | 44.4 | 194 | 2 | US-09-443-067-2 | Sequence 2, Appli | 819 | 4 | 44.4 | 213 | 2 | US-09-181-183-12 | Sequence 12, Appl |
| 747 | 4 | 44.4 | 194 | 2 | US-09-377-497-17 | Sequence 17, Appl | 820 | 4 | 44.4 | 214 | 2 | US-09-280-040-12 | Sequence 12, Appl |
| 748 | 4 | 44.4 | 195 | 2 | US-09-252-991A-21779 | Sequence 21779, A | 821 | 4 | 44.4 | 214 | 2 | US-09-277-700-12 | Sequence 12, Appl |
| 749 | 4 | 44.4 | 195 | 2 | US-09-134-000C-6158 | Sequence 6158, Ap | 822 | 4 | 44.4 | 214 | 2 | US-09-252-991A-21440 | Sequence 21440, A |
| 750 | 4 | 44.4 | 195 | 2 | US-09-270-767-41580 | Sequence 41580, A | 823 | 4 | 44.4 | 214 | 2 | US-09-874-585D-12 | Sequence 12, Appl |
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| 755 | 4 | 44.4 | 196 | 2 | US-09-513-999C-4249 | Sequence 4249, Ap | 828 | 4 | 44.4 | 215 | 2 | US-09-270-767-44174 | Sequence 44174, A |
| 756 | 4 | 44.4 | 197 | 1 | US-08-879-561-5 | Sequence 5, Appli | 829 | 4 | 44.4 | 215 | 2 | | |

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|-----|---|------|-----|---|----------------------|--------------------|-----|---|------|-----|---|----------------------|-------------------|
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| 831 | 4 | 44.4 | 216 | 2 | US-09-488-039A-11454 | Sequence 11454, A | 904 | 4 | 44.4 | 245 | 2 | US-09-949-016-7193 | Sequence 7193, Ap |
| 832 | 4 | 44.4 | 217 | 2 | US-09-543-681A-5490 | Sequence 5490, Ap | 905 | 4 | 44.4 | 246 | 2 | US-09-248-796A-19220 | Sequence 19220, A |
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ALIGNMENTS

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; APPLICANT: Gary Breton et. al
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; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10751
; LENGTH: 382
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US-09-489-039A-10751

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; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ

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; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 691
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-962-756-691

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; APPLICANT: PILLUTLA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-962-756-1425

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; Sequence 338, Application US/09732210

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; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
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; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
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; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
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US-09-732-210-346

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; Patent No. 6537809
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES

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; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
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; PRIOR FILING DATE: 1995-06-07
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; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
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US-09-270-767-60895

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; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
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; PRIOR APPLICATION NUMBER: US 60/096,409
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US-09-248-796A-14343

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|||||
Db 24 TFYV 28

RESULT 9

US-09-668-262A-2
; Sequence 2, Application US/09668262A
; Patent No. 6596926
; GENERAL INFORMATION:
; APPLICANT: Falco, Carl
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Kinney, Tony
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Phosphatidylcholine Biosynthetic Enzyme
; FILE REFERENCE: BB1403 US NA
; CURRENT APPLICATION NUMBER: US/09/668,262A
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155626
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 95
; SEQ ID NO 2
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Zea mays
US-09-668-262A-2

Query Match 55.6%; Score 5; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
Db 128 KVDDT 132

RESULT 10

US-10-427-442-2
; Sequence 2, Application US/10427442
; Patent No. 6960704
; GENERAL INFORMATION:
; APPLICANT: Falco, Carl
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Kinney, Tony
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Phosphatidylcholine Biosynthetic Enzyme
; FILE REFERENCE: BB1403 US NA
; CURRENT APPLICATION NUMBER: US/10/427,442
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: US/09/668,262A
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155626
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 95
; SEQ ID NO 2
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Zea mays
US-10-427-442-2

Query Match 55.6%; Score 5; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

Db 128 KVDDT 132

RESULT 11

US-09-270-767-56930
; Sequence 56930, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56930
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56930

Query Match 55.6%; Score 5; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
Db 87 KVDDT 91

RESULT 12

US-09-270-767-57344
; Sequence 57344, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57344
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57344

Query Match 55.6%; Score 5; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 141 DDTFY 145

RESULT 13

US-09-710-279-2532
; Sequence 2532, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2532


```

; LENGTH: 177
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-2532

Query Match      55.6%; Score 5; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVDVT 5
        |||||
Db      18 KVDVT 22

RESULT 14
US-09-107-532A-4432
; Sequence 4432, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4432:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 202 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...202
; SEQUENCE DESCRIPTION: SEQ ID NO: 4432:
US-09-107-532A-4432

Query Match      55.6%; Score 5; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVDVT 5

; LENGTH: 177
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-2532

Query Match      55.6%; Score 5; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVDVT 5
        |||||
Db      18 KVDVT 22

RESULT 15
US-09-216-393B-31
; Sequence 31, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THE
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-216-393B-31

Query Match      55.6%; Score 5; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVDVT 5
        |||||
Db      168 KVDVT 172

RESULT 16
US-10-101-464A-787
; Sequence 787, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 787
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-787

Query Match      55.6%; Score 5; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 DDTFY 7
        |||||
Db      117 DDTFY 121

RESULT 17
US-08-326-286-5
```

/ Sequence 5, Application US/08326286
/ Patent No. 5866779
/ GENERAL INFORMATION:
/ APPLICANT: Sun, Tai-Ping
/ APPLICANT: Goodman, Howard M.
/ APPLICANT: Ausubel, Frederick M.
/ TITLE OF INVENTION: Recombinant Gibberellin DNA and Uses Thereof
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
/ STREET: 1100 New York Ave., NW
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/326,286
/ FILING DATE: 20-OCT-1994
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/261,769
/ FILING DATE: 17-JUN-1994
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/008,996
/ FILING DATE: 26-JAN-1993
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/844,300
/ FILING DATE: 18-FEB-1992
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Lawrence, B.
/ REGISTRATION NUMBER: 35,086
/ REFERENCE/DOCKET NUMBER: 0609.2070006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 279 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: peptide
US-08-326-286-5

Query Match 55.6%; Score 5; DB 1; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 270 VDDTF 274

RESULT 18
US-09-252-991A-30991
/ Sequence 30991, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ CURRENT APPLICATION NUMBER: 107196.136
/ PRIOR APPLICATION NUMBER: US/09/252,991A
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788

/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 30991
/ LENGTH: 285
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30991

Query Match 55.6%; Score 5; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 196 KVDDT 200

RESULT 19
US-09-328-352-6685
/ Sequence 6685, Application US/09328352
/ Patent No. 6562958
/ GENERAL INFORMATION:
/ APPLICANT: Gary L. Berton et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
/ FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
/ CURRENT APPLICATION NUMBER: US/09/328,352
/ CURRENT FILING DATE: 1999-06-04
/ NUMBER OF SEQ ID NOS: 8252
/ SEQ ID NO 6685
/ LENGTH: 301
/ TYPE: PRT
/ ORGANISM: Acinetobacter baumannii
US-09-328-352-6685

Query Match 55.6%; Score 5; DB 2; Length 301;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 215 KVDDT 219

RESULT 20
US-09-949-016-9786
/ Sequence 9786, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9786
/ LENGTH: 349
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-9786

Query Match 55.6%; Score 5; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7

|||||

Db 208 DDTFY 212

RESULT 21

US-09-134-000C-5050

; Sequence 5050, Application US/09134000C

; Patent No. 6617156

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; FILE REFERENCE: 032796-032

; CURRENT APPLICATION NUMBER: US/09/134,000C

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/055,778

; PRIOR FILING DATE: 1997-08-15

; NUMBER OF SEQ ID NOS: 6812

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5050

; LENGTH: 370

; TYPE: PRT

; ORGANISM: Enterococcus faecalis

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (70)..(70)

; OTHER INFORMATION: Amino acid 70 is Xaa wherein Xaa = any amino acid.

US-09-134-000C-5050

Query Match

Best Local Similarity 55.6%; Score 5; DB 2; Length 370;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5

|||||

Db 145 KVDDT 149

RESULT 22

US-09-914-098-34

; Sequence 34, Application US/09914098

; Patent No. 6855863

; GENERAL INFORMATION:

; APPLICANT: E. I. du Pont de Nemours and Company

; TITLE OF INVENTION: Lysophosphatidic Acid Acetyltransferases

; FILE REFERENCE: BE1332

; CURRENT APPLICATION NUMBER: US/09/914,098

; PRIOR FILING DATE: 2001-08-22

; PRIOR APPLICATION NUMBER: 60/121,119

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 34

; LENGTH: 373

; TYPE: PRT

; ORGANISM: Glycine max

US-09-914-098-34

Query Match

Best Local Similarity 55.6%; Score 5; DB 2; Length 373;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6

|||||

Db 56 VDDTF 60

RESULT 23

US-10-414-759-2

; Sequence 2, Application US/10414759

; Patent No. 6723329
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: MCGUIRE, MICHAEL J.
; TITLE OF INVENTION: Use of Parapox B2L Protein to Modify Immune Responses to Adminis
; TITLE OF INVENTION: Antigens
; FILE REFERENCE: UTSD:664-1US
; CURRENT APPLICATION NUMBER: US/10/414,759
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/336,694
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 378
; TYPE: PRT
; ORGANISM: PARAPOX
US-10-414-759-2

Query Match

Best Local Similarity 55.6%; Score 5; DB 2; Length 378;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6

|||||

Db 325 VDDTF 329

RESULT 24

US-10-414-759-4

; Sequence 4, Application US/10414759

; Patent No. 6723329

; GENERAL INFORMATION:

; APPLICANT: JOHNSTON, STEPHEN A.

; APPLICANT: MCGUIRE, MICHAEL J.

; TITLE OF INVENTION: Use of Parapox B2L Protein to Modify Immune Responses to Adminis

; FILE REFERENCE: UTSD:664-1US

; CURRENT APPLICATION NUMBER: US/10/414,759

; CURRENT FILING DATE: 2003-04-15

; PRIOR APPLICATION NUMBER: US 60/336,694

; PRIOR FILING DATE: 2001-12-07

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 378

; TYPE: PRT

; ORGANISM: PARAPOX

US-10-414-759-4

Query Match

Best Local Similarity 55.6%; Score 5; DB 2; Length 378;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6

|||||

Db 325 VDDTF 329

RESULT 25

US-10-123-058-2

; Sequence 2, Application US/10123058

; Patent No. 6752995

; GENERAL INFORMATION:

; APPLICANT: JOHNSTON, STEPHEN A.

; APPLICANT: MCGUIRE, MICHAEL J.

; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES USEFUL AS

; TITLE OF INVENTION: ADJUVANTS

; FILE REFERENCE: UTSD:664US

; CURRENT APPLICATION NUMBER: US/10/123,058

; CURRENT FILING DATE: 2002-04-15

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 2
; LENGTH: 378
; TYPE: PRT
; ORGANISM: PARAPOX
US-10-123-058-2

Query Match          55.6%; Score 5; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 2 VDDTF 6
Db 325 VDDTF 329

RESULT 26
US-10-123-058-4
; Sequence 4, Application US/10123058
; Patent No. 6752995
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: MCGUIRE, MICHAEL J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES USEFUL AS
; TITLE OF INVENTION: ADJUVANTS
; FILE REFERENCE: UTSD:664US
; CURRENT APPLICATION NUMBER: US/10/123,058
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 378
; TYPE: PRT
; ORGANISM: PARAPOX
US-10-123-058-4

Query Match          55.6%; Score 5; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 2 VDDTF 6
Db 325 VDDTF 329

RESULT 27
US-10-414-609-2
; Sequence 2, Application US/10414609
; Patent No. 6752996
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: MCGUIRE, MICHAEL J.
; TITLE OF INVENTION: Use of Parapox B2L Protein to Modify Immune Responses to Administ
; TITLE OF INVENTION: Antigens
; FILE REFERENCE: UTSD:664-2US
; CURRENT APPLICATION NUMBER: US/10/414,609
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 10/123,058
; PRIOR FILING DATE: 2002-04-15
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 378
; TYPE: PRT
; ORGANISM: PARAPOX
US-10-414-609-2

Query Match          55.6%; Score 5; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 2 VDDTF 6
```

```
Db 325 VDDTF 329

RESULT 28
US-10-414-609-4
; Sequence 4, Application US/10414609
; Patent No. 6752996
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: MCGUIRE, MICHAEL J.
; TITLE OF INVENTION: Use of Parapox B2L Protein to Modify Immune Responses to Administ
; TITLE OF INVENTION: Antigens
; FILE REFERENCE: UTSD:664-2US
; CURRENT APPLICATION NUMBER: US/10/414,609
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 10/123,058
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/336,694
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 378
; TYPE: PRT
; ORGANISM: PARAPOX
US-10-414-609-4

Query Match          55.6%; Score 5; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 2 VDDTF 6
Db 325 VDDTF 329

RESULT 29
US-10-313-332-1
; Sequence 1, Application US/10313332
; Patent No. 6844000
; GENERAL INFORMATION:
; APPLICANT: Dubois-Stringfellow, Natalie
; TITLE OF INVENTION: Use of PARAPOX B2L Protein to Treat Cancer
; TITLE OF INVENTION: and Modify Immune Responses
; FILE REFERENCE: 002973.00092
; CURRENT APPLICATION NUMBER: US/10/313,332
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/336,694
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Parapox ovis strain NZ2
US-10-313-332-1

Query Match          55.6%; Score 5; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 2 VDDTF 6
Db 325 VDDTF 329

RESULT 30
US-10-313-332-3
; Sequence 3, Application US/10313332
; Patent No. 6844000
; GENERAL INFORMATION:
; APPLICANT: Dubois-Stringfellow, Natalie
```

;; TITLE OF INVENTION: Use of PARAPOX B2L Protein to Treat Cancer
;; FILE REFERENCE: 002973.00092
;; CURRENT APPLICATION NUMBER: US/10/313,332
;; CURRENT FILING DATE: 2002-12-06
;; PRIOR APPLICATION NUMBER: US 60/336,694
;; PRIOR FILING DATE: 2001-12-07
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 378
;; TYPE: PRT
;; ORGANISM: Parapox ovis strain D1701
US-10-313-332-3

Query Match 55.6%; Score 5; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
| | | | |
DB 325 VDDTF 329

RESULT 31
US-09-198-452A-720
;; Sequence 720, Application US/09198452A
;; Patent No. 6559294
;; GENERAL INFORMATION:
;; APPLICANT: Griffais, R.
;; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
;; FILE REFERENCE: 9710-003-999
;; CURRENT APPLICATION NUMBER: US/09/198,452A
;; CURRENT FILING DATE: 1998-11-24
;; NUMBER OF SEQ ID NOS: 6849
;; SEQ ID NO 720
;; LENGTH: 428
;; TYPE: PRT
;; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-720

Query Match 55.6%; Score 5; DB 2; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYVV 9
| | | | |
DB 225 TFYVV 229

RESULT 32
US-09-248-796A-17801
;; Sequence 17801, Application US/09248796A
;; Patent No. 6747137
;; GENERAL INFORMATION:
;; APPLICANT: Keith Weinstein et al
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
;; FILE REFERENCE: 107196.132
;; CURRENT APPLICATION NUMBER: US/09/248,796A
;; CURRENT FILING DATE: 1999-02-12
;; PRIOR APPLICATION NUMBER: US 60/074,725
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: US 60/096,409
;; PRIOR FILING DATE: 1998-08-13
;; NUMBER OF SEQ ID NOS: 28208
;; SEQ ID NO 17801
;; LENGTH: 428
;; TYPE: PRT
;; ORGANISM: Candida albicans
US-09-248-796A-17801

Query Match 55.6%; Score 5; DB 2; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
| | | | |
DB 297 VDDTF 301

RESULT 33
US-09-438-185A-682
;; Sequence 682, Application US/09438185A
;; Patent No. 6822071
;; GENERAL INFORMATION:
;; APPLICANT: Stephens, Richard
;; APPLICANT: Mitchell, Wayne
;; APPLICANT: Kalman, Sue
;; APPLICANT: Davis, Ronald
;; TITLE OF INVENTION: The Regents of the University of California
;; FILE REFERENCE: 018941-000411US
;; CURRENT APPLICATION NUMBER: US/09/438,185A
;; CURRENT FILING DATE: 2002-03-13
;; PRIOR APPLICATION NUMBER: US 60/108,279
;; PRIOR FILING DATE: 1998-11-12
;; PRIOR APPLICATION NUMBER: US 60/128,606
;; PRIOR FILING DATE: 1999-04-08
;; NUMBER OF SEQ ID NOS: 1074
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 682
;; LENGTH: 428
;; TYPE: PRT
;; ORGANISM: Chlamydia pneumoniae
;; FEATURE:
;; OTHER INFORMATION: CPN0680
US-09-438-185A-682

Query Match 55.6%; Score 5; DB 2; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYVV 9
| | | | |
DB 225 TFYVV 229

RESULT 34
US-09-889-738-21
;; Sequence 21, Application US/09889738
;; Patent No. 6734343
;; GENERAL INFORMATION:
;; APPLICANT: Gressel, Jonathan
;; APPLICANT: Eyal, Yoram
;; APPLICANT: Fluhr, Robert
;; TITLE OF INVENTION: RHAMNOSYL-TRANSFERASE GENE AND USES THEREOF
;; FILE REFERENCE: 01/22289
;; CURRENT APPLICATION NUMBER: US/09/889,738
;; CURRENT FILING DATE: 2000-01-20
;; PRIOR APPLICATION NUMBER: IL 128193
;; PRIOR FILING DATE: 1999-01-20
;; PRIOR APPLICATION NUMBER: PCT/IL00/00038
;; PRIOR FILING DATE: 2000-01-20
;; NUMBER OF SEQ ID NOS: 21
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 21
;; LENGTH: 452
;; TYPE: PRT
;; ORGANISM: Citrus X paradisi
US-09-889-738-21

Query Match 55.6%; Score 5; DB 2; Length 452;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||

Db 243 KVDDT 247

RESULT 35

US-09-740-002-27
; Sequence 27, Application US/09740002
; Patent No. 6537809
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-27

Query Match 55.6%; Score 5; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||

Db 76 DDTFY 80

RESULT 36

US-09-134-001C-4435
; Sequence 4435, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4435
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4435

Query Match 55.6%; Score 5; DB 2; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||

Db 45 KVDDT 49

RESULT 37

US-10-033-109-12
; Sequence 12, Application US/10033109
; Patent No. 6833492
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Nitrogen Transport Metabolism
; FILE REFERENCE: BB-1210
; CURRENT APPLICATION NUMBER: US/10/033,109
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
; PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Glycine max
US-10-033-109-12

Query Match 55.6%; Score 5; DB 2; Length 486;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||

Db 344 KVDDT 348

RESULT 38

US-08-942-012B-27
; Sequence 27, Application US/08942012B
; Patent No. 6235278
; GENERAL INFORMATION:
; APPLICANT: Miller, Lois K.
; APPLICANT: Lu, Albert
; APPLICANT: Dierks, Peter
; APPLICANT: Black, Bruce
; TITLE OF INVENTION: Biological Insect Control Agents Expressing
; TITLE OF INVENTION: Insect-Specific Toxin Genes, Methods and Compositions
; FILE REFERENCE: 28-96a
; CURRENT APPLICATION NUMBER: US/08/942,012B
; CURRENT FILING DATE: 1997-10-01
; PRIOR APPLICATION NUMBER: 08/729,606
; PRIOR FILING DATE: 2000-10-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Choristoneura fumiferana nucleopolyhedrovirus
US-08-942-012B-27

Query Match 55.6%; Score 5; DB 2; Length 491;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||

Db 328 KVDDT 332

RESULT 39

US-10-033-109-10
; Sequence 10, Application US/10033109
; Patent No. 6833492
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Sakai, Hajime

; TITLE OF INVENTION: Nitrogen Transport Metabolism
; FILE REFERENCE: BB-1210
; CURRENT APPLICATION NUMBER: US/10/033,109
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
; PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 10
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-033-109-10

Query Match 55.6%; Score 5; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDVT 5
DB 347 KVDVT 351

RESULT 40
US-09-252-991A-17363
; Sequence 17363, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17363
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17363

Query Match 55.6%; Score 5; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
DB 133 VDDTF 137

RESULT 41
US-09-398-395A-2
; Sequence 2, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-398-395A-2

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
DB 300 VDDTF 304

RESULT 42
US-09-398-395A-4
; Sequence 4, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-398-395A-4

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
DB 300 VDDTF 304

RESULT 43
US-09-398-395A-6
; Sequence 6, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262

; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-398-395A-6

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 300 VDDTF 304

RESULT 44
US-09-398-395A-8
; Sequence 8, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-398-395A-8

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 300 VDDTF 304

RESULT 45
US-09-398-395A-10
; Sequence 10, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-398-395A-10

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 300 VDDTF 304

RESULT 46
US-09-398-395A-12
; Sequence 12, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; NAME/KEY: VARIANT
; LOCATION: (1)....(548)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-398-395A-12

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 300 VDDTF 304

RESULT 47
US-09-887-586A-2
; Sequence 2, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628

; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-887-586A-2

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
|
|
|
|
Db 300 VDDTF 304

RESULT 48
US-09-887-586A-4
; Sequence 4, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-887-586A-4

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
|
|
|
|
Db 300 VDDTF 304

RESULT 49
US-09-887-586A-6
; Sequence 6, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-887-586A-6

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
|
|
|
|
Db 300 VDDTF 304

RESULT 50
US-09-887-586A-8
; Sequence 8, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-887-586A-8

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
|
|
|
|
Db 300 VDDTF 304

RESULT 51
US-09-887-586A-10
; Sequence 10, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262

; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-887-586A-10

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 52
US-09-887-586A-12
; Sequence 12, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(548)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-887-586A-12

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 53
US-09-895-752-2
; Sequence 2, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-895-752-2

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 54
US-09-895-752-4
; Sequence 4, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-895-752-4

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 55
US-09-895-752-6
; Sequence 6, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752

```

; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-895-752-6

```

```

Query Match          55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 VDDTF 6
      |||||
Db      300 VDDTF 304

```

```

RESULT 56
US-09-895-752-8
; Sequence 8, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-895-752-8

```

```

Query Match          55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 VDDTF 6
      |||||
Db      300 VDDTF 304

```

```

RESULT 57
US-09-895-752-10
; Sequence 10, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.

```

```

; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-895-752-10

```

```

Query Match          55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 VDDTF 6
      |||||
Db      300 VDDTF 304

```

```

RESULT 58
US-09-895-752-12
; Sequence 12, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(548)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-895-752-12

```

```

Query Match          55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 VDDTF 6
      |||||
Db      300 VDDTF 304

```

```

RESULT 59
US-09-903-012B-2

```

; Sequence 2, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-903-012B-2

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 300 VDDTF 304

RESULT 60
US-09-903-012B-4
; Sequence 4, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-903-012B-4

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 300 VDDTF 304

RESULT 61
US-09-903-012B-6
; Sequence 6, Application US/09903012B

; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-903-012B-6

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 300 VDDTF 304

RESULT 62
US-09-903-012B-8
; Sequence 8, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-903-012B-8

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 300 VDDTF 304

RESULT 63
US-09-903-012B-10
; Sequence 10, Application US/09903012B
; Patent No. 6569656

GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-903-012B-10

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 64
US-09-903-012B-12
; Sequence 12, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(548)
; OTHER INFORMATION: xaa = Any Amino Acid
US-09-903-012B-12

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 65

US-09-900-797-2
; Sequence 2, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 66457621, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-900-797-2

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 66
US-09-900-797-4
; Sequence 4, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 66457621, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-900-797-4

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 67
US-09-900-797-6

```
; Sequence 6, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 66457621, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; US-09-900-797-6
```

```
Query Match          55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 VDDTF 6
    |||||
Db 300 VDDTF 304
```

```
RESULT 68
US-09-900-797-8
; Sequence 8, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 66457621, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; US-09-900-797-8
```

```
Query Match          55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 VDDTF 6
    |||||
Db 300 VDDTF 304
```

```
RESULT 69
US-09-900-797-10
; Sequence 10, Application US/09900797
```

```
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 66457621, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; US-09-900-797-10
```

```
Query Match          55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 VDDTF 6
    |||||
Db 300 VDDTF 304
```

```
RESULT 70
US-09-900-797-12
; Sequence 12, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 66457621, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(548)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-900-797-12
```

```
Query Match          55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 VDDTF 6
    |||||
Db 300 VDDTF 304
```

RESULT 71
 US-09-893-820-2
 ; Sequence 2, Application US/09893820
 ; Patent No. 6890752
 ; GENERAL INFORMATION:
 ; APPLICANT: Chappell, Joseph
 ; APPLICANT: No. 68907521, Joseph P.
 ; APPLICANT: Starks, Courtney M.
 ; APPLICANT: Manna, Kathleen R.
 ; TITLE OF INVENTION: SYNTHASES
 ; FILE REFERENCE: 07678-025001
 ; CURRENT APPLICATION NUMBER: US/09/893,820
 ; CURRENT FILING DATE: 2001-06-28
 ; PRIOR APPLICATION NUMBER: US/09/398,395A
 ; PRIOR FILING DATE: 1999-09-17
 ; PRIOR APPLICATION NUMBER: 60/100,993
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/130,628
 ; PRIOR FILING DATE: 1999-04-22
 ; PRIOR APPLICATION NUMBER: 60/150,262
 ; PRIOR FILING DATE: 1999-08-23
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 548
 ; TYPE: PRT
 ; ORGANISM: Nicotiana tabacum
 US-09-893-820-2

Query Match 55.6%; Score 5; DB 2; Length 548;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 300 VDDTF 304

RESULT 72
 US-09-893-820-4
 ; Sequence 4, Application US/09893820
 ; Patent No. 6890752
 ; GENERAL INFORMATION:
 ; APPLICANT: Chappell, Joseph
 ; APPLICANT: No. 68907521, Joseph P.
 ; APPLICANT: Starks, Courtney M.
 ; APPLICANT: Manna, Kathleen R.
 ; TITLE OF INVENTION: SYNTHASES
 ; FILE REFERENCE: 07678-025001
 ; CURRENT APPLICATION NUMBER: US/09/893,820
 ; CURRENT FILING DATE: 2001-06-28
 ; PRIOR APPLICATION NUMBER: US/09/398,395A
 ; PRIOR FILING DATE: 1999-09-17
 ; PRIOR APPLICATION NUMBER: 60/100,993
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/130,628
 ; PRIOR FILING DATE: 1999-04-22
 ; PRIOR APPLICATION NUMBER: 60/150,262
 ; PRIOR FILING DATE: 1999-08-23
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 548
 ; TYPE: PRT
 ; ORGANISM: Nicotiana tabacum
 US-09-893-820-4

Query Match 55.6%; Score 5; DB 2; Length 548;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||

Db 300 VDDTF 304
 RESULT 73
 US-09-893-820-6
 ; Sequence 6, Application US/09893820
 ; Patent No. 6890752
 ; GENERAL INFORMATION:
 ; APPLICANT: Chappell, Joseph
 ; APPLICANT: No. 68907521, Joseph P.
 ; APPLICANT: Starks, Courtney M.
 ; APPLICANT: Manna, Kathleen R.
 ; TITLE OF INVENTION: SYNTHASES
 ; FILE REFERENCE: 07678-025001
 ; CURRENT APPLICATION NUMBER: US/09/893,820
 ; CURRENT FILING DATE: 2001-06-28
 ; PRIOR APPLICATION NUMBER: US/09/398,395A
 ; PRIOR FILING DATE: 1999-09-17
 ; PRIOR APPLICATION NUMBER: 60/100,993
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/130,628
 ; PRIOR FILING DATE: 1999-04-22
 ; PRIOR APPLICATION NUMBER: 60/150,262
 ; PRIOR FILING DATE: 1999-08-23
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 548
 ; TYPE: PRT
 ; ORGANISM: Nicotiana tabacum
 US-09-893-820-6

Query Match 55.6%; Score 5; DB 2; Length 548;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 300 VDDTF 304

RESULT 74
 US-09-893-820-8
 ; Sequence 8, Application US/09893820
 ; Patent No. 6890752
 ; GENERAL INFORMATION:
 ; APPLICANT: Chappell, Joseph
 ; APPLICANT: No. 68907521, Joseph P.
 ; APPLICANT: Starks, Courtney M.
 ; APPLICANT: Manna, Kathleen R.
 ; TITLE OF INVENTION: SYNTHASES
 ; FILE REFERENCE: 07678-025001
 ; CURRENT APPLICATION NUMBER: US/09/893,820
 ; CURRENT FILING DATE: 2001-06-28
 ; PRIOR APPLICATION NUMBER: US/09/398,395A
 ; PRIOR FILING DATE: 1999-09-17
 ; PRIOR APPLICATION NUMBER: 60/100,993
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/130,628
 ; PRIOR FILING DATE: 1999-04-22
 ; PRIOR APPLICATION NUMBER: 60/150,262
 ; PRIOR FILING DATE: 1999-08-23
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 548
 ; TYPE: PRT
 ; ORGANISM: Nicotiana tabacum
 US-09-893-820-8

Query Match 55.6%; Score 5; DB 2; Length 548;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      2 VDDTF 6
Db      300 VDDTF 304

RESULT 75
US-09-893-820-10
; Sequence 10, Application US/09893820
; Patent No. 6890752
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 68907521, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-893-820-10

Query Match      55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VDDTF 6
Db      300 VDDTF 304

RESULT 76
US-09-893-820-12
; Sequence 12, Application US/09893820
; Patent No. 6890752
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 68907521, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: VARIANT

US-09-893-820-12

Query Match      55.6%; Score 5; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VDDTF 6
Db      302 VDDTF 306

RESULT 78
US-08-577-483-8
; Sequence 8, Application US/08577483
; Patent No. 6100451
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: Yin, Shaohui
; APPLICANT: Cornett, Catherine A.G.
; TITLE OF INVENTION: Transcriptional Control Sequences and
```


;; TITLE OF INVENTION: Methods
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson, P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: US
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/577,483
;; FILING DATE: 22-DEC-1995
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Paul T. Clark
;; REGISTRATION NUMBER: 32,164
;; REFERENCE/DOCKET NUMBER: 07678/003001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 542-5070
;; TELEFAX: (617) 542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 550 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-577-483-8

Query Match 55.6%; Score 5; DB 2; Length 550;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
Db 302 VDDTF 306

RESULT 79
US-09-435-380-8
; Sequence 8, Application US/09435380
; Patent No. 6605764
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: Yin, Shaohui
; APPLICANT: Cornett, Catherine A.G.
; TITLE OF INVENTION: Transcriptional Control Sequences and
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/435,380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US/08/443,639
; FILING DATE: 18-MAY-1995

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ferber, Donna M.
;; REGISTRATION NUMBER: 33878
;; REFERENCE/DOCKET NUMBER: 69-94
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (303) 499-8080
;; TELEFAX: (303) 499-8089
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 550 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-435-380-8

Query Match 55.6%; Score 5; DB 2; Length 550;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
Db 302 VDDTF 306

RESULT 80
US-09-398-395A-32
; Sequence 32, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Solanum tuberosum
; US-09-398-395A-32

Query Match 55.6%; Score 5; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
Db 308 VDDTF 312

RESULT 81
US-09-887-586A-32
; Sequence 32, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22

```

; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-09-887-586A-32

```

```

Query Match          55.6%; Score 5; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 VDDTF 6
        |||||
Db      308 VDDTF 312

```

```

RESULT 82
US-09-895-752-32
; Sequence 32, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6559297, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-09-895-752-32

```

```

Query Match          55.6%; Score 5; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 VDDTF 6
        |||||
Db      308 VDDTF 312

```

```

RESULT 83
US-09-903-012B-32
; Sequence 32, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6569656, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B

```

```

; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-09-903-012B-32

```

```

Query Match          55.6%; Score 5; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 VDDTF 6
        |||||
Db      308 VDDTF 312

```

```

RESULT 84
US-09-900-797-32
; Sequence 32, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6645762, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-09-900-797-32

```

```

Query Match          55.6%; Score 5; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 VDDTF 6
        |||||
Db      308 VDDTF 312

```

```

RESULT 85
US-09-893-820-32
; Sequence 32, Application US/09893820
; Patent No. 6890752
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6890752, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; CURRENT FILING DATE: 2001-06-28

```

;; PRIOR APPLICATION NUMBER: US/09/398,395A
;; PRIOR FILING DATE: 1999-09-17
;; PRIOR APPLICATION NUMBER: 60/100,993
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/130,628
;; PRIOR FILING DATE: 1999-04-22
;; PRIOR APPLICATION NUMBER: 60/150,262
;; PRIOR FILING DATE: 1999-08-23
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 32
;; LENGTH: 556
;; TYPE: PRT
;; ORGANISM: Solanum tuberosum
US-09-893-820-32

Query Match 55.6%; Score 5; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
| | | | |
Db 308 VDDTF 312

RESULT 86
US-10-094-749-2545
;; Sequence 2545, Application US/10094749
;; Patent No. 6979557
;; GENERAL INFORMATION:
;; APPLICANT: ISOGAI, TAKAO
;; APPLICANT: SUGIYAMA, TOMOYASU
;; APPLICANT: OTSUKI, TETSUJI
;; APPLICANT: WAKAMATSU, AI
;; APPLICANT: SATO, HIROYUKI
;; APPLICANT: ISHII, SHIZUKO
;; APPLICANT: YAMAMOTO, JUN-ICHI
;; APPLICANT: ISONO, YUUKO
;; APPLICANT: HIO, YURI
;; APPLICANT: OTSUKA, KAORU
;; APPLICANT: NAGAI, KEIICHI
;; APPLICANT: IRIE, RYOTARO
;; APPLICANT: TAMECHIKA, ICHIRO
;; APPLICANT: SEKI, NAOHIKO
;; APPLICANT: YOSHIKAWA, TSUTOMU
;; APPLICANT: OTSUKA, MOTOTYUKI
;; APPLICANT: NAGAHARI, KENJI
;; APPLICANT: MASUHO, YASUHIKO
;; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
;; FILE REFERENCE: 084335/0160
;; CURRENT APPLICATION NUMBER: US/10/094,749
;; CURRENT FILING DATE: 2002-03-12
;; PRIOR APPLICATION NUMBER: 60/350,435
;; PRIOR FILING DATE: 2002-01-24
;; PRIOR APPLICATION NUMBER: JP 2001-328381
;; PRIOR FILING DATE: 2001-09-14
;; NUMBER OF SEQ ID NOS: 3381
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2545
;; LENGTH: 566
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-094-749-2545

Query Match 55.6%; Score 5; DB 2; Length 566;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDVT 5
| | | | |
Db 178 KVDVT 182

RESULT 87
US-09-902-540-11767
;; Sequence 11767, Application US/09902540
;; Patent No. 6833447
;; GENERAL INFORMATION:
;; APPLICANT: Goldman, Barry S.
;; APPLICANT: Hinkle, Gregory J.
;; APPLICANT: Slater, Steven C.
;; APPLICANT: Wiegand, Roger C.
;; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;; FILE REFERENCE: 38-10(15849)B
;; CURRENT APPLICATION NUMBER: US/09/902,540
;; CURRENT FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: 60/217,883
;; PRIOR FILING DATE: 2000-07-10
;; NUMBER OF SEQ ID NOS: 16825
;; SEQ ID NO 11767
;; LENGTH: 567
;; TYPE: PRT
;; ORGANISM: Myxococcus xanthus
US-09-902-540-11767

Query Match 55.6%; Score 5; DB 2; Length 567;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
| | | | |
Db 379 VDDTF 383

RESULT 88
US-09-902-540-12279
;; Sequence 12279, Application US/09902540
;; Patent No. 6833447
;; GENERAL INFORMATION:
;; APPLICANT: Goldman, Barry S.
;; APPLICANT: Hinkle, Gregory J.
;; APPLICANT: Slater, Steven C.
;; APPLICANT: Wiegand, Roger C.
;; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;; FILE REFERENCE: 38-10(15849)B
;; CURRENT APPLICATION NUMBER: US/09/902,540
;; CURRENT FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: 60/217,883
;; PRIOR FILING DATE: 2000-07-10
;; NUMBER OF SEQ ID NOS: 16825
;; SEQ ID NO 12279
;; LENGTH: 581
;; TYPE: PRT
;; ORGANISM: Myxococcus xanthus
US-09-902-540-12279

Query Match 55.6%; Score 5; DB 2; Length 581;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
| | | | |
Db 307 VDDTF 311

RESULT 89
US-09-248-796A-16044
;; Sequence 16044, Application US/09248796A
;; Patent No. 6747137
;; GENERAL INFORMATION:
;; APPLICANT: Keith Weinstock et al
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
;; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 107196.132
;; CURRENT APPLICATION NUMBER: US/09/248,796A
;; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16044
; LENGTH: 584
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16044

Query Match 55.6%; Score 5; DB 2; Length 584;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
DB 80 VDDTF 84

RESULT 90
US-09-248-796A-17444
; Sequence 17444, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17444
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17444

Query Match 55.6%; Score 5; DB 2; Length 651;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||
DB 445 KVDDT 449

RESULT 91
US-09-540-236-2284
; Sequence 2284, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2284
; LENGTH: 783
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2284

Query Match 55.6%; Score 5; DB 2; Length 783;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||
DB 16 KVDDT 20

RESULT 92
US-09-248-796A-20875
; Sequence 20875, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20875
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20875

Query Match 55.6%; Score 5; DB 2; Length 812;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
DB 159 VDDTF 163

RESULT 93
US-09-489-039A-8469
; Sequence 8469, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8469
; LENGTH: 825
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8469

Query Match 55.6%; Score 5; DB 2; Length 825;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
DB 14 VDDTF 18

RESULT 94
US-09-248-796A-18967
; Sequence 18967, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

```
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18967
; LENGTH: 832
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18967

Query Match      55.6%; Score 5; DB 2; Length 832;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVDVT 5
Db      508 KVDVT 512

RESULT 95
US-09-134-000C-5052
; Sequence 5052, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5052
; LENGTH: 869
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (9)..(9)
; OTHER INFORMATION: Amino acid 9 is Xaa wherein Xaa = any amino acid.
US-09-134-000C-5052

Query Match      55.6%; Score 5; DB 2; Length 869;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVDVT 5
Db      670 KVDVT 674

RESULT 96
US-09-134-000C-4697
; Sequence 4697, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4697
```

```
; LENGTH: 899
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4697

Query Match      55.6%; Score 5; DB 2; Length 899;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 DDTFY 7
Db      399 DDTFY 403

RESULT 97
US-09-270-767-42083
; Sequence 42083, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42083
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42083

Query Match      55.6%; Score 5; DB 2; Length 910;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 DDTFY 7
Db      528 DDTFY 532

RESULT 98
US-09-252-991A-27976
; Sequence 27976, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27976
; LENGTH: 1123
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27976

Query Match      55.6%; Score 5; DB 2; Length 1123;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVDVT 5
Db      239 KVDVT 243
```

RESULT 99
US-09-862-027-82
; Sequence 82, Application US/09862027
; Patent No. 6858418
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: No. 6858418el Kinases and Uses Thereof
; FILE REFERENCE: 35800/234862
; CURRENT APPLICATION NUMBER: US/09/862,027
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/345,473
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 1309
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1309)
; OTHER INFORMATION: xaa = Any Amino Acid
US-09-862-027-82

Query Match 55.6%; Score 5; DB 2; Length 1309;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 1078 VDDTF 1082

RESULT 100
US-09-949-016-10490
; Sequence 10490, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10490
; LENGTH: 1912
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10490

Query Match 55.6%; Score 5; DB 2; Length 1912;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 1710 VDDTF 1714

RESULT 101
US-09-747-408-22
; Sequence 22, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:

; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-22

Query Match 44.4%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDD 4
|||
Db 1 KVDD 4

RESULT 102
US-09-996-288-23
; Sequence 23, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-23

Query Match 44.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 7
|||
Db 1 DTFY 4

RESULT 103
US-09-996-288-90
; Sequence 90, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 7

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-90

Query Match 44.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 7
|
|
|
Db 1 DTFY 4

RESULT 104

US-09-996-288-99
; Sequence 99, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-99

Query Match 44.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 7
|
|
|
Db 1 DTFY 4

RESULT 105

US-09-996-265-23
; Sequence 23, Application US/09996265
; Patent No. 6855493
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-23

Query Match 44.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 7
|
|
|
Db 1 DTFY 4

RESULT 106

US-09-996-265-90
; Sequence 90, Application US/09996265
; Patent No. 6855493
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-90

Query Match 44.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 7
|
|
|
Db 1 DTFY 4

RESULT 107

US-09-996-265-99
; Sequence 99, Application US/09996265
; Patent No. 6855493
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-99

Query Match 44.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 7
|
|
|
Db 1 DTFY 4

RESULT 108

US-10-092-263-4
; Sequence 4, Application US/10092263
; Patent No. 6800477
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: STEREoselective REDUCTION OF SUBSTITUTED ACETOPHENONE
; FILE REFERENCE: CT-2657NP
; CURRENT APPLICATION NUMBER: US/10/092,263
; CURRENT FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4

```
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Pichia methanolica
US-10-092-263-4

Query Match      44.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVDD 4
Db      1 KVDD 4

RESULT 109
US-08-166-195A-22
; Sequence 22, Application US/08166195A
; Patent No. 5480799
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5480799th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/166,195A
; FILING DATE: 10 DEC 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470/73
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-166-195A-23

Query Match      44.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVDD 4
Db      3 KVDD 6

RESULT 111
US-08-436-772-22
; Sequence 22, Application US/08436772
; Patent No. 5814456
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5814456th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,772
```


; FILING DATE: 08-MAY-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sibley, Kenneth D.
 ; REGISTRATION NUMBER: 31,665
 ; REFERENCE/DOCKET NUMBER: 5470-73B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-881-3140
 ; TELEFAX: 919-881-3175
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-436-772-22

Query Match 44.4%; Score 4; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDD 4
 Db 6 KVDD 9

RESULT 112
 US-08-436-772-23
 ; Sequence 23 Application US/08436772
 ; Patent No. 5814456
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Rand, Michael G.
 ; APPLICANT: Widgren, Esther E.
 ; APPLICANT: Richardson, Richard T.
 ; APPLICANT: Lea, Isabel
 ; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
 ; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kenneth D. Sibley
 ; STREET: P.O. Box 34009
 ; CITY: Charlotte
 ; STATE: No. 5814456th Carolina
 ; COUNTRY: USA
 ; ZIP: 28234
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/08/436,772
 ; FILING DATE: 08-MAY-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sibley, Kenneth D.
 ; REGISTRATION NUMBER: 31,665
 ; REFERENCE/DOCKET NUMBER: 5470-73B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-881-3140
 ; TELEFAX: 919-881-3175
 ; INFORMATION FOR SEQ ID NO: 23:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-436-772-23

Query Match 44.4%; Score 4; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVDD 4
 Db 3 KVDD 6

RESULT 113
 US-08-436-883B-22
 ; Sequence 22 Application US/08436883B
 ; Patent No. 5820861
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Rand, Michael G.
 ; APPLICANT: Widgren, Esther E.
 ; APPLICANT: Richardson, Richard T.
 ; APPLICANT: Lea, Isabel
 ; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
 ; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kenneth D. Sibley
 ; STREET: P.O. Box 34009
 ; CITY: Charlotte
 ; STATE: No. 5820861th Carolina
 ; COUNTRY: USA
 ; ZIP: 28234
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/436,883B
 ; FILING DATE: 08-MAY-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sibley, Kenneth D.
 ; REGISTRATION NUMBER: 31,665
 ; REFERENCE/DOCKET NUMBER: 5470-73C
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-420-2200
 ; TELEFAX: 919-881-3175
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-436-883B-22

Query Match 44.4%; Score 4; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDD 4
 Db 6 KVDD 9

RESULT 114
 US-08-436-883B-23
 ; Sequence 23 Application US/08436883B
 ; Patent No. 5820861
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Rand, Michael G.
 ; APPLICANT: Widgren, Esther E.
 ; APPLICANT: Richardson, Richard T.
 ; APPLICANT: Lea, Isabel
 ; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
 ; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenneth D. Sibley
STREET: P.O. Box 34009
CITY: Charlotte
STATE: No. 5820861th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,883B
FILING DATE: 08-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-73C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLSCULE TYPE: peptide
US-08-436-883B-23

Query Match 44.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVDD 4
Db 3 KVVDD 6

RESULT 115
US-09-200-757-3
; Sequence 3, Application US/09200757
; Patent No. 6277958
; GENERAL INFORMATION:
; APPLICANT: Aimoto, Saburho
; TITLE OF INVENTION: METHOD FOR PREPARING PEPTIDE THIOL ESTER
; FILE REFERENCE: 31763-138092
; CURRENT APPLICATION NUMBER: US/09/200,757
; CURRENT FILING DATE: 1998-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Asp(OBut)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)
; OTHER INFORMATION: Asp(OBut)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (3)
; OTHER INFORMATION: Asp(OBut)
; FEATURE:
; NAME/KEY: MOD_RES

; LOCATION: (4)
; OTHER INFORMATION: Thr(But)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: Thr(But)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: Lys(Boc)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: Gly(S-C(CH3)2CH2-CO)
; FEATURE:
; OTHER INFORMATION: this peptide has an amidated C-terminus
US-09-200-757-3

Query Match 44.4%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTF 6
Db 2 DDTF 5

RESULT 116
US-09-200-757-4
; Sequence 4, Application US/09200757
; Patent No. 6277958
; GENERAL INFORMATION:
; APPLICANT: Aimoto, Saburho
; TITLE OF INVENTION: METHOD FOR PREPARING PEPTIDE THIOL ESTER
; FILE REFERENCE: 31763-138092
; CURRENT APPLICATION NUMBER: US/09/200,757
; CURRENT FILING DATE: 1998-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: Gly(S-C(CH3)2CH2-CO)
; FEATURE:
; OTHER INFORMATION: this peptide has an amidated C-terminus
US-09-200-757-4

Query Match 44.4%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTF 6
Db 2 DDTF 5

RESULT 117
US-07-712-476A-3
; Sequence 3, Application US/07712476A
; Patent No. 5304496
; GENERAL INFORMATION:
; APPLICANT: Hoyer et al.
; TITLE OF INVENTION: Biological Regulation of
; TITLE OF INVENTION: Mineralization
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5304496ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/712,476A
FILING DATE: 19910610
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Suzanne E. Miller
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN 0473
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568 3100
TELEFAX: (215) 568 3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-712-476A-3

Query Match 44.4%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
DB 6 VDDT 9

RESULT 118
5204097-4
PATENT NO. 5204097
APPLICANT: ARNON, RUTH; HARARI, ILANA; KEUSCH, GERALD T.
DONOHUE-ROLFE, ARTHUR
TITLE OF INVENTION: SHIGA TOXIN B CHAIN POLYPEPTIDES AND
VACCINE THEREOF
NUMBER OF SEQUENCES: 5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/364,506
FILING DATE: 09-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 70,243
FILING DATE: 06-JUL-1987
SEQ ID NO: 4:
LENGTH: 14
5204097-4

Query Match 44.4%; Score 4; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTF 6
DB 5 DDTF 8

RESULT 119
US-08-480-190-171
SEQUENCE 171, Application US/08480190
PATENT NO. 5827516

GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-171

Query Match 44.4%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
DB 1 VDDT 4

RESULT 120
US-08-488-379-171
SEQUENCE 171, Application US/08488379
PATENT NO. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts

/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM PS/2 Model 502 or 55SX
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: WordPerfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/488,379
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/077,255
/ FILING DATE: June 15, 1993
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 171:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-08-488-379-171

Query Match 44.4%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 121
US-08-475-399A-171
/ Sequence 171, Application US/08475399A
/ Patent No. 6509033
/ GENERAL INFORMATION:
/ APPLICANT: Urban, Robert G.
/ APPLICANT: Chiciz, Roman M.
/ APPLICANT: Vignali, Dario A.A.
/ APPLICANT: Hedley, Mary L.
/ APPLICANT: Stern, Lawrence J.
/ APPLICANT: Strominger, Jack L.
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 276
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson, P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows95
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/475,399A
/ FILING DATE: 07-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/077,255
/ FILING DATE: 15-JUN-1993
/ APPLICATION NUMBER: 07/925,460

/ FILING DATE: 11-AUG-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fraser, Janis K.
/ REGISTRATION NUMBER: 34,819
/ REFERENCE/DOCKET NUMBER: 00246/168003
/ TELEPHONE: 617/542-507
/ TELEFAX: 617/542-890
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 171:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-475-399A-171

Query Match 44.4%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 122
US-08-077-255A-171
/ Sequence 171, Application US/08077255A
/ Patent No. 6696061
/ GENERAL INFORMATION:
/ APPLICANT: Robert G. Urban
/ APPLICANT: Roman M. Chiciz
/ APPLICANT: Dario A. A. Vignali
/ APPLICANT: Mary L. Hedley
/ APPLICANT: Lawrence J. Stern
/ APPLICANT: Jack L. Strominger
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 274
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM PS/2 Model 502 or 55SX
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: WordPerfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/077,255A
/ FILING DATE: June 15, 1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 171:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-08-077-255A-171

Query Match 44.4%; Score 4; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDT 5
 Db 1 VDDT 4

RESULT 123

PCT-US93-07545-171
 ; Sequence 171, Application PC/TUS9307545
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Urban
 ; APPLICANT: Roman M. Chicz
 ; APPLICANT: Dario A. A. Vignali
 ; APPLICANT: Mary L. Hedley
 ; APPLICANT: Lawrence J. Stern
 ; APPLICANT: Jack L. Strominger
 ; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
 ; NUMBER OF SEQUENCES: 273
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/07545
 ; FILING DATE: 19930811
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/925,460
 ; FILING DATE: August 11, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 00246/168001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 171:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; PCT-US93-07545-171

Query Match 44.4%; Score 4; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDT 5
 Db 1 VDDT 4

RESULT 124

US-08-480-190-97
 ; Sequence 97, Application US/08480190
 ; Patent No. 5827516
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Urban
 ; APPLICANT: Roman M. Chicz
 ; APPLICANT: Dario A. A. Vignali

; APPLICANT: Mary L. Hedley
 ; APPLICANT: Lawrence J. Stern
 ; APPLICANT: Jack L. Strominger
 ; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
 ; NUMBER OF SEQUENCES: 274
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/480,190
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/077,255
 ; FILING DATE: June 15, 1993
 ; APPLICATION NUMBER: 07/925,460
 ; FILING DATE: August 11, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 00246/168001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 97:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-480-190-97

Query Match 44.4%; Score 4; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDT 5
 Db 1 VDDT 4

RESULT 125

US-08-480-190-108
 ; Sequence 108, Application US/08480190
 ; Patent No. 5827516
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Urban
 ; APPLICANT: Roman M. Chicz
 ; APPLICANT: Dario A. A. Vignali
 ; APPLICANT: Mary L. Hedley
 ; APPLICANT: Lawrence J. Stern
 ; APPLICANT: Jack L. Strominger
 ; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
 ; NUMBER OF SEQUENCES: 274
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

/ COMPUTER: IBM PS/2 Model 502 or 55SX
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: WordPerfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/480,190
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/077,255
/ FILING DATE: June 15, 1993
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 108:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-08-480-190-108

Query Match 44.4%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 VDDT 5
Db 1 VDDT 4

RESULT 126
US-08-488-379-97
/ Sequence 97, Application US/08488379
/ Patent No. 5880103
/ GENERAL INFORMATION:
/ APPLICANT: Robert G. Urban
/ APPLICANT: Roman M. Chicz
/ APPLICANT: Dario A. A. Vignali
/ APPLICANT: Mary L. Hedley
/ APPLICANT: Lawrence J. Stern
/ APPLICANT: Jack L. Strominger
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 274
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM PS/2 Model 502 or 55SX
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: WordPerfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/488,379
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/077,255
/ FILING DATE: June 15, 1993
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.

/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 97:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-08-488-379-97

Query Match 44.4%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 VDDT 5
Db 1 VDDT 4

RESULT 127
US-08-488-379-108
/ Sequence 108, Application US/08488379
/ Patent No. 5880103
/ GENERAL INFORMATION:
/ APPLICANT: Robert G. Urban
/ APPLICANT: Roman M. Chicz
/ APPLICANT: Dario A. A. Vignali
/ APPLICANT: Mary L. Hedley
/ APPLICANT: Lawrence J. Stern
/ APPLICANT: Jack L. Strominger
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 274
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM PS/2 Model 502 or 55SX
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: WordPerfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/488,379
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/077,255
/ FILING DATE: June 15, 1993
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 108:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-08-488-379-108

Query Match 44.4%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDT 5
Db 1 VDDT 4

RESULT 128

US-08-672-345C-65
; Sequence 65, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-391-0525
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-65

Query Match 44.4%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 7
Db 8 DTFY 11

RESULT 129

US-09-214-095D-65
; Sequence 65, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 17
; TYPE: PRT

; ORGANISM: Murinae gen. sp.
US-09-214-095D-65

Query Match 44.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 7
Db 8 DTFY 11

RESULT 130

US-08-475-399A-97
; Sequence 97, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00246/168003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-507
; TELEFAX: 617/542-890
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-475-399A-97

Query Match 44.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDT 5
Db 1 VDDT 4

RESULT 131

US-08-475-399A-108
; Sequence 108, Application US/08475399A
; Patent No. 6509033

GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chiciz, Roman M.
APPLICANT: Vignali, Dario A.A.
APPLICANT: Hedley, Mary L.
APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-108

Query Match 44.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 132
US-08-077-255A-97
Sequence 97, Application US/08077255A
Patent No. 6696061
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chiciz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 17
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-97
Query Match 44.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
QY 2 VDDT 5
Db 1 VDDT 4
RESULT 133
US-08-077-255A-108
Sequence 108, Application US/08077255A
Patent No. 6696061
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chiciz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001


```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-077-255A-108

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Query Match 44.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 VDDT 5
Db 1 VDDT 4

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RESULT 134

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US-09-940-727B-65
; Sequence 65, Application US/09940727B
; Patent No. 6913917
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 17
; TYPE: PRT
; ORGANISM: mouse
; US-09-940-727B-65

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```

Query Match 44.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 DTFY 7
Db 8 DTFY 11

```

RESULT 135

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PCT-US93-07545-97
; Sequence 97, Application PC/TUS9307545
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07545
; FILING DATE: 19930811
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PCT-US93-07545-97

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```

Query Match 44.4%; Score 4; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 2 VDDT 5
Db 1 VDDT 4

```

RESULT 136

```

PCT-US93-07545-108
; Sequence 108, Application PC/TUS9307545
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07545
; FILING DATE: 19930811
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US93-07545-108

Query Match 44.4%; Score 4; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 137
US-08-480-190-106
; Sequence 106, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-480-190-106

Query Match 44.4%; Score 4; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 138
US-08-488-379-106
; Sequence 106, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-488-379-106

Query Match 44.4%; Score 4; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 139
US-08-475-399A-106
; Sequence 106, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Vignali, Dario A.A.

```
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00246/168003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-507
; TELEFAX: 617/542-890
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-475-399A-106

Query Match 44.4%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 140
US-08-077-255A-106
; Sequence 106, Application US/08077255A
; Patent No. 6696061
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
```

```
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/077,255A
; FILING DATE: June 15, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-077-255A-106

Query Match 44.4%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 141
US-09-612-925H-4
; Sequence 4, Application US/09612925H
; Patent No. 6921809
; GENERAL INFORMATION:
; APPLICANT: Cano, Carlos Antonio Durante
; APPLICANT: Nieto, Enrique Gerardo Guillen
; APPLICANT: Acosta, Anabel Alvarez
; APPLICANT: Munoz, Luis Emilio Carpio
; APPLICANT: Vazquez, Diogenes Quintana
; APPLICANT: Rodriguez, Carmen Elena Gomez
; APPLICANT: Rodriguez, Recardo de la Caridad Siva
; APPLICANT: Galvez, Consuelo Nazabal
; APPLICANT: Angulo, Maria de Jesus Leal
; APPLICANT: Dunn, Alejandro Miguel Martin
; TITLE OF INVENTION: Expression System of Heterologous Antigens as Fusion Proteins
; FILE REFERENCE: LEXSA P-13DIV2
; CURRENT APPLICATION NUMBER: US/09/612,925H
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 08/930,917
; PRIOR FILING DATE: 1997-09-16
; PRIOR APPLICATION NUMBER: PCT/CU97/00001
; PRIOR FILING DATE: 1997-01-17
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Neisseria meningitidis (group B)
; US-09-612-925H-4

Query Match 44.4%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 9 VDDT 12
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RESULT 142
PCT-US93-07545-106
; Sequence 106, Application PC/TUS9307545
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07545
; FILING DATE: 19930811
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US93-07545-106
Query Match 44.4%; Score 4; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDT 5
Db 1 VDDT 4
RESULT 143
US-08-480-190-94
; Sequence 94, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston

STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-94
Query Match 44.4%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDT 5
Db 1 VDDT 4
RESULT 144
US-08-480-190-105
; Sequence 105, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255

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; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-480-190-105

Query Match 44.4%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 145
US-08-488-379-94
; Sequence 94, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-488-379-105

Query Match 44.4%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 146
US-08-488-379-105
; Sequence 105, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-488-379-105

Query Match 44.4%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4
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RESULT 147
US-08-475-399A-94
; Sequence 94, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00246/168003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-507
; TELEFAX: 617/542-890
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-475-399A-94
Query Match 44.4%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDT 5
Db 1 VDDT 4
RESULT 148
US-08-475-399A-105
; Sequence 105, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street

; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00246/168003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-507
; TELEFAX: 617/542-890
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-475-399A-105
Query Match 44.4%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDT 5
Db 1 VDDT 4
RESULT 149
US-08-077-255A-94
; Sequence 94, Application US/08077255A
; Patent No. 6696061
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chiciz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/077,255A
; FILING DATE: June 15, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-94

Query Match 44.4%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDT 5
Db 1 VDDT 4

RESULT 150

US-08-077-255A-105
Sequence 105, Application US/08077255A
Patent No. 6696061
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-105

Query Match 44.4%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDT 5
Db 1 VDDT 4

Search completed: May 17, 2006, 06:30:27
Job time : 52 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 17, 2006, 06:12:05 ; Search time 199 Seconds
(without alignments)
41.835 Million cell updates/sec

Title: US-10-764-985-2

Perfect score: 9

Sequence: 1 KVDDTFYV 9

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------|---------------------|
| 1 | 9 | 100.0 | 150 | 1 VHR2_CAMPM | P68643 camelpox vi |
| 2 | 9 | 100.0 | 150 | 1 VHR2_CAMPS | P68642 camelpox vi |
| 3 | 9 | 100.0 | 150 | 1 VHR2_VACCA | P68598 vaccinia vi |
| 4 | 9 | 100.0 | 150 | 1 VHR2_VACCC | P68599 vaccinia vi |
| 5 | 9 | 100.0 | 150 | 1 VHR2_VACCV | P68600 vaccinia vi |
| 6 | 9 | 100.0 | 150 | 1 VHR2_VACV | P33860 variola vir |
| 7 | 9 | 100.0 | 150 | 2 Q49QR1_9POXV | Q49qr1 vaccinia vi |
| 8 | 9 | 100.0 | 150 | 2 Q6RZS8_9POXV | Q6rzs8 rabbitpox v |
| 9 | 9 | 100.0 | 150 | 2 Q76Q66_VAVR | Q76q66 variola min |
| 10 | 9 | 100.0 | 150 | 2 Q76QL6_COWPX | Q76ql6 cowpox viru |
| 11 | 9 | 100.0 | 150 | 2 Q77TN9_VACCT | Q77tn9 vaccinia vi |
| 12 | 9 | 100.0 | 150 | 2 Q8JLI7_9POXV | Q8jli7 ectromelia |
| 13 | 9 | 100.0 | 150 | 2 Q8QN33_COWPX | Q8qn33 cowpox viru |
| 14 | 7 | 77.8 | 512 | 2 Q4WIR3_ASPFU | Q4wir3 aspergillus |
| 15 | 7 | 77.8 | 515 | 2 Q2U7D1_ASPOR | Q2u7d1 aspergillus |
| 16 | 7 | 77.8 | 770 | 2 P73845_SYNV3 | P73845 synechocyst |
| 17 | 6 | 66.7 | 103 | 2 Q8VUM8_STAHO | Q8vum8 staphylococ |
| 18 | 6 | 66.7 | 126 | 2 Q38248_9CAUD | Q3848 lactococcus |
| 19 | 6 | 66.7 | 176 | 2 Q5A2T5_CANAL | Q5a2t5 candida alb |
| 20 | 6 | 66.7 | 205 | 1 RAS3_RHIRA | P22280 rhizomucor |
| 21 | 6 | 66.7 | 231 | 2 Q8T5E9_RICFL | Q8t5e9 ricordea fl |
| 22 | 6 | 66.7 | 232 | 2 Q5TOR6_ANOGA | Q5tor6 anopheles g |
| 23 | 6 | 66.7 | 261 | 2 Q9CAE4_ARATH | Q9cae4 arabidopsis |
| 24 | 6 | 66.7 | 298 | 2 Q2NEH9_9EURY | Q2neh9 methanospira |
| 25 | 6 | 66.7 | 311 | 2 Q4K6A8_PSEF5 | Q4k6a8 pseudomonas |
| 26 | 6 | 66.7 | 330 | 2 Q6DBO7_ERWCT | Q6db07 erwinia car |
| 27 | 6 | 66.7 | 376 | 2 Q5WC87_BACSK | Q5wc87 legionella |
| 28 | 6 | 66.7 | 399 | 2 Q5WX32_LEGPL | Q5wx32 legionella |
| 29 | 6 | 66.7 | 399 | 2 Q5X5Q2_LEGPA | Q5x5q2 legionella |
| 30 | 6 | 66.7 | 399 | 2 Q5ZYV4_LEGPH | Q5zyv4 legionella |
| 31 | 6 | 66.7 | 400 | 1 TRPB_NEIGO | Q849j9 neisseria g |

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| 32 | 6 | 66.7 | 400 | 1 TRPB_NEIMA | Q9jvc0 neisseria m |
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| 35 | 6 | 66.7 | 401 | 2 Q31HH4_THICR | Q31hh4 thiomicrosp |
| 36 | 6 | 66.7 | 404 | 2 Q44BZ8_THICR | Q44bz8 chromohalob |
| 37 | 6 | 66.7 | 405 | 2 Q604P3_METCA | Q604p3 methylococc |
| 38 | 6 | 66.7 | 406 | 2 Q36T45_MARHY | Q36t45 marinobacte |
| 39 | 6 | 66.7 | 409 | 1 TRPB_PSESH | Q849p2 pseudomonas |
| 40 | 6 | 66.7 | 409 | 1 TRPB_PSESM | Q88b61 pseudomonas |
| 41 | 6 | 66.7 | 409 | 2 Q48QG6_PSE14 | Q48qg6 pseudomonas |
| 42 | 6 | 66.7 | 409 | 2 Q500R4_PSEU2 | Q500r4 pseudomonas |
| 43 | 6 | 66.7 | 410 | 2 Q2SJD1_9GAMM | Q2sjd1 hahella che |
| 44 | 6 | 66.7 | 411 | 2 Q35ZW5_9GAMM | Q35zw5 alkalilimni |
| 45 | 6 | 66.7 | 416 | 2 Q3MWU8_9DELT | Q3mwu8 syntrophoba |
| 46 | 6 | 66.7 | 474 | 2 Q3EM85_BACTI | Q3em85 bacillus th |
| 47 | 6 | 66.7 | 482 | 2 Q60051_THREVU | Q60051 thermoactin |
| 48 | 6 | 66.7 | 485 | 2 Q8L9B9_ARATH | Q8l9b9 arabidopsis |
| 49 | 6 | 66.7 | 485 | 2 Q9LNJ3_ARATH | Q9lnj3 arabidopsis |
| 50 | 6 | 66.7 | 499 | 2 Q2V3N3_ARATH | Q2v3n3 arabidopsis |
| 51 | 6 | 66.7 | 500 | 2 Q8RX11_ARATH | Q8rx11 arabidopsis |
| 52 | 6 | 66.7 | 500 | 2 Q9LS40_ARATH | Q9ls40 arabidopsis |
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| 54 | 6 | 66.7 | 512 | 2 Q6HPG6_BACHK | Q6hpg6 bacillus th |
| 55 | 6 | 66.7 | 514 | 2 Q6Z6Q8_ORYSA | Q6z6q8 oryza sativ |
| 56 | 6 | 66.7 | 535 | 2 Q9LYS8_ARATH | Q9lys8 arabidopsis |
| 57 | 6 | 66.7 | 567 | 2 Q50EJ4_LACRE | Q50ej4 lactobacill |
| 58 | 6 | 66.7 | 671 | 2 Q70Q68_PERMR | Q70q68 perla margi |
| 59 | 6 | 66.7 | 678 | 2 Q8FLC6_ECOL6 | Q8flc6 escherichia |
| 60 | 6 | 66.7 | 731 | 2 Q7XJX7_ORYSA | Q7xjx7 oryza sativ |
| 61 | 6 | 66.7 | 870 | 2 Q2Z173_9CAUD | Q2z173 pseudomonas |
| 62 | 6 | 66.7 | 892 | 2 Q9S9U5_ARATH | Q9s9u5 arabidopsis |
| 63 | 6 | 66.7 | 894 | 2 Q8T043_DROME | Q8t043 drosophila |
| 64 | 6 | 66.7 | 900 | 2 Q9VPH1_DROME | Q9vph1 drosophila |
| 65 | 6 | 66.7 | 1080 | 2 Q4I709_GIBZE | Q4i709 gibberella |
| 66 | 6 | 66.7 | 1111 | 1 SECS_NEUCR | Q9hse8 neurospora |
| 67 | 6 | 66.7 | 1256 | 2 Q9XVH4_CABEL | Q9xvh4 caenorhabdi |
| 68 | 6 | 66.7 | 1284 | 2 Q61VN1_CABBR | Q61vn1 caenorhabdi |
| 69 | 6 | 66.7 | 1286 | 2 Q71025_CABEL | Q71025 caenorhabdi |
| 70 | 5 | 55.6 | 51 | 2 Q73C85_BACCI | Q73c85 bacillus ce |
| 71 | 5 | 55.6 | 56 | 2 Q838E6_ENTFA | Q838e6 enterococcu |
| 72 | 5 | 55.6 | 60 | 2 Q514Y7_ENTHI | Q514y7 entamoeba h |
| 73 | 5 | 55.6 | 70 | 2 Q81GV6_BACCR | Q81gv6 bacillus ce |
| 74 | 5 | 55.6 | 78 | 1 RS27A_ASPOF | P31753 asparagus o |
| 75 | 5 | 55.6 | 80 | 1 RS27A_LYCES | P62380 lycopersico |
| 76 | 5 | 55.6 | 80 | 1 RS27A_SOLTU | P62981 solanum tub |
| 77 | 5 | 55.6 | 80 | 2 Q3GRU5_9GAMM | Q3gru9 psychrobact |
| 78 | 5 | 55.6 | 81 | 2 Q48Q06_STRPM | Q48qg6 streptococc |
| 79 | 5 | 55.6 | 87 | 2 Q4FQ61_PSTAR | Q4fq61 psychrobact |
| 80 | 5 | 55.6 | 90 | 1 Y3711_CLOAB | Q04353 clostridium |
| 81 | 5 | 55.6 | 91 | 2 Q8JM27_9NUCL | Q8j27 mamestra co |
| 82 | 5 | 55.6 | 92 | 2 Q63CD4_BACCZ | Q63cd4 bacillus ce |
| 83 | 5 | 55.6 | 92 | 2 Q81RL2_BACAN | Q81rl2 bacillus an |
| 84 | 5 | 55.6 | 92 | 2 Q2Z0L6_9ADEN | Q2z0l6 human adeno |
| 85 | 5 | 55.6 | 94 | 2 Q2WLY5_CLOBE | Q2wly5 clostridium |
| 86 | 5 | 55.6 | 100 | 2 Q4DFB0_TRYCR | Q4dfb0 trypanosoma |
| 87 | 5 | 55.6 | 104 | 2 Q2J0A0_RHOPA | Q2j0a0 rhodopseudo |
| 88 | 5 | 55.6 | 106 | 2 Q65G18_BACLD | Q65g18 bacillus li |
| 89 | 5 | 55.6 | 108 | 2 Q5WEA4_BACSK | Q5wea4 bacillus cl |
| 90 | 5 | 55.6 | 109 | 2 Q4XCY7_PLACH | Q4xcy7 plasmodium |
| 91 | 5 | 55.6 | 116 | 2 Q6Y8R4_MYCHO | Q6y8r4 mycoplasma |
| 92 | 5 | 55.6 | 119 | 2 Q63BU1_BACCZ | Q63bu1 bacillus ce |
| 93 | 5 | 55.6 | 119 | 2 Q6HJB1_BACHK | Q6hjb1 bacillus th |
| 94 | 5 | 55.6 | 119 | 2 Q81D21_BACCR | Q81dz1 bacillus ce |
| 95 | 5 | 55.6 | 119 | 2 Q81R08_BACAN | Q81r08 bacillus an |
| 96 | 5 | 55.6 | 119 | 2 Q738W2_BACCI | Q738w2 bacillus ce |
| 97 | 5 | 55.6 | 120 | 2 Q8U332_PYRFU | Q8u332 pyrococcus |
| 98 | 5 | 55.6 | 120 | 2 Q4MTS5_BACCZ | Q4mts5 bacillus ce |
| 99 | 5 | 55.6 | 126 | 2 Q5DHT7_SCHJA | Q5dht7 schistosoma |
| 100 | 5 | 55.6 | 128 | 2 Q33XT4_9GAMM | Q33xt4 shewanella |
| 101 | 5 | 55.6 | 128 | 2 Q8X3T8_ECO57 | Q8x3t8 escherichia |
| 102 | 5 | 55.6 | 130 | 2 Q7NF95_GLOVI | Q7nf95 gloeobacter |
| 103 | 5 | 55.6 | 134 | 1 PA2_APTCC | Q9bmk4 apis cerana |
| 104 | 5 | 55.6 | 134 | 2 Q8Z174_YERPE | Q8z174 yersinia pe |

| | | | | | | | |
|-----|---|------|-----|---|---------------|---------------------|-----|
| 105 | 5 | 55.6 | 137 | 2 | Q2NCA0_9SPHN | Q2nca0 erythroblast | 178 |
| 106 | 5 | 55.6 | 138 | 1 | RABP2_RAT | P51673 rattus norv | 179 |
| 107 | 5 | 55.6 | 139 | 2 | Q315F6_DSBDG | Q315f6 deulfovibr | 180 |
| 108 | 5 | 55.6 | 140 | 2 | Q4U9J7_THEAN | Q4u9j7 theileria a | 181 |
| 109 | 5 | 55.6 | 141 | 1 | SKB5_SCHPO | Q9u59 schizosacch | 182 |
| 110 | 5 | 55.6 | 142 | 1 | Q4N291_THPEA | Q4n291 theileria p | 183 |
| 111 | 5 | 55.6 | 143 | 2 | Q586G7_9TRYP | Q586g7 trypanosoma | 184 |
| 112 | 5 | 55.6 | 144 | 2 | Q60DU6_ORYSA | Q60du6 oryza sativ | 185 |
| 113 | 5 | 55.6 | 145 | 2 | Q72QM4_LEPIC | Q72qm4 leptospira | 186 |
| 114 | 5 | 55.6 | 146 | 2 | Q8F4Y0_LEPIN | Q8f4y0 leptospira | 187 |
| 115 | 5 | 55.6 | 147 | 2 | Q5IFZ7_9PROT | Q5ifz7 uncultured | 188 |
| 116 | 5 | 55.6 | 148 | 2 | Q3JAM5_9BACT | Q93am5 uncultured | 189 |
| 117 | 5 | 55.6 | 149 | 2 | Q9AF59_9PROT | Q9af59 uncultured | 190 |
| 118 | 5 | 55.6 | 150 | 2 | Q66SU0_YERPE | Q66su0 yersinia ps | 191 |
| 119 | 5 | 55.6 | 151 | 2 | Q8CKF9_YERPE | Q8ckf9 yersinia pe | 192 |
| 120 | 5 | 55.6 | 152 | 2 | Q41753_MAIZE | Q41753 zea mays (m | 193 |
| 121 | 5 | 55.6 | 153 | 2 | Q7WKG7_FORG1 | Q7wkg7 porphyromon | 194 |
| 122 | 5 | 55.6 | 154 | 2 | Q6Q131_RAT | Q6q131 rattus norv | 195 |
| 123 | 5 | 55.6 | 155 | 2 | Q9VJR2_DROME | Q9vjr2 drosophila | 196 |
| 124 | 5 | 55.6 | 156 | 2 | Q7OZ72_CANFA | Q7oz72 canis famil | 197 |
| 125 | 5 | 55.6 | 157 | 2 | Q4UID3_THEAN | Q4uid3 theileria a | 198 |
| 126 | 5 | 55.6 | 158 | 2 | Q43W25_SOLUS | Q43w25 solibacter | 199 |
| 127 | 5 | 55.6 | 159 | 2 | Q4N780_THPEA | Q4n780 theileria p | 200 |
| 128 | 5 | 55.6 | 160 | 2 | Q4ZPM6_PSEU2 | Q4zpm6 pseudomonas | 201 |
| 129 | 5 | 55.6 | 161 | 2 | Q5SVM6_HUMAN | Q5svm6 homo sapien | 202 |
| 130 | 5 | 55.6 | 162 | 2 | Q5CYO6_MONPV | Q5cyo6 monkeypox v | 203 |
| 131 | 5 | 55.6 | 163 | 2 | Q5C0Z6_SCHJA | Q5c0z6 schistosoma | 204 |
| 132 | 5 | 55.6 | 164 | 2 | Q5X255_GUTH | Q5x255 guillardia | 205 |
| 133 | 5 | 55.6 | 165 | 2 | Q6LVZ2_HELPH | Q6lvz2 helicobacter | 206 |
| 134 | 5 | 55.6 | 166 | 2 | Q7VIT4_HELHP | Q7vit4 helicobacter | 207 |
| 135 | 5 | 55.6 | 167 | 2 | Q6WHR4_BPKV4 | Q6whr4 bacterioph | 208 |
| 136 | 5 | 55.6 | 168 | 2 | Q9DHU6_YLDV | Q9dhu6 yaba-like d | 209 |
| 137 | 5 | 55.6 | 169 | 2 | Q5GSB5_WOLTR | Q5gsb5 wolbachia s | 210 |
| 138 | 5 | 55.6 | 170 | 2 | Q4D000_TRYCR | Q4d000 trypanosoma | 211 |
| 139 | 5 | 55.6 | 171 | 2 | Q3ZEE6_SHIDS | Q3zee6 shigella dy | 212 |
| 140 | 5 | 55.6 | 172 | 2 | Q5FJR3_LACAC | Q5fjr3 lactobacill | 213 |
| 141 | 5 | 55.6 | 173 | 2 | Q64LE1_9ADEN | Q64le1 human adeno | 214 |
| 142 | 5 | 55.6 | 174 | 2 | Q5CNC5_CRYHO | Q5cnc5 cryptospori | 215 |
| 143 | 5 | 55.6 | 175 | 2 | Q7YVF2_CRYPV | Q7yvf2 cryptospori | 216 |
| 144 | 5 | 55.6 | 176 | 2 | Q47L35_THEPY | Q47l35 thermobifid | 217 |
| 145 | 5 | 55.6 | 177 | 2 | Q3Y144_ENTFC | Q3y144 enterococu | 218 |
| 146 | 5 | 55.6 | 178 | 2 | Q5MJW8_TOBAC | Q5mjw8 nicotiana t | 219 |
| 147 | 5 | 55.6 | 179 | 2 | Q6C1Q6_YARLI | Q6c1q6 yarrowia li | 220 |
| 148 | 5 | 55.6 | 180 | 2 | Q36SQ4_MARHY | Q36sq4 marinobacte | 221 |
| 149 | 5 | 55.6 | 181 | 2 | Q9RBX9_PSEIN | Q9rbx9 pseudomonas | 222 |
| 150 | 5 | 55.6 | 182 | 2 | Q3FPC2_9BURK | Q3fpc2 rhodofera | 223 |
| 151 | 5 | 55.6 | 183 | 2 | Q76XFP5_9CAUD | Q76xf5 erobobacte | 224 |
| 152 | 5 | 55.6 | 184 | 2 | Q4MN44_BACCE | Q4mn44 bacillus ce | 225 |
| 153 | 5 | 55.6 | 185 | 2 | Q3ZLB4_OREMO | Q3zlb4 oreochromis | 226 |
| 154 | 5 | 55.6 | 186 | 2 | Q3AU66_CHLCH | Q3au66 chlorobium | 227 |
| 155 | 5 | 55.6 | 187 | 2 | Q6L009_PICTO | Q6l009 picrophilus | 228 |
| 156 | 5 | 55.6 | 188 | 2 | Q3QW04_9RHO8 | Q3qw04 silicibacte | 229 |
| 157 | 5 | 55.6 | 189 | 2 | Q3E23_COXBU | Q3e23 coxiella bu | 230 |
| 158 | 5 | 55.6 | 190 | 2 | Q3VVD4_PROAE | Q3vvd4 prosthecoch | 231 |
| 159 | 5 | 55.6 | 191 | 2 | Q3H6V1_TRIER | Q3h6v1 trichodesmi | 232 |
| 160 | 5 | 55.6 | 192 | 2 | Q97A41_THEVO | Q97a41 thermoplas | 233 |
| 161 | 5 | 55.6 | 193 | 2 | Q9V162_PYRAB | Q9v162 pyrococcus | 234 |
| 162 | 5 | 55.6 | 194 | 2 | Q6W6S8_CANFA | Q6w6s8 canis famil | 235 |
| 163 | 5 | 55.6 | 195 | 2 | Q4KED7_PSEF5 | Q4ked7 pseudomonas | 236 |
| 164 | 5 | 55.6 | 196 | 2 | Q3SD18_PARTE | Q3sd18 paramecium | 237 |
| 165 | 5 | 55.6 | 197 | 2 | Q31MT7_NATPD | Q31mt7 natronomona | 238 |
| 166 | 5 | 55.6 | 198 | 2 | Q63F37_BACCZ | Q63f37 bacillus ce | 239 |
| 167 | 5 | 55.6 | 199 | 2 | Q73CJ5_BACCL | Q73cj5 bacillus ce | 240 |
| 168 | 5 | 55.6 | 200 | 2 | Q4UH05_THEAN | Q4uh05 theileria a | 241 |
| 169 | 5 | 55.6 | 201 | 2 | Q3YB22_SARSC | Q3yb22 sarcopetes s | 242 |
| 170 | 5 | 55.6 | 202 | 2 | Q2T8L4_BURTH | Q2t8l4 burkholderi | 243 |
| 171 | 5 | 55.6 | 203 | 2 | Q6C580_YARLI | Q6c580 yarrowia li | 244 |
| 172 | 5 | 55.6 | 204 | 2 | Q341U2_RHOPI | Q341u2 rhodopsedu | 245 |
| 173 | 5 | 55.6 | 205 | 2 | Q81UB2_BACAN | Q81ub2 bacillus an | 246 |
| 174 | 5 | 55.6 | 206 | 2 | Q47FJ7_DSCAR | Q47fj7 dechloromon | 247 |
| 175 | 5 | 55.6 | 207 | 2 | Q6N1B3_RHOPA | Q6n1b3 rhodopsedu | 248 |
| 176 | 5 | 55.6 | 208 | 2 | Q8KU99_ENTFA | Q8ku99 enterococu | 249 |
| 177 | 5 | 55.6 | 209 | 2 | Q371X9_RHOPA | Q371x9 rhodopsedu | 250 |

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|--------|---------------|-----|---|--------------|----------------------|
| Q4hks1 | campylobact | 222 | 2 | Q4HKS1_CAMLA | Q4hks1 campylobact |
| Q8cxq6 | mycoplasma | 226 | 1 | TRMD_MYCP | Q8cxq6 mycoplasma |
| Q6np89 | arabidopsis16 | 226 | 2 | Q6NP89_ARATH | Q6np89 arabidopsis16 |
| Q6c5t8 | yarrowia li | 227 | 2 | Q6C5T8_YARLI | Q6c5t8 yarrowia li |
| Q6aqj7 | aspergillus | 230 | 2 | Q6AQJ7_EMENI | Q6aqj7 aspergillus |
| Q6qj10 | kluyveromyc | 232 | 1 | SNF7_KLULA | Q6qj10 kluyveromyc |
| Q626Y0 | caenorhabdi | 232 | 1 | Q626Y0_CABBR | Q626y0 caenorhabdi |
| Q31cu8 | pseudosalter | 233 | 1 | DSOD_PSEHT | Q31cu8 pseudosalter |
| Q30rv9 | thiomicrosp | 236 | 2 | Q30RV9_THIDN | Q30rv9 thiomicrosp |
| Q31797 | trichoplax | 237 | 2 | Q31797_9METZ | Q31797 trichoplax |
| Q31798 | trichoplax | 237 | 2 | Q31798_9METZ | Q31798 trichoplax |
| Q31799 | trichoplax | 237 | 2 | Q31799_9METZ | Q31799 trichoplax |
| Q5tt21 | anopheles g | 237 | 2 | Q5TT21_ANOGA | Q5tt21 anopheles g |
| Q4Y5S8 | plasmodium | 237 | 2 | Q4Y5S8_PLACH | Q4y5s8 plasmodium |
| Q3feg9 | rhodopsedu | 237 | 2 | Q37EQ9_RHOPA | Q3feg9 rhodopsedu |
| Q6ln97 | photobacter | 237 | 2 | Q6LN97_PHOPR | Q6ln97 photobacter |
| Q58mz0 | cyanophage | 239 | 2 | Q58MZ0_9CAUD | Q58mz0 cyanophage |
| Q5YV13 | nocardia fa | 239 | 2 | Q5YV13_NOCFA | Q5yv13 nocardia fa |
| Q3V3d7 | mus musculus | 240 | 2 | Q3V3D7_MOUSE | Q3v3d7 mus musculus |
| Q4n8m1 | theileria p | 240 | 2 | Q4N8M1_THPEA | Q4n8m1 theileria p |
| Q9xyh3 | babesia big | 240 | 2 | Q9XYH3_BABBI | Q9xyh3 babesia big |
| Q5bx52 | schistosoma | 241 | 2 | Q5BX52_SCHJA | Q5bx52 schistosoma |
| Q3cgg4 | thermoanaer | 242 | 2 | Q3CGG4_THET | Q3cgg4 thermoanaer |
| Q2Q0d5 | methanosa | 242 | 2 | Q2Q0D5_9ZZZZ | Q2q0d5 methanosa |
| Q46e39 | methanogarc | 245 | 2 | Q46E39_METBA | Q46e39 methanogarc |
| Q2ugy7 | aspergillus | 246 | 2 | Q2UQV7_ASPOR | Q2ugy7 aspergillus |
| Q7U328 | helicobacte | 248 | 1 | TRUA_HELHP | Q7u328 helicobacte |
| Q319l1 | psychrobact | 248 | 2 | Q319L1_9GAMM | Q319l1 psychrobact |
| Q4um49 | rickettsia | 249 | 2 | Q4UM49_RICFE | Q4um49 rickettsia |
| Q8vee8 | mus musculus | 251 | 2 | Q8VEE8_MOUSE | Q8vee8 mus musculus |
| Q5cqa1 | cryptospori | 252 | 2 | Q5CQA1_CRYPV | Q5cqa1 cryptospori |
| Q67pc4 | symbiobacte | 252 | 2 | Q67PC4_SYMTB | Q67pc4 symbiobacte |
| Q8H469 | oryza sativ | 255 | 2 | Q8H469_ORYSA | Q8h469 oryza sativ |
| Q5snz3 | bacillus li | 255 | 2 | Q5SNZ3_BACLD | Q5snz3 bacillus li |
| Q5kx41 | geobacillus | 257 | 2 | Q5KX41_GEOKA | Q5kx41 geobacillus |
| Q8Y2a0 | raistonia s | 257 | 2 | Q8Y2A0_RALSO | Q8y2a0 raistonia s |
| Q3c112 | pseudosalter | 259 | 2 | Q3CL12_ALTAT | Q3c112 pseudosalter |
| Q36a47 | shewanella | 261 | 2 | Q36A47_9GAMM | Q36a47 shewanella |
| Q8xng6 | clostridium | 262 | 2 | Q8XNG6_CLOPE | Q8xng6 clostridium |
| Q884r0 | mus musculus | 262 | 2 | Q884R0_MOUSE | Q884r0 mus musculus |
| Q83z90 | enterococu | 263 | 2 | Q83Z90_ENTFA | Q83z90 enterococu |
| Q9KA41 | bachid ha | 263 | 2 | Q9KA41_BACHD | Q9ka41 bachid ha |
| Q9FV80 | arabidopsis | 264 | 2 | Q9FV80_ARATH | Q9fv80 arabidopsis |
| Q4HA89 | deinococcus | 265 | 2 | Q4HA89_9DEIO | Q4ha89 deinococcus |
| Q5WFR4 | bacillus cl | 267 | 2 | Q5WFR4_BACSK | Q5wfr4 bacillus cl |
| Q4XG96 | plasmodium | 269 | 2 | Q4XG96_PLACH | Q4xg96 plasmodium |
| Q2nfz6 | methanospa | 270 | 2 | Q2NFZ6_9EURY | Q2nfz6 methanospa |
| Q31gu6 | pseudosalter | 270 | 2 | Q31GU6_PSEHT | Q31gu6 pseudosalter |
| Q2WRY1 | clostridium | 270 | 2 | Q2WRY1_CLOBE | Q2wry1 clostridium |
| Q4Ypd8 | plasmodium | 271 | 2 | Q4YPD8_PLABE | Q4ypd8 plasmodium |
| Q3fk89 | rhodofera | 271 | 2 | Q3FK89_9BURK | Q3fk89 rhodofera |
| Q317b1 | nitrosococc | 271 | 2 | Q3J7B1_NITOC | Q317b1 nitrosococc |
| Q3mim6 | anabaena va | 271 | 2 | Q3MIM6_ANAVT | Q3mim6 anabaena va |
| Q9Yi68 | bufo marinu | 271 | 2 | Q9YI68_BUFMA | Q9yi68 bufo marinu |
| Q4J9i7 | sulfolobus | 272 | 2 | Q4J9I7_SULAC | Q4j9i7 sulfolobus |
| Q4E0d4 | trypanosoma | 273 | 2 | Q4E0D4_TRYCR | Q4e0d4 trypanosoma |
| Q4Gzf2 | trypanosoma | 275 | 2 | Q4GZF2_9TRYP | Q4gzf2 trypanosoma |
| Q2xek9 | pseudomonas | 275 | 2 | Q2XEK9_PSEPU | Q2xek9 pseudomonas |
| Q51386 | pseudomonas | 275 | 2 | Q51386_PSEAE | Q51386 pseudomonas |
| Q8RSQ3 | pseudomonas | 275 | 2 | Q8RSQ3_PSEPU | Q8rsq3 pseudomonas |
| Q88kt1 | pseudomonas | 275 | 2 | Q88KT1_PSEPK | Q88kt1 pseudomonas |
| Q91433 | pseudomonas | 275 | 2 | Q91433_PSEAK | Q91433 pseudomonas |
| Q88l11 | pseudomonas | 275 | 2 | Q88L11_PSEPK | Q88l11 pseudomonas |
| Q7vwh8 | borderella | 276 | 2 | Q7VWH8_BORPE | Q7vwh8 borderella |
| Q7W148 | borderella | 276 | 2 | Q7W148_BORBR | Q7w148 borderella |
| Q2NFC1 | 9EURY | 279 | 1 | TRMD_DEIRA | Q2nfc1 9EURY |
| Q9HJv3 | thermoplasm | 279 | 2 | Q9HJV3_THEAC | Q9hjv3 thermoplasm |
| Q21lw2 | borderella | 280 | 2 | Q21LW2_BORAV | Q21lw2 borderella |
| Q4L3B6 | staphylococ | 280 | 2 | Q4L3B6_STAHP | Q4l3b6 staphylococ |
| Q5LXJ4 | streptococc | 280 | 2 | Q5LXJ4_STRT1 | Q5lxj4 streptococc |
| Q5m244 | streptococc | 280 | 2 | Q5M244_STRT2 | Q5m244 streptococc |

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|-----|---|------|-----|---|--------------|---------------------|-----|---|------|-----|---|-----------------|---------------------|
| 251 | 5 | 55.6 | 284 | 2 | Q20180_CABEL | Q20180_caenorhabdi | 324 | 5 | 55.6 | 314 | 2 | Q36L59_MARHY | Q36L59_marinobacte |
| 252 | 5 | 55.6 | 284 | 2 | Q579D9_BRUB | Q579D9_brucella ab | 325 | 5 | 55.6 | 314 | 2 | Q7TN47_RAT | Q7TN47_rattus norv |
| 253 | 5 | 55.6 | 284 | 2 | Q8FVC3_BRUS | Q8FVC3_brucella su | 326 | 5 | 55.6 | 315 | 2 | Q37K10_RHOPA | Q37K10_rhodopsuod |
| 254 | 5 | 55.6 | 284 | 2 | Q8YD01_BRUME | Q8YD01_brucella me | 327 | 5 | 55.6 | 315 | 2 | Q39I10_BURS3 | Q39I10_burholderi |
| 255 | 5 | 55.6 | 284 | 2 | Q2YI06_BRUA2 | Q2YI06_brucella ab | 328 | 5 | 55.6 | 315 | 2 | Q2J387_RHOPA | Q2J387_rhodopsuod |
| 256 | 5 | 55.6 | 287 | 2 | Q2UK29_ASPOR | Q2UK29_aspergillus | 329 | 5 | 55.6 | 315 | 2 | Q57TP1_SALCH | Q57TP1_salmonella |
| 257 | 5 | 55.6 | 287 | 2 | Q5DBK4_SCHJA | Q5DBK4_schistosoma | 330 | 5 | 55.6 | 315 | 2 | Q5PDJ3_SALPA | Q5PDJ3_salmonella |
| 258 | 5 | 55.6 | 288 | 2 | Q7PWN1_ANOGA | Q7PWN1_anopheles g | 331 | 5 | 55.6 | 315 | 2 | Q89X49_BRAJA | Q89X49_bradyrhizob |
| 259 | 5 | 55.6 | 291 | 2 | Q2W9S3_MAGSA | Q2W9S3_magnetospir | 332 | 5 | 55.6 | 315 | 2 | Q8ZS13_SALTY | Q8ZS13_salmonella |
| 260 | 5 | 55.6 | 291 | 2 | Q46TN4_RALEJ | Q46TN4_ralstonia e | 333 | 5 | 55.6 | 315 | 2 | Q8Z9R0_SALTY | Q8Z9R0_salmonella |
| 261 | 5 | 55.6 | 291 | 2 | Q6MD42_PARUW | Q6MD42_parachlamyd | 334 | 5 | 55.6 | 316 | 2 | Q8LF62_ARATH | Q8LF62_arabidopsis |
| 262 | 5 | 55.6 | 292 | 2 | Q2SV19_BURTH | Q2SV19_burholderi | 335 | 5 | 55.6 | 316 | 2 | Q8RWV5_ARATH | Q8RWV5_arabidopsis |
| 263 | 5 | 55.6 | 293 | 2 | Q888Y3_PSESM | Q888Y3_pseudomonas | 336 | 5 | 55.6 | 316 | 2 | Q3Z0H1_SHISS | Q3Z0H1_shigella so |
| 264 | 5 | 55.6 | 294 | 1 | NUCG_MOUSE | Q88600_mus musculus | 337 | 5 | 55.6 | 316 | 2 | Q8X4U0_ECOSL | Q8X4U0_escherichia |
| 265 | 5 | 55.6 | 294 | 2 | Q2SRH4_SGAMM | Q2SRH4_hahella che | 338 | 5 | 55.6 | 316 | 2 | Q8FGS4_ECOSL | Q8FGS4_escherichia |
| 266 | 5 | 55.6 | 294 | 2 | Q3R961_XYLFA | Q3R961_xylella fas | 339 | 5 | 55.6 | 317 | 2 | Q21395_CABEL | Q21395_caenorhabdi |
| 267 | 5 | 55.6 | 294 | 2 | Q4JLE9_LACRE | Q4JLE9_lactobacill | 340 | 5 | 55.6 | 317 | 2 | Q9VLN1_DROME | Q9VLN1_drosophila |
| 268 | 5 | 55.6 | 294 | 2 | Q3UN47_MOUSE | Q3UN47_mus musculus | 341 | 5 | 55.6 | 317 | 2 | Q2KU1_BORDTELLA | Q2KU1_bordetella |
| 269 | 5 | 55.6 | 294 | 2 | Q3V5X8_RAT | Q3V5X8_rattus norv | 342 | 5 | 55.6 | 318 | 2 | Q4CK93_TRYCR | Q4CK93_trypanosoma |
| 270 | 5 | 55.6 | 296 | 2 | Q6DBP9_ERWCT | Q6DBP9_erwinia car | 343 | 5 | 55.6 | 318 | 2 | Q650W8_ORYZA | Q650W8_oryza sativ |
| 271 | 5 | 55.6 | 297 | 1 | NUCG_HUMAN | Q14249_homo sapien | 344 | 5 | 55.6 | 319 | 2 | Q31PT7_SYNTP | Q31PT7_synechococc |
| 272 | 5 | 55.6 | 297 | 2 | Q5T281_HUMAN | Q5T281_homo sapien | 345 | 5 | 55.6 | 319 | 2 | Q5N4E1_SYNTP | Q5N4E1_synechococc |
| 273 | 5 | 55.6 | 297 | 2 | Q69L70_ORYSA | Q69L70_oryza sativ | 346 | 5 | 55.6 | 322 | 2 | Q9VEP0_DROME | Q9VEP0_drosophila |
| 274 | 5 | 55.6 | 297 | 2 | Q2ZIE1_CALSA | Q2ZIE1_caldicellul | 347 | 5 | 55.6 | 322 | 2 | Q6LY02_METWP | Q6LY02_methanococc |
| 275 | 5 | 55.6 | 297 | 2 | Q7VCD9_PROMA | Q7VCD9_prochloroco | 348 | 5 | 55.6 | 327 | 2 | Q3IU00_NATPD | Q3IU00_natronomona |
| 276 | 5 | 55.6 | 298 | 2 | Q84PD3_ORYSA | Q84PD3_oryza sativ | 349 | 5 | 55.6 | 327 | 2 | Q5FPT9_GLUOX | Q5FPT9_gluconobact |
| 277 | 5 | 55.6 | 298 | 2 | Q91LM3_WSSV | Q91LM3_white spot | 350 | 5 | 55.6 | 327 | 2 | Q4UI51_THEAN | Q4UI51_thelateria a |
| 278 | 5 | 55.6 | 299 | 1 | NUCG_BOVIN | F38447_bos taurus | 351 | 5 | 55.6 | 327 | 2 | Q62K80_BURMA | Q62K80_burholderi |
| 279 | 5 | 55.6 | 299 | 2 | Q62K14_BURMA | Q62K14_burholderi | 352 | 5 | 55.6 | 327 | 2 | Q63TX8_BURPS | Q63TX8_burholderi |
| 280 | 5 | 55.6 | 299 | 2 | Q63TS0_BURPS | Q63TS0_burholderi | 353 | 5 | 55.6 | 327 | 2 | Q83R08_SHIFL | Q83R08_shigella fl |
| 281 | 5 | 55.6 | 299 | 2 | Q65KZ1_BACLD | Q65KZ1_bacillus li | 354 | 5 | 55.6 | 329 | 1 | NUCI_YEAST | F08466_saccharomyc |
| 282 | 5 | 55.6 | 300 | 2 | Q39979_HYOMU | Q39979_hyocycamus | 355 | 5 | 55.6 | 330 | 2 | Q41KF3_GIBZE | Q41KF3_gibberella |
| 283 | 5 | 55.6 | 302 | 2 | Q5B412_EMENI | Q5B412_aspergillus | 356 | 5 | 55.6 | 330 | 2 | Q625V8_CABEL | Q625V8_caenorhabdi |
| 284 | 5 | 55.6 | 303 | 2 | Q2WML8_CLOBE | Q2WML8_clostridium | 357 | 5 | 55.6 | 330 | 2 | Q9UAT6_CABEL | Q9UAT6_caenorhabdi |
| 285 | 5 | 55.6 | 304 | 2 | Q7MS6_SALCH | Q7MS6_salmonella | 358 | 5 | 55.6 | 330 | 2 | Q663X7_YERPS | Q663X7_yersinia ps |
| 286 | 5 | 55.6 | 304 | 2 | Q5PDQ0_SALPA | Q5PDQ0_salmonella | 359 | 5 | 55.6 | 331 | 2 | Q8Z9Y6_YERPE | Q8Z9Y6_yersinia pe |
| 287 | 5 | 55.6 | 304 | 2 | Q7CQB0_SALTY | Q7CQB0_salmonella | 360 | 5 | 55.6 | 331 | 1 | YIAH_ECOLI | F37669_escherichia |
| 288 | 5 | 55.6 | 304 | 2 | Q8XET1_SALTY | Q8XET1_salmonella | 361 | 5 | 55.6 | 331 | 2 | Q86KC3_DICDI | Q86KC3_dictyostelli |
| 289 | 5 | 55.6 | 306 | 2 | Q3RR04_RALME | Q3RR04_ralstonia m | 362 | 5 | 55.6 | 331 | 2 | Q3IJC0_THICR | Q3IJC0_thiomicrosp |
| 290 | 5 | 55.6 | 306 | 2 | Q9L973_9LACT | Q9L973_lactococcus | 363 | 5 | 55.6 | 331 | 2 | Q3IV57_SHIBS | Q3IV57_shigella bo |
| 291 | 5 | 55.6 | 306 | 2 | Q97HX0_CLOAB | Q97HX0_clostridium | 364 | 5 | 55.6 | 331 | 2 | Q3YVU3_SHISS | Q3YVU3_shigella so |
| 292 | 5 | 55.6 | 306 | 2 | Q8K2G5_MOUSE | Q8K2G5_mus musculu | 365 | 5 | 55.6 | 331 | 2 | Q2W7M4_ECOLI | Q2W7M4_escherichia |
| 293 | 5 | 55.6 | 307 | 2 | Q9L741_ARATH | Q9L741_arabidopsis | 366 | 5 | 55.6 | 331 | 2 | Q57IG3_SALCH | Q57IG3_salmonella |
| 294 | 5 | 55.6 | 308 | 2 | Q38LN0_5TRYP | Q38LN0_trypanosoma | 367 | 5 | 55.6 | 331 | 2 | Q5PLM9_SALPA | Q5PLM9_salmonella |
| 295 | 5 | 55.6 | 308 | 2 | Q8IP99_DROME | Q8IP99_drosophila | 368 | 5 | 55.6 | 331 | 2 | Q8XDM7_ECOS7 | Q8XDM7_escherichia |
| 296 | 5 | 55.6 | 308 | 2 | Q8IPAI_DROME | Q8IPAI_drosophila | 369 | 5 | 55.6 | 331 | 2 | Q8ZLN3_SALTY | Q8ZLN3_salmonella |
| 297 | 5 | 55.6 | 308 | 2 | Q88XV4_LACPL | Q88XV4_lactobacill | 370 | 5 | 55.6 | 331 | 2 | Q8FCE7_ECOSL | Q8FCE7_escherichia |
| 298 | 5 | 55.6 | 308 | 2 | Q80ZV0_MOUSE | Q80ZV0_mus musculu | 371 | 5 | 55.6 | 332 | 2 | Q85J36_SHIFL | Q85J36_shigella fl |
| 299 | 5 | 55.6 | 308 | 2 | Q9DD14_MOUSE | Q9DD14_m 10 days e | 372 | 5 | 55.6 | 332 | 2 | Q41TW8_FERAC | Q41TW8_ferropasma |
| 300 | 5 | 55.6 | 309 | 1 | YEEY_ECOLI | F76369_escherichia | 373 | 5 | 55.6 | 332 | 2 | Q6CSJ8_KJULA | Q6CSJ8_kluyveromyc |
| 301 | 5 | 55.6 | 309 | 2 | Q323J7_SHIBS | Q323J7_shigella bo | 374 | 5 | 55.6 | 332 | 2 | Q7RY75_NEUCR | Q7RY75_neurospora |
| 302 | 5 | 55.6 | 310 | 2 | Q5R6M3_PONPY | Q5R6M3_pongo pygma | 375 | 5 | 55.6 | 332 | 2 | Q328M4_SHIDS | Q328M4_shigella dy |
| 303 | 5 | 55.6 | 311 | 2 | Q2UJN5_ASPOR | Q2UJN5_aspergillus | 376 | 5 | 55.6 | 332 | 2 | Q49ZV4_STAS1 | Q49ZV4_staphylococ |
| 304 | 5 | 55.6 | 311 | 2 | Q9LXU1_ARATH | Q9LXU1_arabidopsis | 377 | 5 | 55.6 | 333 | 2 | Q4MMI0_BACEE | Q4MMI0_bacillus ce |
| 305 | 5 | 55.6 | 312 | 2 | Q8GHF1_PSEPU | Q8GHF1_pseudomonas | 378 | 5 | 55.6 | 333 | 2 | Q63CL9_BACCK | Q63CL9_bacillus th |
| 306 | 5 | 55.6 | 312 | 2 | Q5YQF3_NOCPA | Q5YQF3_nocardia fa | 379 | 5 | 55.6 | 333 | 2 | Q6HK24_BACHK | Q6HK24_bacillus th |
| 307 | 5 | 55.6 | 313 | 2 | Q6UXN9_HUMAN | Q6UXN9_homo sapien | 380 | 5 | 55.6 | 333 | 2 | Q81EN7_BACRC | Q81EN7_bacillus ce |
| 308 | 5 | 55.6 | 313 | 2 | Q4EFR6_LISMO | Q4EFR6_listeria mo | 381 | 5 | 55.6 | 333 | 2 | Q739X3_BACC1 | Q739X3_bacillus ce |
| 309 | 5 | 55.6 | 313 | 2 | Q4ENB4_LISMO | Q4ENB4_listeria mo | 382 | 5 | 55.6 | 335 | 2 | Q4QHT9_LEIMA | Q4QHT9_leishmania |
| 310 | 5 | 55.6 | 313 | 2 | Q71YV3_LISMP | Q71YV3_listeria mo | 383 | 5 | 55.6 | 336 | 2 | Q5CHR4_CRYHO | Q5CHR4_cryptospori |
| 311 | 5 | 55.6 | 313 | 2 | Q8Y6K0_LISMO | Q8Y6K0_listeria mo | 384 | 5 | 55.6 | 336 | 2 | Q5MR15_DROME | Q5MR15_drosophila |
| 312 | 5 | 55.6 | 313 | 2 | Q92AX6_LISIN | Q92AX6_listeria in | 385 | 5 | 55.6 | 337 | 2 | Q6BN78_DEBHA | Q6BN78_debaryomyc |
| 313 | 5 | 55.6 | 313 | 2 | Q8BFQ4_MOUSE | Q8BFQ4_m 12 days e | 386 | 5 | 55.6 | 337 | 2 | Q4PIT0_CABEL | Q4PIT0_caenorhabdi |
| 314 | 5 | 55.6 | 313 | 2 | Q5QJN5_9REOV | Q5QJN5_human rotav | 387 | 5 | 55.6 | 339 | 2 | Q8IGUL_DROME | Q8IGUL_drosophila |
| 315 | 5 | 55.6 | 313 | 2 | Q82052_9REOV | Q82052_human rotav | 388 | 5 | 55.6 | 339 | 2 | Q9BLB5_CABEL | Q9BLB5_caenorhabdi |
| 316 | 5 | 55.6 | 313 | 2 | Q58E77_XENLA | Q58E77_xenopus lae | 389 | 5 | 55.6 | 339 | 2 | Q48ZC4_COLF3 | Q48ZC4_colwellia p |
| 317 | 5 | 55.6 | 313 | 2 | Q5ZMW7_CHICK | Q5ZMW7_gallus gall | 390 | 5 | 55.6 | 340 | 2 | Q7QY86_GIALA | Q7QY86_giardia lam |
| 318 | 5 | 55.6 | 313 | 2 | Q64OJ6_XENLA | Q64OJ6_xenopus lae | 391 | 5 | 55.6 | 340 | 2 | Q3EWR2_BACTI | Q3EWR2_bacillus th |
| 319 | 5 | 55.6 | 313 | 2 | Q6GL39_XENTR | Q6GL39_xenopus tro | 392 | 5 | 55.6 | 341 | 2 | Q7XLD1_ORYZA | Q7XLD1_oryza sativ |
| 320 | 5 | 55.6 | 313 | 2 | Q6NV31_BRARE | Q6NV31_brachydanio | 393 | 5 | 55.6 | 341 | 2 | Q3M183_ANAVT | Q3M183_anabaena va |
| 321 | 5 | 55.6 | 313 | 2 | Q803V6_BRARE | Q803V6_brachydanio | 394 | 5 | 55.6 | 343 | 2 | Q4IQJ0_GIBZE | Q4IQJ0_gibberella |
| 322 | 5 | 55.6 | 314 | 2 | Q5DHI9_SCHJA | Q5DHI9_schistosoma | 395 | 5 | 55.6 | 344 | 2 | Q63646_BABBO | Q63646_babesia bov |
| 323 | 5 | 55.6 | 314 | 2 | Q7QJN9_ANOGA | Q7QJN9_anopheles g | 396 | 5 | 55.6 | 345 | 2 | Q2SVP8_BURTH | Q2SVP8_burholderi |

| | | | | | | | | | | | | | |
|-----|---|------|-----|---|--------------|---------------------|-----|---|------|-----|---|--------------|-----------------------|
| 397 | 5 | 55.6 | 345 | 2 | Q3FB19_9BURK | Q3fb19 burkholderi | 470 | 5 | 55.6 | 385 | 2 | Q8X058_NEUCR | Q8x058 neurospora |
| 398 | 5 | 55.6 | 345 | 2 | Q452G9_9BURK | Q452g9 burkholderi | 471 | 5 | 55.6 | 385 | 2 | Q7N3I2_PHOLL | Q7n3i2 photorhabdu |
| 399 | 5 | 55.6 | 345 | 2 | Q4LRC6_9BURK | Q4lrc6 burkholderi | 472 | 5 | 55.6 | 387 | 2 | Q6YXZ5_ORYSA | Q6yxz5 oryza sativ |
| 400 | 5 | 55.6 | 345 | 2 | Q39CT2_BURS3 | Q39ct2 burkholderi | 473 | 5 | 55.6 | 387 | 2 | Q2IGS4_9DELT | Q2igs4 anaeromyxob |
| 401 | 5 | 55.6 | 345 | 2 | Q3USP5_BURP1 | Q3usp5 burkholderi | 474 | 5 | 55.6 | 389 | 2 | Q76XG1_9CAUD | Q76xg1 enterobacte |
| 402 | 5 | 55.6 | 346 | 2 | Q4BCG5_BURP1 | Q4bcg5 burkholderi | 475 | 5 | 55.6 | 389 | 2 | Q6NX00_BRARE | Q6nx00 brachydanio |
| 403 | 5 | 55.6 | 348 | 2 | Q9MCB6_9VIRU | Q9mc66 lactococcus | 476 | 5 | 55.6 | 391 | 2 | Q8IU02_CABEL | Q8iu02 caenorhabdi |
| 404 | 5 | 55.6 | 348 | 2 | Q9MCB7_9VIRU | Q9mc67 lactococcus | 477 | 5 | 55.6 | 395 | 2 | Q8I3K3_PLAF7 | Q8i3k3 plasmodium |
| 405 | 5 | 55.6 | 348 | 2 | Q3JSM4_BURP1 | Q3jsw4 burkholderi | 478 | 5 | 55.6 | 396 | 2 | Q2ZLK5_SHEPU | Q2zlk5 shewanella |
| 406 | 5 | 55.6 | 350 | 2 | Q58H09_9NEOP | Q58h09 nephelodes | 479 | 5 | 55.6 | 396 | 2 | Q82A13_STRAW | Q82a13 streptomyce |
| 407 | 5 | 55.6 | 350 | 2 | Q61PM4_CABER | Q61pm4 caenorhabdi | 480 | 5 | 55.6 | 397 | 2 | Q5QX66_IDILO | Q5qx66 idiomarina |
| 408 | 5 | 55.6 | 350 | 2 | Q9MCB8_9VIRU | Q9mc68 lactococcus | 481 | 5 | 55.6 | 399 | 1 | TRPB_BACHD | Q9kcb0 lactobacill |
| 409 | 5 | 55.6 | 350 | 2 | Q39980_HYOMU | Q39980 hyoscyamus | 482 | 5 | 55.6 | 399 | 2 | Q38WL3_LACSS | Q38wl3 bacillus ha |
| 410 | 5 | 55.6 | 351 | 2 | Q5M3F7_STRT2 | Q5m3f7 streptococ | 483 | 5 | 55.6 | 399 | 2 | Q5WGS1_BACSK | Q5wgs1 bacillus cl |
| 411 | 5 | 55.6 | 352 | 2 | Q6NEE5_CORDI | Q6nee5 corynebacte | 484 | 5 | 55.6 | 399 | 2 | Q6D6V7_ERWCT | Q6d6v7 erwinia car |
| 412 | 5 | 55.6 | 353 | 1 | VP10_RDVA | Q85447 rice dwarf | 485 | 5 | 55.6 | 402 | 2 | Q2W9V3_MAGSA | Q2w9v3 magnetospi |
| 413 | 5 | 55.6 | 353 | 1 | VP10_RDVF | Q85434 rice dwarf | 486 | 5 | 55.6 | 402 | 2 | Q9JFR8_RAHAB | Q9jfr8 wheat roset |
| 414 | 5 | 55.6 | 353 | 1 | VP10_RDVF | P16594 rice dwarf | 487 | 5 | 55.6 | 404 | 2 | Q470V9_RALEJ | Q470v9 ralestonia e |
| 415 | 5 | 55.6 | 353 | 2 | Q33JP6_METHU | Q33jp6 methanospir | 488 | 5 | 55.6 | 406 | 1 | TRPB_LACCA | P17167 lactobacill |
| 416 | 5 | 55.6 | 353 | 2 | Q86I50_DICDI | Q86i50 dictyosteli | 489 | 5 | 55.6 | 406 | 2 | Q2SLZ3_9SPHI | Q2slz3 salinibacte |
| 417 | 5 | 55.6 | 354 | 2 | Q54I98_DICDI | Q54i98 dictyosteli | 490 | 5 | 55.6 | 406 | 2 | Q5LS43_SLIPO | Q5ls43 silicibacte |
| 418 | 5 | 55.6 | 354 | 2 | Q895Z7_CLOTE | Q895z7 clostridium | 491 | 5 | 55.6 | 407 | 2 | Q43YL7_SOLUS | Q43yl7 solibacter |
| 419 | 5 | 55.6 | 355 | 2 | Q97AJ9_THEVO | Q97aj9 thermoplasm | 492 | 5 | 55.6 | 408 | 2 | Q3WJ20_9ACTO | Q3wj20 frankia sp. |
| 420 | 5 | 55.6 | 356 | 2 | Q55Y83_CRYNE | Q55y83 cryptococcu | 493 | 5 | 55.6 | 408 | 2 | Q5NPZ6_ZYMMP | Q5npz6 zymomonas m |
| 421 | 5 | 55.6 | 356 | 2 | Q5KIQ5_CRYNE | Q5k1q5 cryptococcu | 494 | 5 | 55.6 | 408 | 2 | Q5NDP2_ZYMMP | Q5ndp2 zymomonas m |
| 422 | 5 | 55.6 | 358 | 2 | Q33ZC3_RHOPA | Q33zc3 rhodopseudo | 495 | 5 | 55.6 | 409 | 2 | Q4DVU4_TRYCR | Q4dvu4 trypanosoma |
| 423 | 5 | 55.6 | 358 | 2 | Q3W7S3_ANAVT | Q3w7s3 anabaena va | 496 | 5 | 55.6 | 411 | 2 | Q8FNP9_COREF | Q8fnp9 corynebacte |
| 424 | 5 | 55.6 | 358 | 2 | Q8YNS0_ANASP | Q8yns0 anabaena sp | 497 | 5 | 55.6 | 412 | 1 | PHOA_PENCH | P37274 penicillium |
| 425 | 5 | 55.6 | 358 | 2 | Q3EBK4_ARATH | Q3ebk4 arabidopsis | 498 | 5 | 55.6 | 412 | 2 | Q4B8T9_BURVI | Q4b8t9 burkholderi |
| 426 | 5 | 55.6 | 360 | 2 | Q7X786_ORYSA | Q7x786 oryza sativ | 499 | 5 | 55.6 | 417 | 1 | PHOA_ASPNG | P34724 aspergillus |
| 427 | 5 | 55.6 | 360 | 2 | Q37FH9_RHOPA | Q37fh9 rhodopseudo | 500 | 5 | 55.6 | 417 | 2 | Q5B3F0_EMENI | Q5b3f0 aspergillus |
| 428 | 5 | 55.6 | 360 | 2 | Q3SRN4_NITWN | Q3srn4 nitrobacter | 501 | 5 | 55.6 | 418 | 2 | Q2U0U6_ASPOR | Q2u0u6 aspergillus |
| 429 | 5 | 55.6 | 362 | 2 | Q94BT8_ARATH | Q94bt8 arabidopsis | 502 | 5 | 55.6 | 421 | 1 | PHOX_KIULA | P05540 kluyveromyc |
| 430 | 5 | 55.6 | 363 | 1 | TAGH_LACPL | Q88zh4 lactobacill | 503 | 5 | 55.6 | 421 | 2 | Q7PS87_ANOGA | Q7ps87 desulfobivr |
| 431 | 5 | 55.6 | 364 | 1 | OPSG_SCICA | Q85478 sciurus car | 504 | 5 | 55.6 | 421 | 2 | Q72DX6_DESVH | Q72dx6 desulfoheles g |
| 432 | 5 | 55.6 | 364 | 2 | Q3FFG6_9BURK | Q3ffg6 burkholderi | 505 | 5 | 55.6 | 423 | 2 | Q3SQ87_NITWN | Q3sq87 nitrobacter |
| 433 | 5 | 55.6 | 364 | 2 | Q4NGG3_9MICC | Q4ngg3 arthrobacte | 506 | 5 | 55.6 | 425 | 2 | Q9X8T4_STRCO | Q9x8t4 streptomyc |
| 434 | 5 | 55.6 | 364 | 2 | Q2NUW2_SODGL | Q2nuw2 sodaliga glo | 507 | 5 | 55.6 | 426 | 1 | Y680_CHLPN | Q927m4 chlamydia p |
| 435 | 5 | 55.6 | 364 | 2 | Q51R82_SPETR | Q51r82 spermophiliu | 508 | 5 | 55.6 | 428 | 2 | Q3MPN0_CANAL | Q3mpn0 candida alb |
| 436 | 5 | 55.6 | 367 | 2 | Q4BXS8_CROWT | Q4bxs8 crocospaer | 509 | 5 | 55.6 | 428 | 2 | Q59S52_CANAL | Q59s52 candida alb |
| 437 | 5 | 55.6 | 370 | 2 | Q9APJ9_9RHIZ | Q9apj9 hyphomicrob | 510 | 5 | 55.6 | 428 | 2 | Q35Y70_9GAMM | Q35y70 shewanella |
| 438 | 5 | 55.6 | 370 | 2 | Q8A2F1_BACTN | Q8a2f1 bacteroides | 511 | 5 | 55.6 | 428 | 2 | Q3QF16_9GAMM | Q3qf16 shewanella |
| 439 | 5 | 55.6 | 371 | 2 | Q6C101_YARLI | Q6c101 yarrowia li | 512 | 5 | 55.6 | 428 | 2 | Q9RDL4_STRCO | Q9rdl4 streptomyc |
| 440 | 5 | 55.6 | 371 | 2 | Q553Y1_DICDI | Q553y1 dictyosteli | 513 | 5 | 55.6 | 429 | 2 | Q5AX38_EMENI | Q5ax38 aspergillus |
| 441 | 5 | 55.6 | 371 | 2 | Q6PHL8_XANAC | Q6phl8 xanthomonas | 514 | 5 | 55.6 | 429 | 2 | Q4DZ83_TRYCR | Q4dz83 trypanosoma |
| 442 | 5 | 55.6 | 371 | 2 | Q6NRP1_XENLA | Q6nrl1 xenopus lae | 515 | 5 | 55.6 | 429 | 2 | Q3VBH9_9SPHN | Q3vbn9 sphingopyxi |
| 443 | 5 | 55.6 | 372 | 2 | Q6C7K3_YARLI | Q6c7k3 yarrowia li | 516 | 5 | 55.6 | 431 | 2 | Q4BS69_BURVI | Q4bs69 burkholderi |
| 444 | 5 | 55.6 | 372 | 2 | Q2LW90_9DELT | Q2lw90 syntrophus | 517 | 5 | 55.6 | 431 | 2 | Q5X8G1_LEGPA | Q5x8g1 legionella |
| 445 | 5 | 55.6 | 372 | 2 | Q9KEC2_BACHD | Q9kec2 bacillus ha | 518 | 5 | 55.6 | 432 | 2 | Q37NA2_RHOPA | Q37na2 rhodopseudo |
| 446 | 5 | 55.6 | 373 | 2 | Q4I7X2_GIBZE | Q4i7x2 gibberella | 519 | 5 | 55.6 | 433 | 2 | Q5CIH8_CRYKO | Q5cih8 cryptospori |
| 447 | 5 | 55.6 | 373 | 2 | Q6YRD8_ONYPE | Q6yrd8 onion yellow | 520 | 5 | 55.6 | 435 | 2 | Q3AAB4_CAUCR | Q3aab4 caulobacter |
| 448 | 5 | 55.6 | 374 | 2 | Q6I133_CABBR | Q6i139 caenorhabdi | 521 | 5 | 55.6 | 438 | 2 | Q54LNG_DICDI | Q54lng dictyosteli |
| 449 | 5 | 55.6 | 376 | 1 | CENAZ2_RAT | Q9jk15 rattus norv | 522 | 5 | 55.6 | 438 | 2 | Q8FU11_COREF | Q8fui1 corynebacte |
| 450 | 5 | 55.6 | 378 | 2 | Q3VQB4_9CHLB | Q3vqb4 pelodictyon | 523 | 5 | 55.6 | 439 | 2 | Q2DH09_YLDV | Q2dhq9 yaba-like d |
| 451 | 5 | 55.6 | 378 | 2 | Q6TBP6_9POXV | Q6tbp6 bovine papu | 524 | 5 | 55.6 | 441 | 1 | COAT_SOCNV | P15627 soybean chl |
| 452 | 5 | 55.6 | 378 | 2 | Q6TBP7_9POXV | Q6tbp7 pseudocowpo | 525 | 5 | 55.6 | 441 | 2 | Q3FUT8_TOBAC | Q3fuy8 nicotiana t |
| 453 | 5 | 55.6 | 378 | 2 | Q6TBP8_9POXV | Q6tbp8 orf virus. | 526 | 5 | 55.6 | 441 | 2 | Q604K6_METCA | Q604k6 methylococc |
| 454 | 5 | 55.6 | 378 | 2 | Q6TBP9_9POXV | Q6tbp9 orf virus. | 527 | 5 | 55.6 | 444 | 2 | Q2U0U6_ASPOR | Q2u0u6 aspergillus |
| 455 | 5 | 55.6 | 378 | 2 | Q6TBPQ_9POXV | Q6tbpq orf virus. | 528 | 5 | 55.6 | 445 | 2 | Q6Z412_ORYSA | Q6z412 oryza sativ |
| 456 | 5 | 55.6 | 378 | 2 | Q6TVH7_9POXV | Q6tvh7 bovine papu | 529 | 5 | 55.6 | 445 | 2 | Q35LZ9_9BRAD | Q35lzt9 bradyrhizob |
| 457 | 5 | 55.6 | 378 | 2 | Q6TVV9_9POXV | Q6tvv9 orf virus. | 530 | 5 | 55.6 | 445 | 2 | Q37DJ9_RHOPA | Q37dj9 rhodopseudo |
| 458 | 5 | 55.6 | 378 | 2 | Q6TW89_9POXV | Q6tw89 orf virus. | 531 | 5 | 55.6 | 447 | 2 | Q8X176_ASPFU | Q8x176 aspergillus |
| 459 | 5 | 55.6 | 378 | 2 | Q7T6C4_9POXV | Q7t6c4 orf virus. | 532 | 5 | 55.6 | 447 | 2 | Q7Q943_ANOGA | Q7q943 anopheles g |
| 460 | 5 | 55.6 | 378 | 2 | Q7T6C5_9POXV | Q7t6c5 orf virus. | 533 | 5 | 55.6 | 447 | 2 | Q5CXR2_CRYPV | Q5cxr2 cryptospori |
| 461 | 5 | 55.6 | 378 | 2 | Q84145_9POXV | Q84145 orf virus. | 534 | 5 | 55.6 | 448 | 2 | Q4WK63_ASPFU | Q4wk63 aspergillus |
| 462 | 5 | 55.6 | 379 | 2 | Q4TGG3_TETNG | Q4tgg3 tetraodon n | 535 | 5 | 55.6 | 448 | 2 | Q3WBA1_9ACTO | Q3wba1 frankia sp. |
| 463 | 5 | 55.6 | 380 | 2 | Q2TNC6_ANOGA | Q2tnc6 anopheles g | 536 | 5 | 55.6 | 449 | 2 | Q3PPD3_NITHA | Q3ppd3 nitroacter |
| 464 | 5 | 55.6 | 380 | 2 | Q2IZR4_RHOPA | Q2izr4 rhodopseudo | 537 | 5 | 55.6 | 449 | 2 | Q869J7_9MYRI | Q869j7 glomeris ma |
| 465 | 5 | 55.6 | 382 | 2 | Q4IBJ2_GIBZE | Q4ibj2 gibberella | 538 | 5 | 55.6 | 450 | 2 | Q449P1_SOLUS | Q449p1 solibacter |
| 466 | 5 | 55.6 | 382 | 2 | Q4BEG3_BURVI | Q4beg3 burkholderi | 539 | 5 | 55.6 | 451 | 2 | Q6M8V4_CORGL | Q6m8v4 corynebacte |
| 467 | 5 | 55.6 | 383 | 2 | Q94M47_9CAUD | Q94m47 streptococ | 540 | 5 | 55.6 | 451 | 2 | Q8NU94_CORGL | Q8nu94 corynebacte |
| 468 | 5 | 55.6 | 384 | 2 | Q4WY68_ASPFU | Q4wy68 aspergillus | 541 | 5 | 55.6 | 452 | 2 | Q5TMD5_9CHOR | Q5tmd5 asymmetron |
| 469 | 5 | 55.6 | 384 | 2 | Q4BCU2_BURVI | Q4bcu2 burkholderi | 542 | 5 | 55.6 | 452 | 2 | Q8GVB3_CITWA | Q8gve3 citrus maxi |

| | | | | | | | | | | | | | |
|-----|---|------|-----|---|---------------|--------------------|-----|---|------|-----|---|--------------|---------------------|
| 543 | 5 | 55.6 | 452 | 2 | Q9L173_ARATH | Q9L173_arabidopsis | 616 | 5 | 55.6 | 500 | 2 | Q94D20_ORYSA | Q94D20_oryza sativ |
| 544 | 5 | 55.6 | 452 | 2 | Q5F6L2_NEIGL | Q5f6l2_neisseria g | 617 | 5 | 55.6 | 501 | 2 | Q5WRQ8_CAEEL | Q5wrq8_caenorhabdi |
| 545 | 5 | 55.6 | 452 | 2 | Q9JS21_NEIMA | Q9js21_neisseria m | 618 | 5 | 55.6 | 501 | 2 | Q73EX0_BACCL | Q73ex0_bacillus ce |
| 546 | 5 | 55.6 | 452 | 2 | Q8CN35_STAES | Q8cn35_staphylococ | 619 | 5 | 55.6 | 501 | 2 | Q68F54_XENLA | Q68f54_xenopus lae |
| 547 | 5 | 55.6 | 452 | 2 | Q5HLC7_STAEO | Q5hlc7_staphylococ | 620 | 5 | 55.6 | 503 | 2 | Q5AWQ5_EMENI | Q5awq5_aspergillus |
| 548 | 5 | 55.6 | 453 | 2 | Q67U29_ORYSA | Q67u29_oryza sativ | 621 | 5 | 55.6 | 503 | 2 | Q37MX6_RHOPA | Q37mx6_rhodopseudo |
| 549 | 5 | 55.6 | 453 | 2 | Q9FVL2_LYCPS | Q9fv12_lycopersico | 622 | 5 | 55.6 | 503 | 2 | Q7NST0_CHRVO | Q7nst0_chromobacte |
| 550 | 5 | 55.6 | 454 | 2 | Q3QXN0_XYLFA | Q3qxn0_xylella fas | 623 | 5 | 55.6 | 504 | 2 | Q9AWT3_ORYSA | Q9awt3_oryza sativ |
| 551 | 5 | 55.6 | 454 | 2 | Q4BM51_BURVI | Q4bm51_burkholderi | 624 | 5 | 55.6 | 506 | 2 | Q97VP1_SULSO | Q97vp1_sulfolobus |
| 552 | 5 | 55.6 | 455 | 2 | Q9K0Y8_NEIMB | Q9k0y8_neisseria m | 625 | 5 | 55.6 | 506 | 2 | Q4CYO9_TRYCR | Q4cy09_trypanosoma |
| 553 | 5 | 55.6 | 457 | 2 | Q6C3F9_YARLI | Q6c3f9_yarrowia li | 626 | 5 | 55.6 | 506 | 2 | Q4DZV5_TRYCR | Q4dzv5_trypanosoma |
| 554 | 5 | 55.6 | 457 | 2 | Q2U197_ASPOR | Q2u197_aspergillus | 627 | 5 | 55.6 | 509 | 2 | Q20930_CAEEL | Q20930_caenorhabdi |
| 555 | 5 | 55.6 | 458 | 2 | Q2QVY9_ORYSA | Q2qv99_oryza sativ | 628 | 5 | 55.6 | 510 | 2 | Q5WRQ7_CAEEL | Q5wrq7_caenorhabdi |
| 556 | 5 | 55.6 | 460 | 2 | Q4IUC0_GIBZEA | Q4ijc0_gibberella | 629 | 5 | 55.6 | 511 | 2 | Q6PKS3_CANGA | Q6fks3_candida gla |
| 557 | 5 | 55.6 | 462 | 2 | Q3CTE3_ALTAT | Q3cte3_pseudoalter | 630 | 5 | 55.6 | 511 | 2 | Q4MZP7_THEPA | Q4mzf7_theliera p |
| 558 | 5 | 55.6 | 463 | 2 | Q58LR6_9CAUD | Q58lr6_cyanophaga | 631 | 5 | 55.6 | 513 | 2 | Q5C1H4_CRYHO | Q5c1h4_cryptospori |
| 559 | 5 | 55.6 | 463 | 2 | Q6YZC7_ORYSA | Q6yzc7_oryza sativ | 632 | 5 | 55.6 | 513 | 2 | Q5CXR6_CRYPV | Q5cxr6_cryptospori |
| 560 | 5 | 55.6 | 464 | 2 | Q82866_RHOSU | Q82866_rhodovulum | 633 | 5 | 55.6 | 514 | 2 | Q4N3N3_THEPA | Q4n3n3_theliera p |
| 561 | 5 | 55.6 | 465 | 2 | Q840X0_STRMU | Q840x0_streptococc | 634 | 5 | 55.6 | 514 | 2 | Q8KZ28_3PROT | Q8kz28_burkholderi |
| 562 | 5 | 55.6 | 465 | 2 | Q82877_STRMU | Q82877_streptococc | 635 | 5 | 55.6 | 515 | 2 | Q3JKV0_BURP1 | Q3jkv0_burkholderi |
| 563 | 5 | 55.6 | 465 | 2 | Q8DUS2_STRMU | Q8dus2_streptococc | 636 | 5 | 55.6 | 517 | 2 | Q4ED79_9RICK | Q4ed79_wolbachia e |
| 564 | 5 | 55.6 | 469 | 2 | P91256_CAEEL | P91256_caenorhabdi | 637 | 5 | 55.6 | 518 | 1 | CRTI_RHOS4 | P54980_rhodobacter |
| 565 | 5 | 55.6 | 469 | 2 | Q82G55_STRAW | Q82g55_streptomyce | 638 | 5 | 55.6 | 518 | 2 | Q974J8_SULTO | Q974j8_sulfolobus |
| 566 | 5 | 55.6 | 471 | 2 | Q2NG96_9EURY | Q2ng96_methanosphe | 639 | 5 | 55.6 | 519 | 2 | Q69XG4_ORYSA | Q69xg4_oryza sativ |
| 567 | 5 | 55.6 | 472 | 2 | Q7PEV2_ANOGA | Q7pev2_anopheles g | 640 | 5 | 55.6 | 519 | 2 | Q5FHO9_LACAC | Q5fho9_lactobacill |
| 568 | 5 | 55.6 | 474 | 1 | KPYK_CORRE | Q8fp04_corynebacte | 641 | 5 | 55.6 | 520 | 2 | Q39978_HYOMU | Q39978_hyoscyamus |
| 569 | 5 | 55.6 | 474 | 2 | Q2WYA3_9GAMM | Q2wya3_shewanella | 642 | 5 | 55.6 | 524 | 1 | CRTI_RHOCA | P17054_rhodobacter |
| 570 | 5 | 55.6 | 474 | 2 | Q73GB9_WOLPM | Q73gb9_wolbachia p | 643 | 5 | 55.6 | 525 | 1 | GSH1_PSEPK | Q88r90_pseudomonas |
| 571 | 5 | 55.6 | 475 | 1 | AWT2_AEATH | Q9m5n7_arabidopsis | 644 | 5 | 55.6 | 525 | 2 | Q8MXR4_CAEEL | Q8mxr4_caenorhabdi |
| 572 | 5 | 55.6 | 475 | 2 | Q6L558_ORYSA | Q6l558_oryza sativ | 645 | 5 | 55.6 | 526 | 2 | Q4HSJ1_CAMUP | Q4hsj1_campylobact |
| 573 | 5 | 55.6 | 477 | 2 | Q6MSH0_MYCMS | Q6msh0_mycoplasma | 646 | 5 | 55.6 | 527 | 2 | Q6ML54_BDEBA | Q6ml54_bdellovibri |
| 574 | 5 | 55.6 | 478 | 2 | Q7PVC3_ANOGA | Q7pvc3_anopheles g | 647 | 5 | 55.6 | 528 | 2 | Q757C1_ASHGO | Q757c1_ashleya goss |
| 575 | 5 | 55.6 | 478 | 2 | Q2WKW1_CLOBE | Q2wk1_clostridium | 648 | 5 | 55.6 | 530 | 2 | Q7F9L3_ORYSA | Q7f9l3_oryza sativ |
| 576 | 5 | 55.6 | 478 | 2 | Q3Y079_ENTFC | Q3y079_enterococcu | 649 | 5 | 55.6 | 530 | 2 | Q2XBY1_PSRPU | Q2xbv1_pseudomonas |
| 577 | 5 | 55.6 | 479 | 2 | Q3XB09_METEL | Q3xb09_methylobaci | 650 | 5 | 55.6 | 531 | 2 | Q4IEC4_GIBZE | Q4iec4_gibberella |
| 578 | 5 | 55.6 | 479 | 2 | Q7P6F6_FUSNV | Q7p6f6_fusobacteri | 651 | 5 | 55.6 | 531 | 2 | Q6LKS4_CAEER | Q6lks4_caenorhabdi |
| 579 | 5 | 55.6 | 479 | 2 | Q7NVE1_CHRVV | Q7nve1_chromobacte | 652 | 5 | 55.6 | 533 | 2 | Q8SD85_9CAUD | Q8sd85_pseudomonas |
| 580 | 5 | 55.6 | 479 | 2 | Q82Q54_STRAW | Q82q54_streptomyce | 653 | 5 | 55.6 | 533 | 2 | Q5L7N8_BACFR | Q5l7n8_bacteroides |
| 581 | 5 | 55.6 | 480 | 2 | Q38300_BPLC2 | Q38300_lactococcus | 654 | 5 | 55.6 | 533 | 2 | Q64MV8_BACFR | Q64mv8_bacteroides |
| 582 | 5 | 55.6 | 481 | 2 | Q38239_9CAUD | Q38239_lactococcus | 655 | 5 | 55.6 | 535 | 2 | Q97VY5_SULSO | Q97vy5_sulfolobus |
| 583 | 5 | 55.6 | 481 | 2 | Q6I5E1_ORYSA | Q6i5e1_oryza sativ | 656 | 5 | 55.6 | 537 | 2 | Q6L086_PICTO | Q6l086_picrophilus |
| 584 | 5 | 55.6 | 483 | 2 | Q8TFW0_METKA | Q8tfw0_methanopyru | 657 | 5 | 55.6 | 538 | 1 | ACR7_CAEEL | F45963_caenorhabdi |
| 585 | 5 | 55.6 | 483 | 2 | Q7MAU8_KLUMA | Q7mau8_kluyveromyc | 658 | 5 | 55.6 | 538 | 2 | Q7UKP3_RHOBA | Q7ukp3_rhodopirell |
| 586 | 5 | 55.6 | 483 | 2 | Q9C6M0_ARATH | Q9c6m0_arabidopsis | 659 | 5 | 55.6 | 539 | 2 | Q6L218_CAEER | Q6l218_caenorhabdi |
| 587 | 5 | 55.6 | 483 | 2 | Q9M356_ARATH | Q9m356_arabidopsis | 660 | 5 | 55.6 | 540 | 1 | YM8M_YEAST | Q03263_saccharomyc |
| 588 | 5 | 55.6 | 483 | 2 | Q3RFL1_XYLFA | Q3rfu1_xylella fas | 661 | 5 | 55.6 | 540 | 2 | Q41TF8_FERAC | Q41tf8_ferroplasma |
| 589 | 5 | 55.6 | 484 | 1 | GLGA_BAGSU | P39125_bacillus su | 662 | 5 | 55.6 | 543 | 2 | Q93GZ4_STRAW | Q93gz4_streptomyce |
| 590 | 5 | 55.6 | 484 | 2 | Q87CP1_XYLFT | Q87cp1_xylella fas | 663 | 5 | 55.6 | 544 | 2 | Q974R6_SULTO | Q974r6_sulfolobus |
| 591 | 5 | 55.6 | 486 | 2 | Q84K95_ORYSA | Q84k95_oryza sativ | 664 | 5 | 55.6 | 545 | 2 | Q7SAQ4_NEUCR | Q7saq4_neurospora |
| 592 | 5 | 55.6 | 486 | 2 | Q84KJ7_ORYSA | Q84kj7_oryza sativ | 665 | 5 | 55.6 | 545 | 2 | Q65917_LYCPS | Q65917_lycopersico |
| 593 | 5 | 55.6 | 486 | 2 | Q93X02_LOTJA | Q93x02_lotus japon | 666 | 5 | 55.6 | 547 | 1 | GSPA_AERHY | P45754_aeromonas h |
| 594 | 5 | 55.6 | 486 | 2 | Q92CG1_LISIN | Q92cg1_listeria in | 667 | 5 | 55.6 | 547 | 2 | Q3GLT7_9GAMM | Q3glr7_psychoabact |
| 595 | 5 | 55.6 | 489 | 2 | Q2K5Q1_MAGGR | Q2ked1_magnaporthe | 668 | 5 | 55.6 | 547 | 2 | Q4FS25_PSYAR | Q4fs25_psychoabact |
| 596 | 5 | 55.6 | 490 | 2 | Q5WRQ6_CAEEL | Q5wrq6_caenorhabdi | 669 | 5 | 55.6 | 548 | 1 | SEAS_TOBAC | Q40577_nicotiana t |
| 597 | 5 | 55.6 | 491 | 2 | Q6MSI4_MYCMS | Q6msi4_mycoplasma | 670 | 5 | 55.6 | 548 | 2 | Q9P3K6_NEUCR | Q9p3k6_neurospora |
| 598 | 5 | 55.6 | 491 | 1 | UDPE_NPVCF | Q90157_choristoneu | 671 | 5 | 55.6 | 548 | 2 | Q7X9A3_TOBAC | Q7x9a3_nicotiana t |
| 599 | 5 | 55.6 | 492 | 2 | Q7Q4T4_ANOGA | Q7q4t4_anopheles g | 672 | 5 | 55.6 | 548 | 2 | Q84LF0_9SOLA | Q84lf0_nicotiana a |
| 600 | 5 | 55.6 | 492 | 2 | Q48SF2_STRPM | Q48sf2_streptococc | 673 | 5 | 55.6 | 548 | 2 | Q84LF1_9SOLA | Q84lf1_nicotiana a |
| 601 | 5 | 55.6 | 492 | 2 | Q938L1_9CAUD | Q938l1_temperate p | 674 | 5 | 55.6 | 548 | 2 | Q84LF2_9SOLA | Q84lf2_nicotiana a |
| 602 | 5 | 55.6 | 492 | 2 | Q79XU4_STRP3 | Q79xu4_streptococc | 675 | 5 | 55.6 | 548 | 2 | Q84LG0_9SOLA | Q84lg0_nicotiana a |
| 603 | 5 | 55.6 | 492 | 2 | Q9PCD7_XYLFA | Q9pcd7_xylella fas | 676 | 5 | 55.6 | 549 | 2 | Q9XIZ0_SOUTU | Q9xiz0_solanum tub |
| 604 | 5 | 55.6 | 493 | 1 | AMPA_XANCP | Q8pcr4_xanthomonas | 677 | 5 | 55.6 | 549 | 2 | Q9XJ25_SOUTU | Q9xj25_solanum tub |
| 605 | 5 | 55.6 | 493 | 2 | Q4UOP6_XANCB | Q4uop6_xanthomonas | 678 | 5 | 55.6 | 550 | 2 | Q9SBJ0_SOUTU | Q9sbj0_solanum tub |
| 606 | 5 | 55.6 | 494 | 2 | Q8H251_MEDTR | Q8h251_medicago tr | 679 | 5 | 55.6 | 551 | 2 | Q9ZTQ6_SOUTU | Q9ztq6_solanum tub |
| 607 | 5 | 55.6 | 495 | 2 | Q3QDW7_9GAMM | Q3qdw7_shewanella | 680 | 5 | 55.6 | 552 | 2 | Q46VS9_RALEB | Q46vs9_raibsonia e |
| 608 | 5 | 55.6 | 496 | 2 | Q89ZQ7_BACTN | Q89zq7_bacteroides | 681 | 5 | 55.6 | 554 | 2 | Q4OGE0_9RHOJ | Q4oge0_jannaschia |
| 609 | 5 | 55.6 | 497 | 2 | Q8S230_ORYSA | Q8s230_oryza sativ | 682 | 5 | 55.6 | 554 | 2 | Q8FGS2_ECOL6 | Q8fgs2_escherichia |
| 610 | 5 | 55.6 | 497 | 2 | Q8S233_ORYSA | Q8s233_oryza sativ | 683 | 5 | 55.6 | 556 | 2 | Q9ATN5_CAPAN | Q9atn5_capsicum an |
| 611 | 5 | 55.6 | 497 | 2 | Q3V9X0_9SPHN | Q3v9x0_sphingopyxi | 684 | 5 | 55.6 | 556 | 2 | Q9FVL3_LYCPS | Q9fv13_lycopersico |
| 612 | 5 | 55.6 | 497 | 2 | Q5XAR5_STRP6 | Q5xar5_streptococc | 685 | 5 | 55.6 | 556 | 2 | Q9XJ32_SOUTU | Q9xj32_solanum tub |
| 613 | 5 | 55.6 | 497 | 2 | Q8NZK7_STRP8 | Q8nzr7_streptococc | 686 | 5 | 55.6 | 556 | 2 | Q9ZTQ7_SOUTU | Q9ztq7_solanum tub |
| 614 | 5 | 55.6 | 497 | 2 | Q9AOP2_STRP1 | Q9aop2_streptococc | 687 | 5 | 55.6 | 557 | 2 | Q9ZTQ8_SOUTU | Q9ztq8_solanum tub |
| 615 | 5 | 55.6 | 498 | 2 | Q3NQ88_SHEPR | Q3ng98_shewanella | 688 | 5 | 55.6 | 558 | 2 | Q3WTR7_9RHIZ | Q3wtr7_mesorhizobi |

| | | | | | | | | | | | | | |
|-----|---|------|-----|---|----------------|---------------------|-----|---|------|-----|---|---------------|--------------------|
| 689 | 5 | 55.6 | 559 | 2 | Q4WB27 ASPFU | Q4wb27 aspergillus | 762 | 5 | 55.6 | 628 | 2 | Q9SN07 ARATH | Q9sn07 arabidopsis |
| 690 | 5 | 55.6 | 559 | 2 | Q6ATB2_ORYSA | Q6atb2 oryza sativ | 763 | 5 | 55.6 | 631 | 2 | Q4CMJ1_TRYCR | Q4cmj1 trypanosoma |
| 691 | 5 | 55.6 | 560 | 2 | Q9SDN9_CARPAN | Q9sdn9 capricum an | 764 | 5 | 55.6 | 631 | 2 | Q5QYD8_IDILO | Q5qyd8 idiomarina |
| 692 | 5 | 55.6 | 561 | 2 | Q580M8_9TRYP | Q580m8 trypanosoma | 765 | 5 | 55.6 | 632 | 2 | Q6CSY9_YARLI | Q6csy9 yarrowia li |
| 693 | 5 | 55.6 | 562 | 2 | Q4MZFB_TSEHT | Q4mzf8 theileria p | 766 | 5 | 55.6 | 632 | 2 | Q8H106_ARATH | Q8h106 arabidopsis |
| 694 | 5 | 55.6 | 565 | 2 | Q31IEG3_PSEHT | Q3ieg3 pseudalter | 767 | 5 | 55.6 | 633 | 2 | Q6ET07_ORYSA | Q6et07 oryza sativ |
| 695 | 5 | 55.6 | 566 | 2 | Q972D3_SULSO | Q972d3 sulfolobus | 768 | 5 | 55.6 | 634 | 2 | Q7PY63_ANOGA | Q7py63 anopheles g |
| 696 | 5 | 55.6 | 566 | 2 | Q4KMX2_HUMAN | Q4kmx2 homo sapien | 769 | 5 | 55.6 | 637 | 2 | Q81IL8_PLAF7 | Q81il8 plasmodium |
| 697 | 5 | 55.6 | 566 | 2 | Q5VTB9_HUMAN | Q5vtb9 homo sapien | 770 | 5 | 55.6 | 638 | 2 | Q3ZLT0_BURKE | Q3zlt0 burkholderi |
| 698 | 5 | 55.6 | 566 | 2 | Q8HXD5_MACFA | Q8hxd5 macca fasc | 771 | 5 | 55.6 | 639 | 2 | Q416M5_GIBZE | Q416m5 gibberella |
| 699 | 5 | 55.6 | 566 | 2 | Q6PDX6_MOUSE | Q6pdx6 mus musculu | 772 | 5 | 55.6 | 639 | 2 | Q4L530_STAHL | Q4l530 staphylococ |
| 700 | 5 | 55.6 | 567 | 2 | Q9HGH9_ASPOR | Q9hgh9 aspergillus | 773 | 5 | 55.6 | 640 | 1 | HTPG_FREDE | HTpg frede |
| 701 | 5 | 55.6 | 569 | 2 | Q6PUF9_TOBAC | Q6puf9 nicotiana t | 774 | 5 | 55.6 | 641 | 2 | Q87RQ5_VIBPA | Q87rq5 vibrio para |
| 702 | 5 | 55.6 | 571 | 2 | Q8MXR5_CAEEL | Q8mxr5 caenorhabdi | 775 | 5 | 55.6 | 643 | 1 | ICB1_HUMAN | ICb1 human |
| 703 | 5 | 55.6 | 572 | 1 | DPOL_BPZA | DPolBPza bacterioph | 776 | 5 | 55.6 | 643 | 2 | Q61L64_CAEUR | Q61l64 caenorhabdi |
| 704 | 5 | 55.6 | 573 | 2 | Q4V9N6_BRARE | Q4v9n6 brachydanio | 777 | 5 | 55.6 | 646 | 2 | Q7RZK4_NEUCR | Q7rzk4 neurospora |
| 705 | 5 | 55.6 | 574 | 1 | VB18_VACCA | Q57263 vaccinia vi | 778 | 5 | 55.6 | 655 | 2 | Q5FVW8_XENTR | Q5fvw8 xenopus tro |
| 706 | 5 | 55.6 | 574 | 1 | VB18_VACCC | P21076 vaccinia vi | 779 | 5 | 55.6 | 662 | 2 | Q9VLK1_DROME | Q9vlk1 drosophila |
| 707 | 5 | 55.6 | 574 | 1 | VB18_VACCV | Q01222 vaccinia vi | 780 | 5 | 55.6 | 664 | 2 | Q4WJTA_ASPFU | Q4wtj4 aspergillus |
| 708 | 5 | 55.6 | 574 | 1 | VB18_VACV | P33824 variola vir | 781 | 5 | 55.6 | 665 | 2 | Q5AHK1_CANAL | Q5ahk1 candida alb |
| 709 | 5 | 55.6 | 574 | 2 | Q41R24_GIBZE | Q4ir24 gibberella | 782 | 5 | 55.6 | 665 | 2 | Q3AHX7_CANAL | Q3ahr7 candida alb |
| 710 | 5 | 55.6 | 574 | 2 | Q72753_COMPLEX | Q72753 compox viru | 783 | 5 | 55.6 | 665 | 2 | Q3SR82_NITWN | Q3sr82 nitrobacter |
| 711 | 5 | 55.6 | 574 | 2 | Q6RZB3_9POXV | Q6rzb3 rabbitpox v | 784 | 5 | 55.6 | 668 | 2 | Q4LSC5_FERAC | Q4lsc5 ferroplasma |
| 712 | 5 | 55.6 | 574 | 2 | Q76PT5_VARV | Q76pt5 variola min | 785 | 5 | 55.6 | 671 | 2 | Q5JLP9_ORYSA | Q5jlp9 oryza sativ |
| 713 | 5 | 55.6 | 574 | 2 | Q89114_VARV | Q89114 variola vir | 786 | 5 | 55.6 | 677 | 2 | Q5V0F1_HALMA | Q5v0f1 haloarcula |
| 714 | 5 | 55.6 | 574 | 2 | Q89523_VARV | Q89523 variola vir | 787 | 5 | 55.6 | 678 | 2 | Q54PF9_DICDI | Q54pf9 dictyosteli |
| 715 | 5 | 55.6 | 574 | 2 | Q8QMN6_COMPLEX | Q8qmn6 compox viru | 788 | 5 | 55.6 | 680 | 2 | Q6NUC4_XENLA | Q6nuc4 xenopus lae |
| 716 | 5 | 55.6 | 574 | 2 | Q9JF35_VACCT | Q9jf35 vaccinia vi | 789 | 5 | 55.6 | 680 | 2 | Q34BQ7_RHOPA | Q34bq7 rhodopseuo |
| 717 | 5 | 55.6 | 575 | 1 | DPOL_BPPH2 | P03680 bacterioph | 790 | 5 | 55.6 | 681 | 2 | Q8XSL2_RALSO | Q8xsl2 ralstonia s |
| 718 | 5 | 55.6 | 575 | 2 | Q38545_BPPH2 | Q38545 bacterioph | 791 | 5 | 55.6 | 683 | 2 | Q3ZVL7_SPTCI | Q3zvl7 spiroplasma |
| 719 | 5 | 55.6 | 577 | 2 | Q6C526_YARLI | Q6c526 yarrowia li | 792 | 5 | 55.6 | 683 | 2 | Q8D097_YERPE | Q8d097 yersinia pe |
| 720 | 5 | 55.6 | 577 | 2 | Q2SS55_MYCCA | Q2ss55 mycoplasma | 793 | 5 | 55.6 | 683 | 2 | Q9L6C8_SALET | Q9l6c8 salmonella |
| 721 | 5 | 55.6 | 578 | 2 | Q5SVMS_HUMAN | Q5svms homo sapien | 794 | 5 | 55.6 | 683 | 2 | Q57NC1_SALCH | Q57nc1 salmonella |
| 722 | 5 | 55.6 | 578 | 2 | Q2W5C2_ORYSA | Q2w5c2 oryza sativ | 795 | 5 | 55.6 | 683 | 2 | Q5PHK7_SALPA | Q5phk7 salmonella |
| 723 | 5 | 55.6 | 578 | 2 | Q2W5C6_MAGSA | Q2w5c6 magnetospir | 796 | 5 | 55.6 | 683 | 2 | Q6BWM0_YERPS | Q6bwm0 yersinia ps |
| 724 | 5 | 55.6 | 579 | 2 | Q9U1W0_CAEEL | Q9u1w0 caenorhabdi | 797 | 5 | 55.6 | 683 | 2 | Q8ZFD4_YERPE | Q8zfd4 yersinia pe |
| 725 | 5 | 55.6 | 579 | 2 | Q54FY7_DICDI | Q54fy7 dictyosteli | 798 | 5 | 55.6 | 683 | 2 | Q8ZWN9_SALTY | Q8zwn9 salmonella |
| 726 | 5 | 55.6 | 579 | 2 | Q42947_TOBAC | Q42947 nicotiana t | 799 | 5 | 55.6 | 686 | 2 | Q8Z5X7_SALTI | Q8z5x7 salmonella |
| 727 | 5 | 55.6 | 580 | 2 | Q4D3V7_TRYCR | Q4d3v2 trypanosoma | 800 | 5 | 55.6 | 686 | 2 | Q75CQ8_ASHGO | Q75cq8 ashbya gosb |
| 728 | 5 | 55.6 | 580 | 2 | Q4D7V3_TRYCR | Q4d7v3 trypanosoma | 801 | 5 | 55.6 | 686 | 2 | Q3Z2J6_SHISS | Q3z2j6 shigella so |
| 729 | 5 | 55.6 | 585 | 2 | Q97918_THEVO | Q97918 thermoplasm | 802 | 5 | 55.6 | 686 | 2 | Q32HB7_SHIDS | Q32hb7 shigella dy |
| 730 | 5 | 55.6 | 585 | 2 | Q7UZ29_RHOBA | Q7uz29 rhodopirell | 803 | 5 | 55.6 | 686 | 2 | Q8XCK4_ECO57 | Q8xck4 escherichia |
| 731 | 5 | 55.6 | 587 | 2 | Q6D3Z9_ERWCT | Q6d3z9 erwinia car | 804 | 5 | 55.6 | 686 | 2 | Q83R69_SHIFL | Q83r69 shigella fl |
| 732 | 5 | 55.6 | 588 | 2 | Q61BC2_CABBR | Q61bc2 caenorhabdi | 805 | 5 | 55.6 | 687 | 2 | Q4YX27_PLABE | Q4yx27 plasmodium |
| 733 | 5 | 55.6 | 588 | 2 | Q3RTQ2_RALME | Q3rtq2 ralstonia m | 806 | 5 | 55.6 | 687 | 2 | Q2JV15_9CYAN | Q2jv15 cyanobacter |
| 734 | 5 | 55.6 | 592 | 2 | Q81LM1_PLAF7 | Q81lm1 plasmodium | 807 | 5 | 55.6 | 688 | 2 | Q95YGI_PENJP | Q95ygi penaeus jap |
| 735 | 5 | 55.6 | 594 | 2 | Q9JFS6_9POXV | Q9jfs6 ectromelia | 808 | 5 | 55.6 | 689 | 2 | Q96U83_NEUCR | Q96u83 neurospora |
| 736 | 5 | 55.6 | 600 | 2 | Q41I86_GIBZE | Q4i186 gibberella | 809 | 5 | 55.6 | 689 | 2 | Q474V0_RALSTO | Q474v0 ralstonia e |
| 737 | 5 | 55.6 | 600 | 2 | Q49B63_WOLPI | Q49b63 wolbachia p | 810 | 5 | 55.6 | 689 | 2 | Q2NTH7_SODGL | Q2nth7 sodalis glo |
| 738 | 5 | 55.6 | 600 | 2 | Q6TEM7_BRARE | Q6tem7 brachydanio | 811 | 5 | 55.6 | 690 | 2 | Q381Q3_9TRYP | Q381q3 trypanosoma |
| 739 | 5 | 55.6 | 606 | 1 | Y609_ENCCU | Q8svf3 encephalito | 812 | 5 | 55.6 | 693 | 2 | Q2UKD4_ASPOR | Q2ukd4 aspergillus |
| 740 | 5 | 55.6 | 608 | 2 | Q2ZA86_9GAMM | Q2za86 shewanella | 813 | 5 | 55.6 | 693 | 2 | Q3SOP0_RALME | Q3sop0 ralstonia m |
| 741 | 5 | 55.6 | 609 | 2 | Q2ZNY0_SHEPU | Q2zny0 shewanella | 814 | 5 | 55.6 | 695 | 2 | Q7MTR1_PORGI | Q7mtr1 porphyromon |
| 742 | 5 | 55.6 | 610 | 2 | Q2X645_9GAMM | Q2x645 shewanella | 815 | 5 | 55.6 | 696 | 2 | Q8UDAI_AGR5 | Q8udai agrobacteri |
| 743 | 5 | 55.6 | 610 | 2 | Q8EFW1_SHEON | Q8efw1 shewanella | 816 | 5 | 55.6 | 697 | 2 | Q5OY29_ENTHI | Q5oy29 entamoeba h |
| 744 | 5 | 55.6 | 611 | 2 | Q4XFQ2_PLACH | Q4xfq2 plasmodium | 817 | 5 | 55.6 | 704 | 2 | Q8PJ59_XANAC | Q8pj59 xanthomonas |
| 745 | 5 | 55.6 | 611 | 2 | Q3Q0P3_9GAMM | Q3q0p3 shewanella | 818 | 5 | 55.6 | 705 | 2 | Q7RUR8_NEUCR | Q7rur8 neurospora |
| 746 | 5 | 55.6 | 613 | 2 | Q4Q8F9_LEIMA | Q4q8f9 leishmania | 819 | 5 | 55.6 | 712 | 2 | Q3AG94_SYNSC | Q3ag94 synecococc |
| 747 | 5 | 55.6 | 613 | 2 | Q9VBJ6_DROME | Q9vbj6 drosophila | 820 | 5 | 55.6 | 712 | 2 | Q6LRA0_PHOPR | Q6lra0 photobacter |
| 748 | 5 | 55.6 | 615 | 2 | Q7NFU9_GLOVI | Q7nfu9 gloeobacter | 821 | 5 | 55.6 | 715 | 2 | Q852G7_ORYSA | Q852g7 oryza sativ |
| 749 | 5 | 55.6 | 616 | 2 | Q8VXX2_ARATH | Q8vxx2 arabidopsis | 822 | 5 | 55.6 | 715 | 2 | Q852G7_ORYSA | Q852g7 oryza sativ |
| 750 | 5 | 55.6 | 616 | 2 | Q9FF13_ARATH | Q9ff13 arabidopsis | 823 | 5 | 55.6 | 716 | 2 | Q4URK3_THEAN | Q4urk3 theileria a |
| 751 | 5 | 55.6 | 616 | 2 | Q5ZL71_CHICK | Q5zl71 gallus gall | 824 | 5 | 55.6 | 716 | 2 | Q6LQ86_PHOPR | Q6lq86 photobacter |
| 752 | 5 | 55.6 | 617 | 1 | VF33B_HUMAN | Q52171 homo sapien | 825 | 5 | 55.6 | 718 | 2 | Q9B107_ENTHI | Q9b107 entamoeba h |
| 753 | 5 | 55.6 | 617 | 1 | VF33B_MOUSE | P59016 mus musculu | 826 | 5 | 55.6 | 719 | 2 | Q54D68_DICDI | Q54d68 dictyosteli |
| 754 | 5 | 55.6 | 617 | 1 | VF33B_RAT | Q8c076 rattus norv | 827 | 5 | 55.6 | 719 | 2 | Q4LB15_PRESH | Q4lb15 pseudomonas |
| 755 | 5 | 55.6 | 617 | 1 | Q8C076_MOUSE | Q8c076 mus musculu | 828 | 5 | 55.6 | 719 | 2 | Q4ZMG8_PSEU2 | Q4zmg8 pseudomonas |
| 756 | 5 | 55.6 | 620 | 1 | ACE1_CAEER | Q27459 caenorhabdi | 829 | 5 | 55.6 | 719 | 2 | Q3TIM6_MOUSE | Q3tim6 mus musculu |
| 757 | 5 | 55.6 | 622 | 2 | Q8ANR5_CANAL | Q5a8n5 candida alb | 830 | 5 | 55.6 | 722 | 2 | Q87541_POTY | Q87541 barley mild |
| 758 | 5 | 55.6 | 623 | 2 | Q7UFK6_RHOBA | Q7ufk6 rhodopirell | 831 | 5 | 55.6 | 722 | 2 | Q4CS27_TRYCR | Q4cs27 trypanosoma |
| 759 | 5 | 55.6 | 624 | 2 | Q9QSK5_IRVB | Q9qsk5 chilo iride | 832 | 5 | 55.6 | 722 | 2 | Q4E4F4_TRYCR | Q4e4f4 trypanosoma |
| 760 | 5 | 55.6 | 625 | 2 | Q3QEQ8_9GAMM | Q3qeq8 shewanella | 833 | 5 | 55.6 | 723 | 2 | Q3JA75_NITOC | Q3ja75 nitrococc |
| 761 | 5 | 55.6 | 628 | 2 | Q2TY93_ASPOR | Q2ty93 aspergillus | 834 | 5 | 55.6 | 723 | 2 | Q5FTK2_GUOX | Q5ftk2 gluconobact |

| | | | | | | | | | | | | | | |
|-----|---|------|-----|---|--------------|---------------------|--------------|-----|------|------|------|--------------|---------------------|--------------------|
| 835 | 5 | 55.6 | 724 | 1 | KS6A1_MOUSE | P18653 | mus musculus | 908 | 5 | 55.6 | 869 | 2 | Q87ZB5_PSESM | Q87ZB5_pseudomonas |
| 836 | 5 | 55.6 | 724 | 2 | Q4Y8T8_PLABE | Q4Y8T8_plasmodium | 909 | 5 | 55.6 | 869 | 2 | Q88KZ9_PSEPK | Q88KZ9_pseudomonas | |
| 837 | 5 | 55.6 | 724 | 2 | Q60C15_METCA | Q60C15_methylococc | 910 | 5 | 55.6 | 870 | 2 | Q76NP4_CABEL | Q76NP4_caenorhabdi | |
| 838 | 5 | 55.6 | 727 | 2 | Q4N2E9_THEPA | Q4N2E9_theliera p | 911 | 5 | 55.6 | 870 | 2 | Q86S28_CABEL | Q86S28_caenorhabdi | |
| 839 | 5 | 55.6 | 729 | 2 | Q5QLC6_ORYSA | Q5QLC6_oryza sativ | 912 | 5 | 55.6 | 870 | 2 | Q48GW6_PSE14 | Q48GW6_pseudomonas | |
| 840 | 5 | 55.6 | 732 | 2 | Q4RME1_TETNG | Q4RME1_tetradodon n | 913 | 5 | 55.6 | 870 | 2 | Q4ZRA3_PSEU2 | Q4ZRA3_pseudomonas | |
| 841 | 5 | 55.6 | 732 | 2 | Q7ZVH8_BRAAE | Q7ZVH8_brachydanio | 914 | 5 | 55.6 | 879 | 2 | Q36KV0_MARHY | Q36KV0_marinobacte | |
| 842 | 5 | 55.6 | 735 | 1 | KS6A1_HUMAN | Q15418_homo sapien | 915 | 5 | 55.6 | 880 | 2 | Q4DYN0_TRYCR | Q4DYN0_trypanosoma | |
| 843 | 5 | 55.6 | 735 | 1 | KS6A1_RAT | Q63531_rattus norv | 916 | 5 | 55.6 | 882 | 2 | Q8BPJ3_XANAC | Q8BPJ3_xanthomonas | |
| 844 | 5 | 55.6 | 735 | 2 | Q5SVN8_HUMAN | Q5SVN8_homo sapien | 917 | 5 | 55.6 | 885 | 2 | Q8BPJ3_XANAC | Q8BPJ3_xanthomonas | |
| 845 | 5 | 55.6 | 735 | 2 | Q2RUL9_RHOUR | Q2RUL9_rhodospiril | 918 | 5 | 55.6 | 889 | 2 | Q8BL87_MOUSE | Q8BL87_mus musculu | |
| 846 | 5 | 55.6 | 735 | 2 | Q3UPZ5_MOUSE | Q3UPZ5_mus musculu | 919 | 5 | 55.6 | 893 | 2 | Q4UBT9_THEAN | Q4UBT9_theliera a | |
| 847 | 5 | 55.6 | 735 | 2 | Q50YN6_MOUSE | Q50YN6_mus musculu | 920 | 5 | 55.6 | 893 | 2 | Q832P7_ENTFA | Q832P7_enterococcu | |
| 848 | 5 | 55.6 | 736 | 2 | Q6TBY5_ORYSA | Q6TBY5_oryza sativ | 921 | 5 | 55.6 | 896 | 2 | Q6BR11_DBBHA | Q6BR11_debaryomyce | |
| 849 | 5 | 55.6 | 738 | 2 | Q8TBA4_ASTPE | Q8TBA4_asterina pe | 922 | 5 | 55.6 | 896 | 2 | Q8DH74_SYNEL | Q8DH74_synechococc | |
| 850 | 5 | 55.6 | 738 | 2 | Q4HFMA_CAMCO | Q4HFMA_campylobact | 923 | 5 | 55.6 | 897 | 2 | Q3C661_9CLOT | Q3C661_alkaliphilu | |
| 851 | 5 | 55.6 | 739 | 2 | Q7KRQ2_DROME | Q7KRQ2_drosophila | 924 | 5 | 55.6 | 897 | 2 | Q5NIG1_PPRAT | Q5NIG1_francisella | |
| 852 | 5 | 55.6 | 739 | 2 | Q9PIZ8_CAMJE | Q9PIZ8_campylobact | 925 | 5 | 55.6 | 898 | 2 | Q7RJ73_PLAYO | Q7RJ73_plasmodium | |
| 853 | 5 | 55.6 | 741 | 2 | Q8SX87_DROME | Q8SX87_drosophila | 926 | 5 | 55.6 | 898 | 2 | Q6MRC8_DBBBA | Q6MRC8_dbellovibri | |
| 854 | 5 | 55.6 | 742 | 2 | Q6FY80_CANGA | Q6FY80_candida gla | 927 | 5 | 55.6 | 901 | 1 | GLR21_ARATH | Q04660_arabidopsis | |
| 855 | 5 | 55.6 | 752 | 1 | KS6AA_CHICK | P18652_gallus gall | 927 | 5 | 55.6 | 901 | 1 | GLR21_ARATH | Q04660_arabidopsis | |
| 856 | 5 | 55.6 | 752 | 2 | Q9UIV9_CAEEL | Q9UIV9_caenorhabdi | 928 | 5 | 55.6 | 902 | 2 | Q8PVX0_METMA | Q8PVX0_methanosarc | |
| 857 | 5 | 55.6 | 756 | 2 | Q751Y0_ASHGO | Q751Y0_ashbya goss | 929 | 5 | 55.6 | 902 | 2 | Q9Q8X9_9POXV | Q9Q8X9_rabbit fibr | |
| 858 | 5 | 55.6 | 756 | 2 | Q86S27_CABEL | Q86S27_caenorhabdi | 930 | 5 | 55.6 | 902 | 2 | Q3JUK1_BURP1 | Q3JUK1_burkholderi | |
| 859 | 5 | 55.6 | 759 | 2 | Q5W1J6_XENLA | Q5W1J6_xenopus lae | 931 | 5 | 55.6 | 907 | 2 | Q62A11_BURMA | Q62A11_burkholderi | |
| 860 | 5 | 55.6 | 760 | 2 | Q7S1T3_NEUCR | Q7S1T3_neurospora | 932 | 5 | 55.6 | 907 | 2 | Q3JUK1_BURP1 | Q3JUK1_burkholderi | |
| 861 | 5 | 55.6 | 760 | 2 | Q60X52_CAEER | Q60X52_caenorhabdi | 933 | 5 | 55.6 | 907 | 2 | Q62A11_BURMA | Q62A11_burkholderi | |
| 862 | 5 | 55.6 | 767 | 2 | Q4XY12_PLACH | Q4XY12_plasmodium | 934 | 5 | 55.6 | 909 | 2 | Q3QFH6_9GAMM | Q3QFH6_shevanella | |
| 863 | 5 | 55.6 | 769 | 2 | Q647S8_9ARCH | Q647S8_uncultured | 935 | 5 | 55.6 | 916 | 2 | Q2T710_BURTH | Q2T710_burkholderi | |
| 864 | 5 | 55.6 | 771 | 2 | Q4A675_MYCS5 | Q4A675_mycoplasma | 936 | 5 | 55.6 | 917 | 2 | Q3H993_TRIER | Q3H993_trichodeemi | |
| 865 | 5 | 55.6 | 773 | 2 | Q81OV8_MOUSE | Q81OV8_mus musculu | 937 | 5 | 55.6 | 919 | 2 | Q4REZ5_TENG | Q4REZ5_tetradodon n | |
| 866 | 5 | 55.6 | 777 | 2 | Q7RBN5_PLAYO | Q7RBN5_plasmodium | 938 | 5 | 55.6 | 920 | 2 | Q4AC93_HUMAN | Q4AC93_homo sapien | |
| 867 | 5 | 55.6 | 777 | 2 | Q86JF9_DICDI | Q86JF9_dictyosteli | 939 | 5 | 55.6 | 921 | 2 | Q8IK22_PLAP7 | Q8IK22_plasmodium | |
| 868 | 5 | 55.6 | 778 | 2 | Q3PRZ3_NITHA | Q3PRZ3_nitrobacter | 940 | 5 | 55.6 | 923 | 2 | Q908G5_RHILO | Q908G5_rhizobium l | |
| 869 | 5 | 55.6 | 780 | 2 | Q3A744_PELCD | Q3A744_pelobacter | 941 | 5 | 55.6 | 924 | 2 | Q60UX1_CAEER | Q60UX1_caenorhabdi | |
| 870 | 5 | 55.6 | 783 | 2 | Q7UHE0_RHOBA | Q7UHE0_rhodopirell | 942 | 5 | 55.6 | 936 | 2 | Q9W365_DROME | Q9W365_drosophila | |
| 871 | 5 | 55.6 | 784 | 2 | Q5AK17_CANAL | Q5AK17_candida alb | 943 | 5 | 55.6 | 937 | 2 | Q2ZYD7_STRSU | Q2ZYD7_streptococc | |
| 872 | 5 | 55.6 | 785 | 2 | Q2XQA9_PSEPU | Q2XQA9_pseudomonas | 944 | 5 | 55.6 | 940 | 2 | Q2ZYD7_STRSU | Q2ZYD7_streptococc | |
| 873 | 5 | 55.6 | 789 | 2 | Q7RTK8_SCHMA | Q7RTK8_schistosoma | 945 | 5 | 55.6 | 940 | 2 | Q3S8A4_9ADEN | Q3S8A4_human adeno | |
| 874 | 5 | 55.6 | 791 | 2 | Q38B12_9TRYP | Q38B12_trypanosoma | 946 | 5 | 55.6 | 942 | 2 | Q8TJ74_METAC | Q8TJ74_methanosarc | |
| 875 | 5 | 55.6 | 796 | 2 | Q45019_9BURK | Q45019_burkholderi | 947 | 5 | 55.6 | 947 | 2 | Q6YVX3_ORYSA | Q6YVX3_oryza sativ | |
| 876 | 5 | 55.6 | 796 | 2 | Q4LPG2_9BURK | Q4LPG2_burkholderi | 948 | 5 | 55.6 | 948 | 2 | Q7R7T5_PLAYO | Q7R7T5_plasmodium | |
| 877 | 5 | 55.6 | 797 | 2 | Q4CST5_TRYCR | Q4CST5_trypanosoma | 949 | 5 | 55.6 | 950 | 2 | Q8VZ08_ARATH | Q8VZ08_arabidopsis | |
| 878 | 5 | 55.6 | 798 | 2 | Q4BKH4_BURVI | Q4BKH4_burkholderi | 950 | 5 | 55.6 | 953 | 1 | IF2_STRP1 | Q9VY91_streptococc | |
| 879 | 5 | 55.6 | 800 | 2 | Q5AV46_EMENI | Q5AV46_aspergillus | 951 | 5 | 55.6 | 953 | 1 | IF2_STRP3 | Q8K644_streptococc | |
| 880 | 5 | 55.6 | 800 | 2 | Q73IS7_WOLPM | Q73IS7_wolbachia p | 952 | 5 | 55.6 | 953 | 1 | IF2_STRP6 | Q5XAH1_streptococc | |
| 881 | 5 | 55.6 | 807 | 2 | Q48724_ARATH | Q48724_arabidopsis | 953 | 5 | 55.6 | 953 | 1 | IF2_STRP8 | Q8XU77_streptococc | |
| 882 | 5 | 55.6 | 812 | 2 | Q61V33_CAEER | Q61V33_caenorhabdi | 954 | 5 | 55.6 | 953 | 2 | Q48RUB_STRPM | Q48RUB_streptococc | |
| 883 | 5 | 55.6 | 813 | 2 | Q6ASW7_ORYSA | Q6ASW7_oryza sativ | 955 | 5 | 55.6 | 956 | 2 | Q3KKN5_CHLTA | Q3KKN5_chlamydia t | |
| 884 | 5 | 55.6 | 817 | 2 | Q98KX1_RHILO | Q98KX1_rhizobium l | 956 | 5 | 55.6 | 956 | 2 | Q84812_CHLTR | Q84812_chlamydia t | |
| 885 | 5 | 55.6 | 820 | 2 | Q5B0F8_EMENI | Q5B0F8_aspergillus | 957 | 5 | 55.6 | 957 | 2 | Q60J73_CAEER | Q60J73_caenorhabdi | |
| 886 | 5 | 55.6 | 821 | 2 | Q966D4_CAEEL | Q966D4_caenorhabdi | 958 | 5 | 55.6 | 971 | 1 | SW11_SCHPO | Q9UUM2_schizosacch | |
| 887 | 5 | 55.6 | 826 | 1 | VP91_NPVEP | Q91GH8_epiphyas po | 959 | 5 | 55.6 | 976 | 2 | Q73SX6_MYCPA | Q73SX6_mycobacteri | |
| 888 | 5 | 55.6 | 829 | 2 | Q5SAU1_DICDI | Q5SAU1_dictyosteli | 960 | 5 | 55.6 | 979 | 2 | Q4DKR7_TRYCR | Q4DKR7_trypanosoma | |
| 889 | 5 | 55.6 | 833 | 2 | Q4DLW0_TRYCR | Q4DLW0_trypanosoma | 961 | 5 | 55.6 | 981 | 2 | Q5AQL1_EMENI | Q5AQL1_aspergillus | |
| 890 | 5 | 55.6 | 833 | 2 | Q4SVN6_TETNG | Q4SVN6_tetradodon n | 962 | 5 | 55.6 | 982 | 2 | Q24KX5_DICDI | Q24KX5_dictyosteli | |
| 891 | 5 | 55.6 | 835 | 2 | Q2QNH1_ORYSA | Q2QNH1_oryza sativ | 963 | 5 | 55.6 | 982 | 2 | Q2WC39_9VICR | Q2WC39_enterobacte | |
| 892 | 5 | 55.6 | 837 | 2 | Q55176_CRYNE | Q55176_cryptococcu | 964 | 5 | 55.6 | 982 | 2 | Q4UGD2_BSP6 | Q4UGD2_enterobacte | |
| 893 | 5 | 55.6 | 837 | 2 | Q5K7R1_CRYNE | Q5K7R1_cryptococcu | 965 | 5 | 55.6 | 989 | 2 | Q6UGM0_THEAN | Q6UGM0_theliera a | |
| 894 | 5 | 55.6 | 837 | 2 | Q8G518_BIFLO | Q8G518_bifidobacte | 966 | 5 | 55.6 | 991 | 2 | Q72SC6_LEPIC | Q72SC6_leptospira | |
| 895 | 5 | 55.6 | 841 | 1 | PSP1_YEAST | P50896_saccharomyc | 967 | 5 | 55.6 | 991 | 2 | Q8F398_LEPIN | Q8F398_leptospira | |
| 896 | 5 | 55.6 | 844 | 2 | Q4BCV2_BURVI | Q4BCV2_burkholderi | 968 | 5 | 55.6 | 994 | 2 | Q6CHE0_YARLI | Q6CHE0_yarrowia li | |
| 897 | 5 | 55.6 | 846 | 2 | Q7R2T7_GIALA | Q7R2T7_giardia lam | 969 | 5 | 55.6 | 1002 | 2 | Q8EFG0_SHEON | Q8EFG0_shevanella | |
| 898 | 5 | 55.6 | 849 | 2 | Q8ZTP7_PYRAE | Q8ZTP7_pyrobaculum | 970 | 5 | 55.6 | 1003 | 2 | Q9AHP2_9ACTO | Q9AHP2_arcanobacte | |
| 899 | 5 | 55.6 | 851 | 2 | Q81IE2_PLAP7 | Q81IE2_plasmodium | 971 | 5 | 55.6 | 1014 | 2 | Q4Q946_LEIMA | Q4Q946_leishmania | |
| 900 | 5 | 55.6 | 851 | 2 | Q44E08_CHRSL | Q44E08_chromohalob | 972 | 5 | 55.6 | 1019 | 2 | Q4Z9Z8_9CAUD | Q4Z9Z8_bacteriopho | |
| 901 | 5 | 55.6 | 855 | 2 | Q4CCN3_CLOIM | Q4CCN3_clostridium | 973 | 5 | 55.6 | 1019 | 2 | Q6Y7Q4_9CAUD | Q6Y7Q4_staphylococ | |
| 902 | 5 | 55.6 | 861 | 2 | Q3ZVJ3_SPIC1 | Q3ZVJ3_spiroplasma | 974 | 5 | 55.6 | 1019 | 2 | Q2FJW0_ENTFC | Q2FJW0_enterococcu | |
| 903 | 5 | 55.6 | 863 | 2 | Q3FQJ8_9BURK | Q3FQJ8_rhodoferax | 975 | 5 | 55.6 | 1022 | 2 | Q61907_CABEL | Q61907_caenorhabdi | |
| 904 | 5 | 55.6 | 864 | 1 | SYL_WIGER | Q8D333_wiggleswort | 976 | 5 | 55.6 | 1023 | 2 | Q2T7E3_BURTH | Q2T7E3_burkholderi | |
| 905 | 5 | 55.6 | 864 | 2 | Q2JG16_9ACTO | Q2JG16_franksia sp. | 977 | 5 | 55.6 | 1028 | 2 | Q5TML1_ANGOA | Q5TML1_anopheles g | |
| 906 | 5 | 55.6 | 865 | 2 | Q2M0U7_DROPS | Q2M0U7_drosophila | 978 | 5 | 55.6 | 1034 | 2 | Q6CKS6_KULUA | Q6CKS6_kluyveromyc | |
| 907 | 5 | 55.6 | 869 | 2 | Q755W6_ASHGO | Q755W6_ashbya goss | 979 | 5 | 55.6 | 1042 | 2 | Q6D806_ERWCT | Q6D806_erwinia car | |
| | | | | | | | | | | | 1044 | 2 | Q9ZH24_PSEAE | Q9ZH24_pseudomonas |

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981 5 55.6 1045 2 Q9RG59 PSEAE Q9RG59 pseudomonas
982 5 55.6 1046 2 Q5A115 CANAL Q5A115 candida alb
983 5 55.6 1046 2 Q2ZNG8 PSEAE Q2ZNG8 pseudomonas
984 5 55.6 1053 2 Q6FQAB CANGA Q6FQAB candida gia
985 5 55.6 1070 2 Q7R2W4 GIALA Q7R2W4 giardia lam
986 5 55.6 1071 2 Q2Z867 9GAMM Q2Z867 shewanella
987 5 55.6 1080 2 Q69PR5 ORYSA Q69PR5 oryza sativ
988 5 55.6 1083 2 Q43ZL3 SOLUS Q43ZL3 solibacter
989 5 55.6 1084 2 Q2KEZ1 MAGGR Q2KEZ1 magnaporthe
990 5 55.6 1088 2 Q6ZUM6 HUMAN Q6ZUM6 homo sapien
991 5 55.6 1104 2 Q7MZ50 PHOLL Q7MZ50 photorhabd
992 5 55.6 1108 2 Q4ESI0 LISMO Q4ESI0 listeria m
993 5 55.6 1113 2 Q511P5 ENTHI Q511P5 entamoeba h
994 5 55.6 1117 2 Q388R2 TRYYP Q388R2 trypanosoma
995 5 55.6 1138 2 Q4H7T0 9DEIO Q4H7T0 deinoxococcus
996 5 55.6 1144 2 Q54BG8 DICDI Q54BG8 dictyosteli
997 5 55.6 1144 2 Q54ZAI DICDI Q54ZAI dictyosteli
998 5 55.6 1144 2 Q55Z15 DICDI Q55Z15 dictyosteli
999 5 55.6 1144 2 Q55D49 DICDI Q55D49 dictyosteli
1000 5 55.6 1144 2 Q9GQ49 DICDI Q9GQ49 dictyosteli

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ALIGNMENTS

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RESULT 1
VHR2 CAMPM
ID VHR2 CAMPM STANDARD; PRT; 150 AA.
AC P68643; Q8V2Z8;
DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.
DT 07-DEC-2004, sequence version 1.
DE Probable host range protein 6.
GN OrderedLocusNames=CMV019;
OS Camelox virus (strain M-96).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=203173;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22031204; PubMed=1203760; DOI=10.1006/viro.2001.1343;
RA Alfonso C.L., Tulman E.R., Lu Z., Zsak L., Sandybaev N.T.,
RA Kerembekova U.Z., Zaitsev V.L., Kutish G.F., Rock D.L.;
RT "The genome of camelox virus.";
RL Virology 255:1-9(2002).
CC -!- FUNCTION: Plays a role for multiplication of the virus in
CC different cell types (By similarity).
CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
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-----
EMBL; AF438165; AAL73726.1; -; Genomic_DNA.
DR InterPro; IPR004967; Pox C7 F8A.
DR Pfam; PF03287; Pox C7 F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
FT CHAIN 1 150
FT SEQUENCE 150 AA; 18069 MW; 3D5557A68AF83D95 CRC64;
SQ
Query Match 100.0%; Score 9; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDTFYV 9
DB 74 KVDDTFYV 82
RESULT 2
VHR2 CAMPS
ID VHR2 CAMPS STANDARD; PRT; 150 AA.
AC P68642; Q8V2Z8;
DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.
DT 07-DEC-2004, sequence version 1.
DE Probable host range protein 2.
GN OrderedLocusNames=CMV19L;
OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=203172;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=9263813; PubMed=9601507; DOI=10.1006/viro.1998.9123;
RA Antoine G., Scheiflinger F., Dörner F., Falkner F.G.;
RA Submitt (APR-2004) to the EMBL/GenBank/DBJ databases.
RT "The complete genomic sequence of the modified vaccinia Ankara strain:
RT comparison with other orthopoxviruses.";
RL Virology 244:365-396(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Isolate Acambis 3000;
RA Esposito J.J., Frace M., Sammons S.A., Olsen-Rasmussen M.S.,
RA Osborne J., Khristova M., Wohlhueter R.M.;
RL Submitt (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays a role for multiplication of the virus in
CC different cell types (By similarity).
CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
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-----
EMBL; AF438165; AAL73726.1; -; Genomic_DNA.
DR InterPro; IPR004967; Pox C7 F8A.
DR Pfam; PF03287; Pox C7 F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
FT CHAIN 1 150
FT SEQUENCE 150 AA; 18069 MW; 3D5557A68AF83D95 CRC64;
SQ
Query Match 100.0%; Score 9; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDTFYV 9
DB 74 KVDDTFYV 82
RESULT 3
VHR2 VACCA
ID VHR2 VACCA STANDARD; PRT; 150 AA.
AC P68598; P17363; Q762Y7;
DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.
DT 07-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Host range protein 2.
GN OrderedLocusNames=MVA018L, ACAM3000_MVA_018;
OS Vaccinia virus (strain Ankara) (VACV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=126794;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=9263813; PubMed=9601507; DOI=10.1006/viro.1998.9123;
RA Antoine G., Scheiflinger F., Dörner F., Falkner F.G.;
RT "The complete genomic sequence of the modified vaccinia Ankara strain:
RT comparison with other orthopoxviruses.";
RL Virology 244:365-396(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Isolate Acambis 3000;
RA Esposito J.J., Frace M., Sammons S.A., Olsen-Rasmussen M.S.,
RA Osborne J., Khristova M., Wohlhueter R.M.;
RL Submitt (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays a role for multiplication of the virus in
CC different cell types (By similarity).
CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
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EMBL; AF438165; AAL73726.1; -; Genomic_DNA.
DR InterPro; IPR004967; Pox C7 F8A.
DR Pfam; PF03287; Pox C7 F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
FT CHAIN 1 150
FT SEQUENCE 150 AA; 18069 MW; 3D5557A68AF83D95 CRC64;
SQ
Query Match 100.0%; Score 9; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDTFYV 9
DB 74 KVDDTFYV 82

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DR EMBL; U94848; AAB96405.1; -; Genomic DNA.
DR EMBL; AY603355; AAT10416.1; -; Genomic DNA.
DR PIR; A33348; WZVZB1.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
KW Early protein.
FT CHAIN 1 150 Host range protein 2.
FT SEQUENCE 150 AA; 17999 MW; 47CDF841D563COA4 CRC64;
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563COA4 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
Db 74 KVDDTFYV 82

RESULT 4
VHR2_VACCC
ID VHR2_VACCC STANDARD; PRT; 150 AA.
AC P68599; P17363;
DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.
DT 07-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Host range protein 2.
DE ORFNames=C7L;
GN Vaccinia virus (strain Copenhagen) (VACV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10249;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=91021027; PubMed=2219723;
RA Goebel S.J., Johnson G.P., Perkins M.E., Winslow J.P.,
RA Paoletti E.;
RT "The complete DNA sequence of vaccinia virus.";
RL Virology 179:247-266(1990).
RN [2]
RP COMPLETE GENOME.
RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
RA Paoletti E.;
RT "Appendix to 'The complete DNA sequence of vaccinia virus'.";
RL Virology 179:517-563(1990).
CC -!- FUNCTION: Plays a role for multiplication of the virus in
CC different cell types (By similarity).
CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
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CC
DR EMBL; M35027; AAA47993.1; -; Genomic DNA.
DR PIR; A33348; WZVZB1.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
KW Early protein.
FT CHAIN 1 150 Host range protein 2.
FT SEQUENCE 150 AA; 17999 MW; 47CDF841D563COA4 CRC64;
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563COA4 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
Db 74 KVDDTFYV 82

RESULT 5
VHR2_VARY
ID VHR2_VARY STANDARD; PRT; 150 AA.
AC P33860;
DT 01-FEB-1994, integrated into UniProtKB/Swiss-Prot.

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VHR2_VACCV
ID VHR2_VACCV STANDARD; PRT; 150 AA.
AC P68600; P17363; Q76ZY7;
DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.
DT 07-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Host range protein 2.
DE OrderedLocNames=VACVOR21; ORFNames=C7L;
OS Vaccinia virus (strain Western Reserve / WR) (VACV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10254;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=89073756; PubMed=2849238;
RA Kotwal G.J., Moss B.;
RT "Analysis of a large cluster of nonessential genes deleted from a
RT vaccinia virus terminal transposition mutant.";
RL Virology 167:524-537(1988).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Esposito J.J., Frace A.M., Sammons S.A., Olsen-Rasmussen M.,
RA Osborne J., Wohlhueter R.;
RT "Sequencing of the coding region of Vaccinia-WR to an average 9-fold
RT redundancy and an error rate of 0.16/10kb.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION.
RX MEDLINE=91021030; PubMed=2171207;
RA Perkus M.E., Goebel S.J., Davis S.W., Johnson G.P., Limbach K.,
RA Norton E.K., Paoletti E.;
RT "Vaccinia virus host range genes.";
RL Virology 179:276-286(1990).
RN [4]
RP FUNCTION.
RX MEDLINE=93329391; PubMed=8336123;
RA Ogutlura N., Spehner D., Drilien R.;
RT "Detection of a protein encoded by the vaccinia virus C7L open reading
RT frame and study of its effect on virus multiplication in different
RT cell lines.";
RL J. Gen. Virol. 74:1409-1413(1993).
CC -!- FUNCTION: Plays a role for multiplication of the virus in
CC different cell types.
CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
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CC
DR EMBL; M22812; AAA69601.1; -; Genomic DNA.
DR EMBL; AY243312; AAO89300.1; -; Genomic DNA.
DR PIR; A33348; WZVZB1.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
KW Early protein.
FT CHAIN 1 150 Host range protein 2.
FT SEQUENCE 150 AA; 17999 MW; 47CDF841D563COA4 CRC64;
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563COA4 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
Db 74 KVDDTFYV 82

RESULT 6
VHR2_VARV
ID VHR2_VARV STANDARD; PRT; 150 AA.
AC P33860;
DT 01-FEB-1994, integrated into UniProtKB/Swiss-Prot.

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DT 01-FEB-1994, sequence version 1.
DE 07-FEB-2006, entry version 30.
DE Host range protein 2.
GN ORFNames=C7L, B15L, D8L;
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]_TaxID=10255;
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=India-1967 / isolate Ind3;
RX MEDLINE=93202281; PubMed=8384139; DOI=10.1016/0014-5793(93)80041-R;
RA Shchelkunov S.N., Blinov V.M., Sandakchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.";
RL FEBS Lett. 319:80-83(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=Bangladesh-1975;
RX MEDLINE=9408747; PubMed=8264798; DOI=10.1038/366748a0;
RA Massung R.F., Esposito J.J., Liu L.I., Qi J., Uterback T.R.,
RA Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
RA Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
RA Venter C.J.;
RT "Potential virulence determinants in terminal regions of variola
RT smallpox virus genome.";
RL Nature 366:748-751(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=Congo-1965, Garcia-1966, and Somalia-1977;
RA Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
RA Totmenin A.V., Shchelkunov S.N., Esposito J.J.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays a role for multiplication of the virus in
CC different cell types (By similarity).
CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
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CC
DR EMBL; X69198; CAA48949.1; -; Genomic DNA.
DR EMBL; L22579; AAA60756.1; -; Genomic DNA.
DR EMBL; U18340; AAA69419.1; -; Genomic DNA.
DR EMBL; U18337; AAA69313.1; -; Genomic DNA.
DR EMBL; U18338; AAA69354.1; -; Genomic DNA.
DR PIR; F72151; F72151.
DR PIR; H36837; H36837.
DR PIR; T28446; T28446.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
FT CHAIN 1 150 Host range protein 2.
FT /FTID=PRO_0000099389.
SQ SEQUENCE 150 AA; 18027 MW; 50FDF841C253CE94 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
DB 74 KVDDTFYV 82

RESULT 7
Q49QR1_9POXV PRELIMINARY; PRT; 150 AA.
AC Q49QR1;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein.
GN ORFNames=m8020L, m0020L;

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OS Vaccinia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10245;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=L16m8, and L16m0;
RX PubMed=16140764; DOI=10.1128/JVI.79.18.11873-11891.2005;
RA Morikawa S., Sakiyama T., Hasegawa H., Saijo M., Maeda A., Kurane I.,
RA Maeno G., Kimura J., Hirama C., Yoshida T., Asahi-Ozaki Y., Sata T.,
RA Kurata T., Kojima A.;
RT "An attenuated L16m8 smallpox vaccine: analysis of full-genome
RT sequence and induction of immune protection.";
RL J. Virol. 79:11873-11891(2005).
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CC
DR EMBL; AY678275; AAW23413.1; -; Genomic DNA.
DR EMBL; AY678277; AAW23695.1; -; Genomic DNA.
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
KW Hypothetical protein.
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
DB 74 KVDDTFYV 82

RESULT 8
Q6RZS8_9POXV PRELIMINARY; PRT; 150 AA.
AC Q6RZS8;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE RPXV013.
GN ORFNames=RPXV013;
OS Rabbitpox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=32606;
RN [1]_TaxID=32606;
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16227218; DOI=10.1099/vir.0.81331-0;
RA Li G., Chen N., Roper R.L., Feng Z., Hunter A., Danila M.,
RA Lefkowitz E.J., Buller R.M., Upton C.;
RT "Complete coding sequences of the rabbitpox virus genome.";
RL J. Gen. Virol. 86:2969-2977(2005).
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CC
DR EMBL; AY484669; AAS49726.1; -; Genomic DNA.
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
DB 74 KVDDTFYV 82

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Db          74 KVDDTFYV 82

RESULT 9
Q76066 VARV PRELIMINARY; PRT; 150 AA.
AC Q76066
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE B14L protein.
DE Name=B14L;
OS Variola minor virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=53258;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Garcia-1966;
RA Shchelkunov S.N., Totmenin A.V., Gutorov V.V., Safronov P.F.,
RA Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
RA Reposito J.J., Sosnovtsev S.;
RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL; Y16780; CAB54608.1; -; Genomic DNA.
GO; GO:0016032; P:Viral life cycle; IEA.
InterPro; IPR004967; Pox_C7_F8A.
Pfam; PF03287; Pox_C7_F8A; 1.
PIRSF; PIRSF003779; VAC_C7L; 1.
SQ SEQUENCE 150 AA; 18027 MW; 50DF841C253CE94 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
Db          74 KVDDTFYV 82

RESULT 10
Q760L6 COMPX PRELIMINARY; PRT; 150 AA.
AC Q760L6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE C13L protein.
DE Name=C13L;
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GRI-90;
RX MEDLINE=97068532; PubMed=8963248;
RA Safronov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V.,
RA Shchelkunov S.N., Sandakhchiev L.S.;
RA "Genes of a circle of hosts for the cowpox virus.";
RL Dokl. Akad. Nauk SSSR 349:829-833(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GRI-90;
RX MEDLINE=98229462; PubMed=9568042; DOI=10.1006/viro.1998.9039;
RA Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
RA Ryzankina O.I., Gutorov V.V., Kotwal G.J.;
RA "The genomic sequence analysis of the left and right species-specific
RT terminal region of a cowpox virus strain reveals unique sequences and
RT a cluster of intact ORFs for immunomodulatory and host range
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proteins.";
RL Virology 243:432-460(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GRI-90;
RA Shchelkunov S.N., Safronov P.F., Totmenin A.V., Miheev M.V.,
RA Ryzankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.J.,
RA Sandakhchiev L.S.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL; X94355; CAA64098.1; -; Genomic DNA.
GO; GO:0016032; P:Viral life cycle; IEA.
InterPro; IPR004967; Pox_C7_F8A.
Pfam; PF03287; Pox_C7_F8A; 1.
PIRSF; PIRSF003779; VAC_C7L; 1.
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
Db          74 KVDDTFYV 82

RESULT 11
Q77TN9 VACCT PRELIMINARY; PRT; 150 AA.
AC Q77TN9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE TC7L.
OS Vaccinia virus (strain Tian Tan) (VACV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10253;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Tian Tan;
RA Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang X.K.,
RA Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;
RA Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL; AF095689; AAF33872.1; -; Genomic DNA.
GO; GO:0016032; P:Viral life cycle; IEA.
InterPro; IPR004967; Pox_C7_F8A.
Pfam; PF03287; Pox_C7_F8A; 1.
PIRSF; PIRSF003779; VAC_C7L; 1.
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
Db          74 KVDDTFYV 82

RESULT 12
Q8JLI7 9POXV PRELIMINARY; PRT; 150 AA.
ID Q8JLI7_9POXV
AC Q8JLI7;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
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DT 07-FEB-2006, entry version 12.
DE SVM015.
GN Name=EVN015;
OS Ectromelia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=12643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Moscow;
RX MEDLINE=95266283; PubMed=7747448;
RA Moseman K., Upton C., Buller R.M., McFadden G.;
RT "Species specificity of ectromelia virus and vaccinia virus
interferon-gamma binding proteins.";
RL Virology 208:762-769(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Moscow;
RX MEDLINE=20192152; PubMed=10725549; DOI=10.1016/S0168-1702(99)00135-5;
RA Chen N., Buller R.M., Wall E.M., Upton C.;
RT "Analysis of host response modifier ORFs of ectromelia virus, the
causative agent of mousepox.";
RL Virus Res. 66:155-173(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Moscow;
RX MEDLINE=98154919; PubMed=9495531; DOI=10.1016/S0168-1702(97)00122-6;
RA Wall E.M., Cao J.X., Chen N., Buller R.M.L., Upton C.;
RT "A novel poxvirus gene and its human homolog are similar to an E. coli
lysophospholipase.";
RL Virus Res. 52:157-167(1997).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Moscow;
RX MEDLINE=98154919; PubMed=9495531; DOI=10.1016/S0168-1702(97)00122-6;
RA Wall E.M., Cao J.X., Chen N., Buller R.M.L., Wang C., Han X.,
Lefkowitz E., Upton C.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.
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CC -----
EMBL; AF012825; AAM92321.1; -; Genomic DNA.
DR GO; GO:0016032; P:viral life cycle; IEA.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
SQ SEQUENCE 150 AA; 18130 MW; 4DD4FC55F62422BE CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYV 9
Db 74 KVDDTFYV 82

RESULT 13
QBQN33_COMPX PRELIMINARY; PRT; 150 AA.
AC QBQN33;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE CPXV029 protein.
GN Name=CPXV029 CDS;
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Brighton Red;
```

```
RX MEDLINE=83117629; PubMed=6961398;
RA Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;
RT "Sequence of terminal regions of cowpox virus DNA: arrangement of
repeated and unique sequence elements.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Brighton Red;
RX MEDLINE=90177240; PubMed=2309453;
RA Parsons B.L., Pickup D.J.;
RT "Transcription of orthopoxvirus telomeres at late times during
infection.";
RL Virology 175:69-80(1990).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Brighton Red;
RX MEDLINE=91196263; PubMed=2014645;
RA Hu F.Q., Pickup D.J.;
RT "Transcription of the terminal loop region of vaccinia virus DNA is
initiated from the telomere sequences directing DNA resolution.";
RL Virology 181:716-720(1991).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Brighton Red;
RX MEDLINE=94378510; PubMed=8091665;
RA Hu F.Q., Smith C.A., Pickup D.J.;
RT "Cowpox virus contains two copies of an early gene encoding a soluble
secreted form of the type II TNF receptor.";
RL Virology 204:343-356(1994).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Brighton Red;
RA Dietrich F.S., Ray C.A., Sharma D.A., Allen A., Pickup D.J.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBSJ databases.
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CC -----
EMBL; AF482758; AAM13476.1; -; Genomic DNA.
DR GO; GO:0016032; P:viral life cycle; IEA.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
SQ SEQUENCE 150 AA; 17954 MW; 6B5C029714B02944 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYV 9
Db 74 KVDDTFYV 82

RESULT 14
QBQWIR3_ASPTU PRELIMINARY; PRT; 512 AA.
AC QBQWIR3;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-MAR-2006, entry version 6.
DE Possible beta-xylosidase, family 43 of glycosyl hydrolases.
GN ORFNames=Afu2g00930;
OS Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5085;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Af293 / CBS 101355 / FGSC A1100;
RX PubMed=16372009; DOI=10.1038/nature04332;
RA Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,
Arroyo J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,
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RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
 RA Farman M., Fedorova N.D., Fedorova N.D., Feldblyum T.V., Fischer R.,
 RA Fokker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
 RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,
 RA Haas H., Harris D.E., Horiuchi H., Huang J., Humphray S., Jimenez J.,
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Konack S.,
 RA Kulkarni R., Kumagai T., Lafton A., Latge J.P., Li W., Lord A.,
 Lu C., Majors W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,
 RA Monod M., Mouyina I., Mulligan S., Murphy L.D., O'Neill S., Paulsen I.,
 RA Penalta M., Perte M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabinowitsch E., Rawlins N., Rajandream M.A., Reichard U.,
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
 RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrell B.G., Denning D.W.,
 RA "Genomic sequence of the pathogenic and allergenic filamentous fungus
 RT *Aspergillus fumigatus*,"
 RL Nature 438:1151-1156(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC -----
 CC EMBL; AAH01000008; EAL87192.1; -; Genomic DNA.
 DR DR GO; GO:0016787; F:hydrolase activity; IEA_
 DR DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 KW Complete proteome; Hydrolase.
 SQ SEQUENCE 512 AA; 55648 MW; 5E174A037C55B830 CRC64;
 Query Match 77.8%; Score 7; DB 2; Length 512;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTFY 8
 Db 26 VDDTFY 32
 |||||
 [1]
 RESULT 15
 ID Q2U7D1 ASPOR PRELIMINARY; PRT; 515 AA.
 AC Q2U7D1;
 DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 24-JAN-2006, sequence version 1.
 DT 07-MAR-2006, entry version 3.
 DE Beta-xylosidase.
 GN ORFNames=AO090701000886;
 OS *Aspergillus oryzae*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.
 OX NCBI_TaxID=5062;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RIB 40;
 RX PubMed=16372010; DOI=10.1038/nature04300;
 RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,
 RA Horiuchi K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,
 RA Kusuuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
 RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,
 RA Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotch O., Horikawa H.,
 RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,
 RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
 RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
 RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
 RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
 RA Komori T., Kovama Y., Minetoki T., Suhanan S., Tanaka A., Isono K.,
 RA Kuwara S., Ogasawara N., Kikuchi H.;
 RT "Genome sequencing and analysis of *Aspergillus oryzae*,"

RL Nature 438:1157-1161(2005).
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 CC -----
 CC EMBL; AP007164; BA662534.1; -; Genomic DNA.
 SQ SEQUENCE 515 AA; 56635 MW; 3EDFD2B09FF52176 CRC64;
 Query Match 77.8%; Score 7; DB 2; Length 515;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTFY 8
 Db 39 VDDTFY 45
 |||||
 [1]
 RESULT 16
 ID P73845 SYN3 PRELIMINARY; PRT; 770 AA.
 AC P73845;
 DT 01-FEB-1997, integrated into UniProtKB/TrEMBL.
 DT 01-FEB-1997, sequence version 1.
 DT 07-FEB-2006, entry version 26.
 DE S111608 protein.
 DE S111608 protein.
 GN OrderedLocusNames=s111608;
 OS *Synechocystis* sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; *Synechocystis*.
 OX NCBI_TaxID=1148;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=97061201; PubMed=8905231; DOI=10.1093/dnares/3.3.109;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hikosawa M., Sugita M., Sugita M., Saito S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
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 CC -----
 CC EMBL; BA000022; BAA17904.1; -; Genomic DNA.
 DR PIR; S75042; S75042.
 DR BioCyc; SSP1148:SL11608-MONOMER; -.
 DR InterPro; IPR002931; Trnsglutase like.
 DR Pfam; PF01841; Transglut_core; 1.
 DR SMART; SM00460; Tgc; 1.
 KW Complete proteome.
 SQ SEQUENCE 770 AA; 87815 MW; F58C2EA34EC8873C CRC64;
 Query Match 77.8%; Score 7; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTFY 8
 Db 286 VDDTFY 292
 |||||
 [1]
 RESULT 17
 ID Q8VUM8 STAHO PRELIMINARY; PRT; 103 AA.
 AC Q8VUM8;
 DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2002, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE ORF19.
 OS *Staphylococcus hominis*.
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.

```

OX NCBI_TaxID=1290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=GI/FU12263;
RC MEDLINE=22586405; PubMed=12700250;
RX DOI=10.1128/JB.185.9.2711-2722.2003;
RA Kobayashi Y., Takeuchi F., Ito T., Ma X.X., Ui-Mizutani Y.,
RA Kobayashi I., Hiramatsu K.;
RT "Identification in methicillin-susceptible Staphylococcus hominis of
RT an active primordial mobile genetic element for the staphylococcal
RT cassette chromosome mec of methicillin-resistant Staphylococcus
RT aureus";
RL J. Bacteriol. 185:2711-2722(2003).
CC
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CC -----
CC EMBL; AB063171; BAB83490.1; -; Genomic_DNA.
DR InterPro; IPR009303; DUF960_STA_app.
DR Pfam; PF06124; DUF960; 1.
SQ SEQUENCE 103 AA; 12599 MW; 13194326CCE4617D CRC64;

Query Match 66.7%; Score 6; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
DB 91 DTFYV 96
|||||

RESULT 18
Q38248 9CAUD PRELIMINARY; PRT; 126 AA.
ID Q38248_9CAUD PRELIMINARY; PRT; 126 AA.
AC Q38248;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE DNA polymerase subunit.
OS Lactococcus phage bIL67.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC c2-like viruses.
OX NCBI_TaxID=36343;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95111629; PubMed=7812447;
RA Schouler C., Ehrlich S.D., Chopin M.C.;
RT "Sequence and organization of the lactococcal prolate-headed bIL67
RT phage genome.";
RL Microbiology 140:3061-3069(1994).
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CC -----
CC EMBL; L33769; AAA74342.1; -; Genomic_DNA.
SQ SEQUENCE 126 AA; 14843 MW; 1768C9622ED7749B CRC64;

Query Match 66.7%; Score 6; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDTTF 6
DB 100 KVDTTF 105
|||||

RESULT 19
Q5A2T5 CANAL PRELIMINARY; PRT; 176 AA.
ID Q5A2T5 CANAL PRELIMINARY; PRT; 176 AA.
AC Q5A2T5;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
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DE Hypothetical protein.
GN ORFNames=CaO19.2181, CaO19.9727;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=SC5314;
RC PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL; AACQ01000075; EAK97013.1; -; Genomic_DNA.
DR EMBL; AACQ01000076; EAK96954.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 176 AA; 19448 MW; D04B9BE79CA86853 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 117 VDDTFY 122
|||||

RESULT 20
RAS3 RHIRA
ID _RAS3 RHIRA STANDARD; PRT; 205 AA.
AC P22280;
DT 01-AUG-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1991, sequence version 1.
DT 07-MAR-2006, entry version 37.
DE Ras-like protein 3.
GN Name=RAS3;
OS Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC Mucor.
OX NCBI_TaxID=4841;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX STRAIN=ATCC 1216B; PubMed=1701021;
RA Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;
RT "Expression of a gene family in the dimorphic fungus Mucor racemosus
RT which exhibits striking similarity to human ras genes.";
RL Mol. Cell. Biol. 10:6654-6663(1990).
CC -!- ENZYME REGULATION: Alternate between an inactive form bound to GDP
CC and an active form bound to GTP. Activated by a guanine
CC nucleotide-exchange factor (GEF) and inactivated by a GTPase-
CC activating protein (GAP).
CC -!- SUBCELLULAR LOCATION: Cell membrane; lipid-anchor.
CC -!- DEVELOPMENTAL STAGE: In sporulating mycelium and much less in
CC germling and yeast.
CC -!- SIMILARITY: Belongs to the small GTPase superfamily. Ras family.
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CC -----
CC EMBL; M55177; AAA83379.1; -; Genomic_DNA.
DR PIR; C36365; C36365.
DR HSSP; P01112; 1PLL.
DR InterPro; IPR003579; GTPase_Rab.
```

DE ENSANGP00000029666.
GN ORFNames=ENSANGG00000022851;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
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CC -----
CC EMBL; AAAB01008962; EAL39783.1; -; Genomic_DNA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00628; PHD; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
DR SEQUENCE 232 AA; 25290 MW; 78A98241F2283718 CRC64;
Qy Query Match 66.7%; Score 6; DB 2; Length 232;
Db Best Local Similarity 100.0%; Pred.No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 2 VDDTFY 7
Db 16 VDDTFY 21
|||||

RESULT 23
Q9CAE4 ARATH
ID Q9CAE4 ARATH PRELIMINARY; PRT; 261 AA.
AC Q9CAE4;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein F13M14.33 (At3g10400).
GN Name=F13M14.33; OrderedLocusNames=At3g10400;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsi
NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Town C.D., Kaul S.;
RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC Shinn P., Chen H., Cheuk R., Kim C.J., Ecker J.R.;
RA "Arabidopsis cDNA clones."
RT "Arabidopsis cDNA clones."


```
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Kim C.-J., Chen H., Cheuk R., Shinn P., Ecker J.R.;
RT "Arabidopsis ORF clones.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AC011560; AAG51392.1; -; Genomic DNA.
DR EMBL; BT015938; AAV31168.1; -; mRNA.
DR EMBL; BT021922; AAX49371.1; -; mRNA.
DR HSSP; O08583; 1N08.
DR TAIR; At3g10400; -.
DR GO; GO:0046872; F-metal ion binding; IEA.
DR GO; GO:0003676; F-nucleic acid binding; IEA.
DR GO; GO:0001666; F-nucleotide binding; IEA.
DR GO; GO:0008270; F-zinc ion binding; IEA.
DR InterPro; IPR012677; a_b_plait_nuc_bd.
DR InterPro; IPR000504; RNPI_RNA_bd.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00076; RRM_1; 1.
DR Pfam; PF00098; ZF_CCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00360; RRM; 1.
DR SMART; SM00343; Znf_C2HC; 1.
DR PROSITE; PS0102; RRM; 1.
DR PROSITE; PS0158; ZF_CCHC; 1.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 261 AA; 29367 MW; 4A3767C92819D22 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFFY 8
DB 14 DDTFFY 19

RESULT 24
Q2NEH9_9EURY PRELIMINARY; PRT; 298 AA.
AC Q2NEH9.
DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DT 07-FEB-2006, entry version 1.
DE CofD.
GN Name=CofD; ORFName=Msp 1403;
OS Methanospaera stadmanae DSM 3091.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanospaera.
OX NCBI_TaxID=339860;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 3091;
RX PubMed=16385054; DOI=10.1128/JB.188.2.642-658.2006;
RA Fricke W.F., Seedorf H., Henne A., Krueer M., Liesegang H.,
RA Hedderich R., Gottschalk G., Thauer R.K.;
RT "The Genome Sequence of Methanospaera stadmanae Reveals Why This
RT Human Intestinal Archaeon Is Restricted to Methanol and H2 for Methane
RT Formation and ATP Synthesis.";
RL J. Bacteriol. 188:642-658(2006).
CC -----
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CC -----
DR EMBL; CP000102; ABC57774.1; -; Genomic DNA.
SQ SEQUENCE 298 AA; 33234 MW; FF70D402A75C4C8 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 68 VDDTFY 73

RESULT 25
Q4K6A8_PSEF5 PRELIMINARY; PRT; 311 AA.
AC Q4K6A8;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Transcriptional regulator, MerR family.
GN OrderedLocNames=PFL_5146;
OS Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C.M., Ravel J., Kobayashi D.Y., Myers G.S.A.,
RA Mavrodi D.V., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin A.S., Brinkac L.M., Daugherty S.C., Sullivan S.A.,
RA Rosovitz M.J., Gwinn M.B., Zhou L., Schneider D.J., Cartinhour S.W.,
RA Nelson W.C., Weidman J., Thomasow L.S., Loper J.E.;
RT Pierson L.S. III, Thomashow L.S., Loper J.E.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5.";
RL Nat. Biotechnol. 23:873-878(2005).
CC -----
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CC -----
DR EMBL; CP000076; AAY94368.1; -; Genomic DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000551; HTH_MerR.
DR Pfam; PF00376; MerR; 1.
DR SMART; SM00422; HTH_MER; 1.
DR PROSITE; PS0937; HTH_MER_2; 1.
KW Complete proteome; DNA-binding.
SQ SEQUENCE 311 AA; 34959 MW; AB8C46F939674EFF CRC64;

Query Match 66.7%; Score 6; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTF 6
DB 122 KVDDTF 127

RESULT 26
Q6DB07_ERWCT PRELIMINARY; PRT; 330 AA.
AC Q6DB07.
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Putative membrane protein.
GN OrderedLocNames=ECA0095;
OS Erwinia carotovora subsp. atroseptica (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
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RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Akin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmund G.P.C., Birch P.R.J., Parkhill J., Toth I.K.,
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
CC -----
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CC -----
CC EMBL; BX950851; CAG73015.1; -; Genomic DNA.
DR GO; GO:0016747; F:transferase activity, transferring groups o. .; IEA.
DR InterPro; IPR002656; Acyl_transf_3.
DR Pfam; PF01757; Acyl_transf_3; 1.
KW Complete proteome.
SQ SEQUENCE 330 AA; 36965 MW; D8F8B183D34D1D09 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
DB 179 DTFYV 184
|||||

RESULT 27
Q5WC87_BACSK PRELIMINARY; PRT; 376 AA.
ID Q5WC87;
AC Q5WC87;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Hypothetical protein.
GN OrderedLocNames=ABC3490;
OS Bacillus clausii (strain KSM-K16).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=66692;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Takaki Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,
RA Kawai S., Ito S., Horiuchi K.;
RT "The complete genome sequence of the alkaliphilic Bacillus clausii
RT KSM-K16.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AP006627; BAD66023.1; -; Genomic DNA.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 376 AA; 42123 MW; FC8A63EA03CD4362 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 172 VDDTFY 177
|||||

RESULT 28
Q5WX32_LEGPL PRELIMINARY; PRT; 399 AA.
ID Q5WX32;
AC Q5WX32;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.

```

```

DE Tryptophan synthase beta subunit.
GN Name-trpB; OrderedLocNames=lp11267;
OS Legionella pneumophila (strain Lens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297245;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
CC -----
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CC -----
CC EMBL; CR628337; CAH15507.1; -; Genomic DNA.
DR Legiolist; lp11267; -
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004834; F:tryptophan synthase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006568; P:tryptophan metabolism; IEA.
DR InterPro; IPR001926; B6 enzyme beta.
DR InterPro; IPR006653; Trp synth_b rel.
DR Pfam; PF00291; PALP; 1.
DR TIGRFAMs; TIGR00263; trpB; 1.
DR PROSITE; PS00168; TRP SYNTHASE_BETA; 1.
KW Complete proteome; Pyridoxal phosphate.
SQ SEQUENCE 399 AA; 43301 MW; 25720A677000BAA0 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 186 VDDTFY 191
|||||

RESULT 29
Q5X5Q2_LEGPA PRELIMINARY; PRT; 399 AA.
ID Q5X5Q2;
AC Q5X5Q2;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Tryptophan synthase beta subunit.
GN Name-trpB; OrderedLocNames=lp1268;
OS Legionella pneumophila (strain Paris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297246;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
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CC -----
CC EMBL; CR628336; CAH12419.1; -; Genomic DNA.
DR Legiolist; lp1268; -
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004834; F:tryptophan synthase activity; IEA.

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DR GO: GO:0008152; P:metabolism; IEA.
DR GO: GO:0006568; P:tryptophan metabolism; IEA.
DR InterPro: IPR001926; B6_enzyme_beta.
DR InterPro: IPR006653; Trp_synth_beta.
DR InterPro: IPR006654; Trp_synth_beta.
DR Pfam: PF00291; PALP; 1.
DR TIGRFAMs: TIGR00263; trpB; 1.
DR PROSITE: PS00168; TRP SYNTHASE BETA; 1.
KW Complete proteome; Pyridoxal phosphate.
SQ SEQUENCE 399 AA; 43301 MW; 25720A677000BAA0 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 186 VDDTFY 191

RESULT 30
ID Q5ZVY4_LEGPH PRELIMINARY; PRT; 399 AA.
AC Q5ZVY4;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Tryptophan synthetase, beta subunit (EC 4.2.1.20).
GN OrderedLocNames=lp31304;
OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=272624;

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15448271; DOI=10.1126/science.1099776;
RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA Asanani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,
RA Steshenko V., Park S.H., Zhao B., Teplickaya E., Edwards J.R.,
RA Pampou S., Georgiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
RA Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
RA Segal G., Qu X., Rzhetsky A., Zhang P., Cayanis E., De Jong P.J.,
RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
RT "The genomic sequence of the accidental pathogen Legionella pneumophila.";
RL Science 305:1966-1968(2004).

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CC -----
DR EMBL: AE017354; AAU27387.1; -; Genomic_DNA.
DR GO: GO:0016829; F:lyase activity; IEA.
DR GO: GO:0004834; F:tryptophan synthase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR GO: GO:0006568; P:tryptophan metabolism; IEA.
DR InterPro: IPR001926; B6_enzyme_beta.
DR InterPro: IPR006653; Trp_synth_beta.
DR Pfam: PF00291; PALP; 1.
DR TIGRFAMs: TIGR00263; trpB; 1.
DR PROSITE: PS00168; TRP SYNTHASE BETA; 1.
KW Complete proteome; Lyase; Pyridoxal phosphate.
SQ SEQUENCE 399 AA; 43300 MW; E5BFCB1A797BE32 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 186 VDDTFY 191

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RESULT 31
TRPB_NEIGO
ID TRPB_NEIGO STANDARD; PRT; 400 AA.
AC Q84GT9;
DT 22-AUG-2003, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Tryptophan synthase beta chain (EC 4.2.1.20).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;

RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=MS11;
RA Jose J., Otto G.W., Meyer T.F.;
RT "Integration site of the Iga gene in commensal Neisseria sp.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: The beta subunit is responsible for the synthesis of L-tryptophan from indole and L-serine.
CC -!- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate = L-tryptophan + glyceraldehyde 3-phosphate.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate; step 5 [final step].
CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By similarity).
CC -!- SIMILARITY: Belongs to the trpB family.

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CC -----
DR EMBL: AY165022; AAG65176.1; -; Genomic_DNA.
DR HSSP: P00933; 2WSV.
DR HAMAP: MP_00133; -; 1.
DR InterPro: IPR001926; B6_enzyme_beta.
DR InterPro: IPR006653; Trp_synth_beta.
DR Pfam: PF00291; PALP; 1.
DR TIGRFAMs: TIGR00263; trpB; 1.
DR PROSITE: PS00168; TRP SYNTHASE BETA; 1.
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Lyase;
KW Pyridoxal phosphate; Tryptophan biosynthesis.
FT CHAIN 1 400 Tryptophan synthase beta chain.
FT BINDING 92 92 Pyridoxal phosphate (covalent) (By similarity).
FT SEQUENCE 400 AA; 43549 MW; 3765C02F97627ACA CRC64;

Query Match 66.7%; Score 6; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 186 VDDTFY 191

RESULT 32
TRPB_NEIMA
ID TRPB_NEIMA STANDARD; PRT; 400 AA.
AC Q9JVC0;
DT 19-OCT-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2000, sequence version 1.
DT 07-MAR-2006, entry version 28.
DE Tryptophan synthase beta chain (EC 4.2.1.20).
GN Name=trpB; OrderedLocNames=NNA0904;
OS Neisseria meningitidis serogroup A.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;

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RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Baaham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moulé S., Murgall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491."
RL Nature 404:502-506(2000).
CC
CC -I- FUNCTION: The beta subunit is responsible for the synthesis of L-
CC tryptophan from indole and L-serine.
CC -I- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate
CC = L-tryptophan + glyceraldehyde 3-phosphate.
CC -I- COFACTOR: Pyridoxal phosphate (By similarity).
CC -I- PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-
CC tryptophan from chorismate; step 5 [final step].
CC -I- SUBUNIT: Tetramer of two alpha and two beta chains (By
CC similarity).
CC -I- SIMILARITY: Belongs to the trpB family.
CC
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CC
CC EMBL; AL162754; CAB84181.1; -; Genomic_DNA.
CC PIR; H81936; H81936.
CC HSSP; P00933; 2WSY.
CC GenomeReviews; AL157959 GR; NMA0904.
CC BioCyc; NMEN65699:NMA0904-MONOMER; -.
CC HAMAP; MF_00133; -; 1.
CC InterPro; IPR001926; B6 enzyme beta.
CC InterPro; IPR006653; Trp synth_b rel.
CC Pfam; PF00291; PALP; 1.
CC TIGRFAMs; TIGR00263; trpB; 1.
CC PROSITE; PS00168; TRP SYNTHASE BETA; 1.
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW Complete proteome; Lyase; Pyridoxal phosphate;
KW Tryptophan biosynthesis.
FT CHAIN 1 400 Tryptophan synthase beta chain.
FT BINDING 92 92 /FTID=PRO_0000098972.
FT FT Pyridoxal phosphate (covalent) (By
FT similarity).
SQ SEQUENCE 400 AA; 43193 MW; 82001AE125A99F80 CRC64;

Query Match 66.7%; Score 6; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
Db 186 VDDTFY 191

RESULT 33
TRPB_NEIMB
ID TRPB_NEIMB STANDARD; PRT; 400 AA.
AC Q9K05;
DT 19-OCT-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2000, sequence version 1.
DT 07-MAR-2006, entry version 29.
DE Tryptophan synthase beta chain (EC 4.2.1.20).
GN Name-trpB; OrderedLocNames=NMB0699;
OS Neisseria meningitidis serogroup B.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
[1]
RN STRAIN=MC58 / Serogroup B;
RC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

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RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.P., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.P.,
RA Dickson E.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Cittiore H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Massignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
CC
CC -I- FUNCTION: The beta subunit is responsible for the synthesis of L-
CC tryptophan from indole and L-serine.
CC -I- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate
CC = L-tryptophan + glyceraldehyde 3-phosphate.
CC -I- COFACTOR: Pyridoxal phosphate (By similarity).
CC -I- PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-
CC tryptophan from chorismate; step 5 [final step].
CC -I- SUBUNIT: Tetramer of two alpha and two beta chains (By
CC similarity).
CC -I- SIMILARITY: Belongs to the trpB family.
CC
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CC
CC EMBL; AE002098; NAF41116.1; -; Genomic_DNA.
CC PIR; B81169; B81169.
CC HSSP; P00933; 2WSY.
CC GenomeReviews; AE002098 GR; NMB0699.
CC TIGR; NMB0699; -.
CC BioCyc; NMEN491:NMB0699-MONOMER; -.
CC HAMAP; MF_00133; -; 1.
CC InterPro; IPR001926; B6 enzyme beta.
CC InterPro; IPR006653; Trp synth_b rel.
CC Pfam; PF00291; PALP; 1.
CC TIGRFAMs; TIGR00263; trpB; 1.
CC PROSITE; PS00168; TRP SYNTHASE BETA; 1.
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW Complete proteome; Lyase; Pyridoxal phosphate;
KW Tryptophan biosynthesis.
FT CHAIN 1 400 Tryptophan synthase beta chain.
FT BINDING 92 92 /FTID=PRO_0000098973.
FT FT Pyridoxal phosphate (covalent) (By
FT similarity).
SQ SEQUENCE 400 AA; 43209 MW; 86FCC42EF6F64210 CRC64;

Query Match 66.7%; Score 6; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
Db 186 VDDTFY 191

RESULT 34
QSF9W3_NEIG1
ID QSF9W3_NEIG1 PRELIMINARY; PRT; 400 AA.
AC QSF9W3;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Putative tryptophan synthase.
GN OrderedLocNames=NGO0274;
OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=242231;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

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RA Lewis L.A., Gillaespy A.F., McLaughlin R.E., Gipson M., Ducey T.F.,
RA Ownbey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
RA Song L., Lin S., Xuan X., Najjar P., Zhan M., Ren Q., Zhu H., Qi S.,
RA Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
RT "The complete genome sequence of Neisseria gonorrhoeae.";
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; A5004969; AAW89024.1; -; Genomic DNA.
DR GO; GO:0016829; Flyase activity; IEA.
DR GO; GO:0004834; F:tryptophan synthase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006568; P:tryptophan metabolism; IEA.
DR InterPro; IPR001926; B6_enzyme_beta.
DR InterPro; IPR006653; Trp_synth_b_rel.
DR InterPro; IPR006654; Trp_synth_beta.
DR Pfam; PF00291; PALP; 1.
DR TIGRFAMs; TIGR00263; trpB; 1.
DR PROSITE; PS00168; TRP_SYNTHASE_BETA; 1.
KW Complete proteome; Lyase; Pyridoxal phosphate.
SQ SEQUENCE 400 AA; 43459 MW; C31E408696C60AE7 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 186 VDDTFY 191

RESULT 35
Q31HH4 THICR PRELIMINARY; PRT; 401 AA.
ID Q31HH4;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, entry version 1.
DE Tryptophan synthase, beta subunit.
GN ORFNames=trc_0803;
OS Thiomicrospira crunogena (strain XCL-2).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales;
OC Piscirickettsiaceae; Thiomicrospira.
OX NCBI_TaxID=317025;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=XCL-2;
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Chain P., Malfatti S., Shin M.,
RA Vergez L., Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A.,
RA Richardson P.;
RT "Complete sequence of Thiomicrospira crunogena XCL-2.";
RT Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CP000109; ABB41399.1; -; Genomic DNA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004834; F:tryptophan synthase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006568; P:tryptophan metabolism; IEA.
DR Pyridoxal phosphate.
SQ SEQUENCE 401 AA; 43363 MW; A98F7BF3778EDC2B CRC64;

Query Match 66.7%; Score 6; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 186 VDDTFY 191

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DB 188 VDDTFY 193

RESULT 36
Q44BZ8 CHRSL PRELIMINARY; PRT; 404 AA.
ID Q44BZ8;
AC Q44BZ8;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Tryptophan synthase, beta chain.
GN ORFNames=cealDRAFT_0124;
OS Chromohalobacter salexigens DSM 3043.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
OC Halomonadaceae; Chromohalobacter.
OX NCBI_TaxID=290398;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 3043;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Chromohalobacter
RT salexigens DSM 3043.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 3043;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Chromohalobacter
RT salexigens DSM 3043.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAH201000035; EAM22248.1; -; Genomic DNA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004834; F:tryptophan synthase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006568; P:tryptophan metabolism; IEA.
DR InterPro; IPR001926; B6_enzyme_beta.
DR InterPro; IPR006653; Trp_synth_b_rel.
DR InterPro; IPR006654; Trp_synth_beta.
DR Pfam; PF00291; PALP; 1.
DR TIGRFAMs; TIGR00263; trpB; 1.
DR PROSITE; PS00168; TRP_SYNTHASE_BETA; 1.
KW Pyridoxal phosphate.
SQ SEQUENCE 404 AA; 43777 MW; FECB7C0B2BD168AE CRC64;

Query Match 66.7%; Score 6; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 190 VDDTFY 195

RESULT 37
Q604P3 METCA PRELIMINARY; PRT; 405 AA.
ID Q604P3 METCA;
AC Q604P3;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Tryptophan synthase, beta subunit (EC 4.2.1.20).
GN Name=trpB; OrderedLocusNames=MCA2495;

```


FT CHAIN 1 409 Tryptophan synthase beta chain.
 FT FTID=PRO_0000098984.
 FT BINDING 95 95 Pyridoxal_phosphate (covalent) (By
 FT similarity).
 SQ SEQUENCE 409 AA; 44542 MW; D6311A4BB6C9BABF CRC64;

Query Match 66.7%; Score 6; DB 1; Length 409;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 |||||
 Db 189 VDDTFY 194

RESULT 40

TRPB_PSESM
 ID TRPB_PSESM STANDARD; PRT; 409 AA.
 AC Q88B61;
 DT 31-OCT-2003, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-2003, sequence version 1.
 DT 07-MAR-2006, entry version 21.
 DE Tryptophan synthase beta chain (EC 4.2.1.20).
 GN Name=trpB; OrderedLocusNames=PSPT00158;
 OS Pseudomonas syringae pv. tomato.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=323;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=DC3000;
 RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
 RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
 RA Gwin M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
 RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
 RA Nelson W.C., Davidson T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
 RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
 RA Unterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
 RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
 RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
 RA Bender C.L., White O., Fraser C.M., Collmer A.;
 RT "The complete genome sequence of the Arabidopsis and tomato pathogen
 Pseudomonas syringae pv. tomato DC3000."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
 CC -!- FUNCTION: The beta subunit is responsible for the synthesis of L-
 tryptophan from indole and L-serine.
 CC -!- CATALYTIC ACTIVITY: L-serine + L-(indol-3-yl)glycerol 3-phosphate
 = L-tryptophan + glyceraldehyde 3-phosphate.
 CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -!- PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-
 tryptophan from chorismate; step 5 [final step].
 CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By
 similarity).
 CC -!- SIMILARITY: Belongs to the trpB family.
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EMBL; AE016853; AA053712.1; -; Genomic_DNA.

HSSP; P00933; 2WSY.

GenomeReviews; AE016853_GR; PSPT00158.

TIGR; PSPT00158; -.

BioCyc; PSYR223283:PSPT00158-MONOMER; -.

HMAP; MF_00133; -; 1.

InterPro; IPR001926; B6_enzyme_beta.

InterPro; IPR006653; Trp_synth_b_rel.

InterPro; IPR006654; Trp_synth_beta.

Pfam; PF00291; PALP; 1.

TIGRFAMs; TIGR00263; trpB; 1.

PROSITE; PS00168; TRP_SYNTHASE_BETA; 1.

KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;

KW Complete proteome; Lyase; Pyridoxal phosphate;

KW Tryptophan biosynthesis.

FT CHAIN 1 409 Tryptophan synthase beta chain.
 FT FTID=PRO_0000098985.
 FT BINDING 95 95 Pyridoxal_phosphate (covalent) (By
 FT similarity).
 SQ SEQUENCE 409 AA; 44547 MW; 25A56962380CC284 CRC64;

Query Match 66.7%; Score 6; DB 1; Length 409;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 |||||
 Db 189 VDDTFY 194

RESULT 41

Q48QG6_PSE14
 ID Q48QG6_PSE14 PRELIMINARY; PRT; 409 AA.
 AC Q48QG6;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE Tryptophan synthase, beta subunit.
 GN Name=trpB; OrderedLocusNames=PSPPH_0036;
 OS Pseudomonas syringae pv. phaseolicola (strain 1448A / Race 6).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=264730;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=16159782; DOI=10.1128/JB.187.18.6488-6498.2005;
 RA Joardar V., Lindeberg M., Jackson R., Selengut J., Dodson R.,
 RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gwin M.L., Madupu R., Nelson W.C., Rosovitz M.J., Sullivan S.A.,
 RA Crabtree J., Creasy T., Davidson T.M., Haft D.H., Zafar N., Zhou L.,
 RA Halpin R., Holley T., Khouri H.M., Feldblyum T.V., White O.,
 RA Fraser C.M., Chatterjee A.K., Cartinhour S., Schneider D.,
 RA Mansfield J., Collmer A., Buell R.;
 RT "Whole-genome sequence analysis of Pseudomonas syringae pv.
 phaseolicola 1448A reveals divergence among pathogens in genes
 involved in virulence and transposition."
 RL J. Bacteriol. 187:6488-6498(2005).
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EMBL; CP000058; AA234189.1; -; Genomic DNA.

DR GO; GO:0016829; F:lyase activity; IEA.

DR GO; GO:0004834; F:tryptophan synthase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR GO; GO:0006588; P:tryptophan metabolism; IEA.

DR InterPro; IPR001926; B6_enzyme_beta.

DR InterPro; IPR006653; Trp_synth_b_rel.

DR InterPro; IPR006654; Trp_synth_beta.

DR Pfam; PF00291; PALP; 1.

DR TIGRFAMs; TIGR00263; trpB; 1.

DR PROSITE; PS00168; TRP_SYNTHASE_BETA; 1.

KW Complete proteome; Lyase; Pyridoxal phosphate.

SQ SEQUENCE 409 AA; 44516 MW; C2604B0EA298BFA CRC64;

Query Match 66.7%; Score 6; DB 2; Length 409;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 |||||
 Db 189 VDDTFY 194

RESULT 42

Q500R4_PSEU2
 ID Q500R4_PSEU2 PRELIMINARY; PRT; 409 AA.
 AC Q500R4;

DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DE 07-FEB-2006, entry version 8.
GN TrpTryptophan synthase, beta chain (EC 4.2.1.20).
OS Pseudomonas syringae pv. syringae (strain B728a).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205918;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16043691; DOI=10.1073/pnas.0504930102;
RA Feil H., Feil W.S., Chain P., Larimer F., Dibartolo G., Copeland A.,
RA Lykidis A., Trong S., Nolan M., Goldsman E., Thiel J., Malfatti S.,
RA Loper J.E., Lapidus A., Detter J.C., Land M., Richardson P.M.,
RA Kyriakides N.C., Ivanova N., Lindow S.E.;
RT "Comparison of the complete genome sequences of Pseudomonas syringae
pv. syringae B728a and pv. tomato DC3000".
RL Proc. Natl. Acad. Sci. U.S.A. 102:11064-11069(2005).
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CC
CC EMBL; CP000075; AAY35108.1; -; Genomic DNA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0004834; P:tryptophan synthase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006568; P:tryptophan metabolism; IEA.
DR InterPro; IPR001926; B6 enzyme beta.
DR InterPro; IPR006653; Trp_synth_beta.
DR InterPro; IPR006654; Trp_synth_beta.
DR Pfam; PF00291; PALP; 1.
DR TIGRFAMs; TIGR00263; trpB; 1.
DR PROSITE; PS00168; TRP SYNTHASE BETA; 1.
DR PROSITE; PS00168; TRP SYNTHASE BETA; 1.
KW Complete proteome; Lyase; Pyridoxal phosphate.
SQ SEQUENCE 409 AA; 44452 MW; D6B775F530D7E4B CRC64;
Query Match 66.7%; Score 6; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTFY 7
Db 189 VDDTFY 194
RESULT 43
ID Q2SJD1_9GAMM PRELIMINARY; PRT; 410 AA.
AC Q2SJD1;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DE 07-MAR-2006, entry version 3.
DE Tryptophan synthase, beta subunit (EC 4.2.1.20).
GN Name=trpB1; ORFNames=HCH_02436;
OS Haemella chejuensis KCTC 2396.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
OC Haemellaceae; Haemella.
OX NCBI_TaxID=349521;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KCTC 2396;
RX PubMed=16352867; DOI=10.1093/nar/gki1016;
RA Jeong H., Yim J.H., Lee C., Choi S.-H., Park Y.K., Yoon S.H.,
RA Hur C.-G., Kang H.-Y., Kim D., Lee H.H., Park K.H., Park S.-H.,
RA Park H.-S., Lee H.K., Oh T.K., Kim J.P.;
RT "Genomic blueprint of Haemella chejuensis, a marine microbe producing
an algicidal agent".
RL Nucleic Acids Res. 33:7066-7073(2005).
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CC

DR EMBL; CP000155; ABC29243.1; -; Genomic DNA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Lyase; Pyridoxal phosphate.
SQ SEQUENCE 410 AA; 45093 MW; 2389625857C5E998 CRC64;
Query Match 66.7%; Score 6; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTFY 7
Db 197 VDDTFY 202
RESULT 44
ID Q352W5_9GAMM PRELIMINARY; PRT; 411 AA.
AC Q352W5;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DE 07-MAR-2006, entry version 4.
DE Tryptophan synthase, beta chain (EC 4.2.1.20).
GN ORFNames=MgDRAFT_2774;
OS Alkalilimnicola ehrlichei MLHE-1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC Ectothiorhodospiraceae; Alkalilimnicola.
OX NCBI_TaxID=187272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MLHE-1;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.,
RT "Sequencing of the draft genome and assembly of Alkalilimnicola
ehrichtei MLHE-1".
RT Submitted (OCT-2005) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MLHE-1;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.,
RT "Annotation of the draft genome of Alkalilimnicola ehrlichei MLHE-1".
RL Submitted (NOV-2005) to the EMBL/GenBank/DBSJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
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CC
CC EMBL; AALK01000001; EAP35688.1; -; Genomic DNA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0004834; P:tryptophan synthase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006568; P:tryptophan metabolism; IEA.
KW Lyase; Pyridoxal phosphate.
SQ SEQUENCE 411 AA; 44619 MW; B8952DA9644A4C26 CRC64;
Query Match 66.7%; Score 6; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTFY 7
Db 198 VDDTFY 203
RESULT 45
ID Q3MKU8_9DELTA PRELIMINARY; PRT; 416 AA.
AC Q3MKU8;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.

DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=SfumDRAFT_0032;
OS Syntrophobacter fumaroxidans MPOB.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Syntrophobacterales;
CC Syntrophobacteraceae; Syntrophobacter.
OX NCBI_TaxID=335543;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MPOB;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.,
RT "Sequencing of the draft genome and assembly of Syntrophobacter
RT fumaroxidans MPOB.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MPOB;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.,
RT "Annotation of the draft genome assembly of Syntrophobacter
RT fumaroxidans MPOB.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
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CC -----
DR EMBL; AAJF01000066; EAO19414.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 416 AA; 46643 MW; CE2F7754D4B3F249 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTF 6
Db 136 KVDDTF 141

RESULT 46
Q3EM85 BACTI PRELIMINARY; PRT; 474 AA.
AC Q3EM85;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Phosphoenolpyruvate synthase [EC 2.7.9.2].
GN ORFNames=RETH_02591;
OS Bacillus thuringiensis serovar israelensis ATCC 35646.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
CC Bacillus cereus group.
OX NCBI_TaxID=339854;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35646;
RA Anderson I., Sorokin A., Kapatral V., Reznik G., Bhattacharya A.,
RA Mikhailova N., Burd H., Joukov V., Kaznadzey D., Walunas T.,
RA D'Souza M., Larsen N., Pusch G., Liolios K., Grechkin Y., Lapidus A.,
RA Goltsman E., Chu L., Fonstein M., Ehrlich D., Overbeek R.,
RA Kyrpides N., Ivanova N.,
RT "Comparative genome analysis of Bacillus cereus group genomes with
RT Bacillus subtilis.";
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAJW01000430; EAO52421.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008986; F:pyruvate, water dikinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016310; P:phosphorylation; IEA.
DR InterPro; IPR002192; P:PPDK_PEP_bd.
DR Pfam; PF01326; P:PPDK_N; 1.
KW Pyruvate; Transferase.
SQ SEQUENCE 474 AA; 52575 MW; 1COA641BE2374B57 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
Db 300 VDDTFY 305

RESULT 47
Q60051 THEVU PRELIMINARY; PRT; 482 AA.
AC Q60051;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 27.
DE Alpha-amylase precursor [EC 3.2.1.1].
GN Name=amyTV;
OS Thermoactinomyces vulgaris.
OC Bacteria; Firmicutes; Bacillales; Thermoactinomycetaceae;
CC Thermoactinomycetes.
OX NCBI_TaxID=2026;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K94;
RX MEDLINE=95031040; PubMed=7944369;
RA Hofemeister B., Koenig S., Hoang V., Engel J., Mayer G., Hansen G.,
RA Hofemeister J.,
RT "The gene amyE (TVI) codes for a nonglucogenic alpha-amylase from
RT Thermoactinomyces vulgaris 94-2A in Bacillus subtilis.";
RL Appl. Environ. Microbiol. 60:3381-3389(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K94;
RA Hofemeister J.W.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; X69807; CAA49465.1; -; Genomic_DNA.
DR PIR; S31478; S31478.
DR HSSP; P10529; 7TAA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016738; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006589; Alp_aryl_cat_sub.
DR InterPro; IPR006048; Alpha_aryl_C.
DR InterPro; IPR006047; Alpha_aryl_cat.
DR Pfam; PF00128; Alpha-amylase; 13.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy_C; 1.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 29 potential.
FT CHAIN 30 482 alpha-amylase.
SQ SEQUENCE 482 AA; 54483 MW; D8F98C370B579025 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7

Db 409 VDDTFY 414

RESULT 48

Q9L9B9 ARATH
ID Q9L9B9 ARATH PRELIMINARY; PRT; 485 AA.
AC Q9L9B9;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Chloroplast nucleoid DNA binding protein, putative.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22088475; PubMed=12093376;
RA Haas B.J., Volkovskiy N., Town C.D., Troughan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22088475; PubMed=12093376;
RA Haas B.J., Volkovskiy N., Town C.D., Troughan M., Alexandrov N.,
RA Feldmann K., Flavell R.,
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
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CC

DR EMBL; AY085528; AAM66061.1; -; mRNA.
DR HSSP; P42210; IQDM.
DR GO; GO:0004584; F:pepsin A activity; IEA.
DR GO; GO:0006198; P:proteolysis; IEA.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR009007; Pept_Aspartc_cat.
DR InterPro; IPR001461; Peptidase_A1.
DR PANTHER; PTHR13683; Peptidase_A1; 2.
DR Pfam; PF00026; Asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 2.
SQ SEQUENCE 485 AA; 52314 MW; D205E7EA9B283787 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 485;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9

Db 327 DTFYV 332

RESULT 49

Q9LNJ3 ARATH
ID Q9LNJ3 ARATH PRELIMINARY; PRT; 485 AA.
AC Q9LNJ3;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE F6F3.10 protein (Chloroplast nucleoid DNA binding protein, putative)
DE (Atg01300).
GN Name=F6F3.10; OrderedLocusNames=Atg01300;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

OX NCBI_TaxID=3702;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Pederspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
RA Buehler E., Chao Q., Chin C., Chlou J., Choi E., Gonzalez A.,
RA Hwang B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
RA Lenz C., Liu A., Liu S., Mukharly N., Pham P., Sakano H., Shinn P.,
RA Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.

RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Barth J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.

RA Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,

RA Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.

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CC

DR EMBL; AC023628; AAF97328.1; -; Genomic_DNA.
DR EMBL; AY128344; AAM91547.1; -; mRNA.
DR EMBL; BT006619; AAP31963.1; -; mRNA.
DR FIR; C86143; C86143.
DR HSSP; P42210; IQDM.
DR TAIR; At1G01300; -.

DR GO; GO:0009505; C:cell wall (sensu Magnoliophyta); IDA.

DR InterPro; IPR001969; Pept_Asp_AS.

DR InterPro; IPR009007; Pept_Aspartc_cat.

DR InterPro; IPR001461; Peptidase_A1.

DR PANTHER; PTHR13683; Peptidase_A1; 2.

DR Pfam; PF00026; Asp; 1.

DR PRINTS; PR00792; PEPsin.

DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 2.

SQ SEQUENCE 485 AA; 52175 MW; 1A1782027531709 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 485;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9

Db 327 DTFYV 332

RESULT 50

Q2V3N3 ARATH
ID Q2V3N3 ARATH PRELIMINARY; PRT; 499 AA.
AC Q2V3N3;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Protein At3g59080.
GN OrderedLocusNames=At3g59080;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

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RC STRAIN=ev. Columbia;
RX MEDLINE=21016720; PubMed=11130713; DOI=10.1038/35048706;
RA Salanoubat M., Lencke K., Rieger M., Ansoerge W., Unselid M.,
RA Farmanan B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Delsen M., Boutry M., Grivell L.A., Mache R., Pulgomenech P.,
RA De Simone V., Choise N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Schaefer M., Schoen O., Barges M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Waits A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Ideawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yaeuda M., Tabata S.,
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:820-822 (2000).
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CC
SQ TAIR; AC3959080; -.
SQ SEQUENCE 499 AA; 55354 MW; 87B60A948079617C CRC64;
Query Match 66.7%; Score 6; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DTFYTV 9
DB 338 DTFYTV 343
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Nucleotide Sequence
ID Q8RXI1 ARATH PRELIMINARY; PRT; 500 AA.
AC Q8RXI1
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Putative chloroplast nucleoid DNA-binding protein.
GN Name=At3g18490;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yanada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashiaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC
CC -!- INTERACTION:
CC Q42403:TRX3; NbExp=1; IntAct=EBI-449501; EBI-449157;

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CC
EMBL; AY080874; AAL87345.1; -; mRNA.
DR HSSP; P20142; IAVF.
DR IntAct; Q8RXI1; -.
DR GO; GO:0005515; F:protein binding; IPT.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR009007; Pept_Aspartc_cat.
DR PANTHER; PTHR13683; Peptidase A1.
DR Pfam; PF00026; Peptidase_1.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
KW DNA-binding.
SQ SEQUENCE 500 AA; 53220 MW; AOCF7BC606BBABE9 CRC64;
Query Match 66.7%; Score 6; DB 2; Length 500;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DTFYTV 9
DB 342 DTFYTV 347
|||||
Nucleotide Sequence
ID Q9LS40 ARATH PRELIMINARY; PRT; 500 AA.
AC Q9LS40
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 21-FEB-2006, entry version 18.
DE CN41, chloroplast nucleoid DNA binding protein-like (Putative
DE chloroplast nucleoid DNA-binding protein).
GN OrderedLocusNames=At3g18490;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20277480; PubMed=10819329; DOI=10.1093/dnares/7.2.131;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Yanada K., Chan M.M., Chang C.H., Dale J.M., Huan V.W., Lee J.M.,
RA Quach H.L., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
RA Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
RA Ecker J.R., Theologis A.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yanada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashiaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC
CC -!- INTERACTION:
CC Q42403:TRX3; NbExp=1; IntAct=EBI-449501; EBI-449157;

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DR InterPro; IPR009007; Pept_Aspartic_cat.
DR InterPro; IPR001461; Peptidase_A1.
DR PANTHER; PTHR13683; Peptidase_A1; 1.
DR Pfam; PF00026; Asp; 1.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
DR DNA-binding.
SQ SEQUENCE 500 AA; 53234 MW; F5DF2E1CF9CB306C CRC64;

Query Match 66.7%; Score 6; DB 2; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVV 9
DB 342 DTFYVV 347

RESULT 53
Q63G23_BACCH
ID Q63G23_BACCH PRELIMINARY; PRT; 512 AA.
AC Q63G23;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Hypothetical protein.
GN OrderedLocusNames=BCE33L0203;
OS Bacillus cereus (strain ZK / E33L).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK ";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
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KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 512 AA; 58358 MW; DC9F2EFDDA617B50 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVV 9
DB 299 DTFYVV 304

RESULT 54
Q6HPG6_BACHK
ID Q6HPG6_BACHK PRELIMINARY; PRT; 512 AA.
AC Q6HPG6;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Hypothetical protein.
GN OrderedLocusNames=BT9727_0199;
OS Bacillus thuringiensis subsp. konkukian.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=97-27;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;

"Complete genome sequence of Bacillus thuringiensis 97-27.";
Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 514 AA; 54891 MW; 77653ACBD68094E1 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVV 9
DB 352 DTFYVV 357

RESULT 56
Q9LYS8_ARATH
ID Q9LYS8_ARATH PRELIMINARY; PRT; 535 AA.
AC Q9LYS8;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Hypothetical protein F17J16_130 (AT3G59080/F17J16_130) (Hypothetical
DE protein At3G59080).
GN Name=F17J16_130; OrderedLocusNames=At3G59080;

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OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA D'Angelo M., Vezzi A., Modesto D., Pigazzi M., Valle G., Mewes H.W.,
 RA Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
 RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RN NUCLEOTIDE SEQUENCE.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
 RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RN NUCLEOTIDE SEQUENCE.
 RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RL [5]
 RN NUCLEOTIDE SEQUENCE.
 RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RL [6]
 RN NUCLEOTIDE SEQUENCE.
 RA GO; GO:0004194; F:pepsin A activity; IEA.
 DR EMBL; AF424562; AAL11556.1; -; mRNA.
 DR EMBL; BT000326; AAN15645.1; -; mRNA.
 DR EMBL; AV099818; AAM20669.1; -; mRNA.
 DR PIR; T47790; T47790.
 DR HSP; P07267; IFMX.
 DR TAIR; At3G59080; -.
 DR GO; GO:0006150; F:proteolysis; IEA.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR InterPro; IPR009007; Pept_Aspartc_cat.
 DR InterPro; IPR001461; Peptidase_A1.
 DR PANTHER; PTHR13683; Peptidase_A1; 2.
 DR Pfam; PF00026; Asp; 1.
 DR PRINTS; PS00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 535 AA; 59242 MW; 4C20AF38A2B66472 CRC64;
 Query Match 66.7%; Score 6; DB 2; Length 535;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 DTFYTV 9
 DB 374 DTFYTV 379

RESULT 57
 ID Q50EJ4 LACRE PRELIMINARY; PRT; 567 AA.
 AC Q50EJ4;
 DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
 DT 07-JUN-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE ATP-dependent nuclease subunit B (Fragment).
 OS Lactobacillus reuteri.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1598;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CRL1098;
 RA Vera J.L., Santos F., Sesma F.J.M., Font de Valdez G., Hugenholtz J.;
 RA Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
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 DR EMBL; AY780645; AAX14552.1; -; Genomic_DNA.
 DR NON_TER 567
 SQ SEQUENCE 567 AA; 64982 MW; E5AA0430AC8C53AC CRC64;
 Query Match 66.7%; Score 6; DB 2; Length 567;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFYV 8
 DB 33 DDTFYV 38

RESULT 58
 ID Q70Q68 PERMR PRELIMINARY; PRT; 671 AA.
 AC Q70Q68;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Hemocyanin subunit 2 precursor.
 GN Name=hc2;
 OS Perla marginata (Stonefly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Plecoptera; Perlidae; Perlidae; Perlidae; Perla.
 OX NCBI_TaxID=227363;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14715904; DOI=10.1073/pnas.0305872101;
 RA Hagner-Holler S., Schoen A., Erker W., Marden J.;
 RT "A respiratory hemocyanin from an insect.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:871-874(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Burmester I.;
 RA Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
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 DR EMBL; AJ555404; CAD87763.1; -; mRNA.
 DR GO; GO:0005344; F:oxygen transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000896; Hemocyanin.
 DR InterPro; IPR005203; hemocyanin_C.
 DR InterPro; IPR005204; hemocyanin_N.
 DR InterPro; IPR002227; Tyrosinase.
 DR PANTHER; PTHR11511; Hemocyanin; 1.
 DR Pfam; PF03723; Hemocyanin_C; 1.
 DR Pfam; PF00372; Hemocyanin_M; 1.

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DR Pfam: PF03722; Hemocyanin N; 1.
DR PRINTS: PR00187; HAEMOCYANIN.
DR PROSITE: PS00209; HAEMOCYANIN_1; 1.
DR PROSITE: PS00210; HAEMOCYANIN_2; UNKNOWN_1.
DR PROSITE: PS00498; TYROSINASE_2; UNKNOWN_1.
DR SIGNAL.
FT CHAIN 1 16 Potential.
FT CHAIN 17 671 hemocyanin subunit 2.
SQ SEQUENCE 671 AA; 77870 MW; 39A84D01C1DA98AD CRC64;

Query Match
Best Local Similarity 66.7%; Score 6; DB 2; Length 671;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTFY 7
Db 19 VDDTFY 24

RESULT 59
Q8FLC6_ECOL6
ID Q8FLC6_ECOL6 PRELIMINARY; PRT; 678 AA.
AC Q8FLC6;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 21-FEB-2006, entry version 11.
DE Putative glutamate dehydrogenase.
GN ORFNames=c_0018;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;

[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC.
RX MEDLINE=22398234; PubMed=124711157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Rosch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
CC

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EMBL: AE014075; AN78518.1; -; Genomic_DNA.
DR BLoCyc; ECOL199310:C0018-MONOMER; -.
KW Complete proteome.
SQ SEQUENCE 678 AA; 78223 MW; C9329675AC896AB9 CRC64;

Query Match
Best Local Similarity 66.7%; Score 6; DB 2; Length 678;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTFY 7
Db 496 VDDTFY 501

RESULT 60
Q7XJX7_ORYSA
ID Q7XJX7_ORYSA PRELIMINARY; PRT; 731 AA.
AC Q7XJX7; Q7X732;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2004, entry version 2.
DE OSJNBa0063C18.16 protein (OSJNBa0033G05.2 protein).
GN OSJNBa0063C18.16; Synonyms=OSJNBa0033G05.2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;

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OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;

[1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=2237377; PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Wang Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320 (2002).
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EMBL: AL731607; CA05975.2; -; Genomic DNA.
DR EMBL; AL606454; CAD41901.2; -; Genomic_DNA.
DR Gramene; Q7XJX7; -.
DR GO; GO:0007049; P:cell cycle; IEA.
DR InterPro; IPR001373; Cullin.
DR Pfam; PF00888; Cullin; 1.
DR SMART; SM00182; CULLIN; 1.
DR PROSITE; PS50069; CULLIN_2; 1.
SQ SEQUENCE 731 AA; 84804 MW; 6A02220495C5048B CRC64;

Query Match
Best Local Similarity 66.7%; Score 6; DB 2; Length 731;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFFY 8
Db 620 DDTFFY 625

RESULT 61
Q2Z173_9CAUD
ID Q2Z173_9CAUD PRELIMINARY; PRT; 870 AA.
AC Q2Z173;
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
OS Pseudomonas phage phiEL.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=273133;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22684572; PubMed=12798231; DOI=10.1016/S0923-2508(03)00070-6;
RA Krylov V.N., Pleteneva E.A., Bourkalsteva M.V., Shaburova O.V.,
RA Volckaert G., Sykklinda N.N., Kurochkina L.P., Mesyanzhinov V.V.;
RT "Myoviridae bacteriophages of Pseudomonas aeruginosa: a long and
complex evolutionary pathway.";
RL Res. Microbiol. 154:269-275 (2003).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22389089; PubMed=12500672;
RA Burkal'tseva M.V., Krylov V.N., Pleteneva E.A., Shaburova O.V.,
RA Krylov S.V., Volckaert G., Sykklinda N.N., Kurochkina L.P.,
RA Mesyanzhinov V.V.;
RT "Phenogenetic characterization of a group of giant Phi KZ-like
bacteriophages of Pseudomonas aeruginosa.";
RL Genetika 38:1470-1479 (2002).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=15033869; DOI=10.1093/bioinformatics/btg456;
RA Lavigne R., Sun W.D., Volckaert G.;
RT "PHIRE, a deterministic approach to reveal regulatory elements in

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RT bacteriophage genomes." ;
RL Bioinformatics 20:629-635(2004).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16256135;
RA Hertveldt K., Lavigne R., Pleteneva E., Sernova N., Kurochkina L.,
RA Korchevskii R., Robben J., Mesyanzhinov V., Krylov V.N., Volckaert G.;
RT "Genome Comparison of Pseudomonas aeruginosa Large Phages.";
RL J. Mol. Biol. 354:536-545(2005).
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CC -----
CC EMBL: AJ697969; CAG27102.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 870 AA; 100611 MW; 57347C91B488C432 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 870;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
DB 60 DTFYV 65

RESULT 62
Q9S9U5 ARATH PRELIMINARY; PRT; 892 AA.
AC Q9S9U5;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE F15P11.3 protein.
GN Name=F15P11.3;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Washu;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA McPherson C., Wohldmann P., Scronce D.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL: AF160760; RAD48936.1; -; Genomic_DNA.
DR InterPro: IPR006595; CtlH_C.
DR InterPro: IPR006594; Lish.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 4.
DR SMART: SM00668; CtlH; 1.
DR SMART: SM00667; Lish; 1.
DR SMART: SM00320; WD40; 2.
DR PROSITE: PS50897; CtlH; 1.
DR PROSITE: PS50896; Lish; 1.
DR PROSITE: PS50082; WD REPEATS 2; 1.
SQ SEQUENCE 892 AA; 39780 MW; 2487A7C97E027AEF CRC64;

Query Match 66.7%; Score 6; DB 2; Length 892;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KVDDTF 6
DB 520 KVDDTF 525

RESULT 63
Q8T043 DROME PRELIMINARY; PRT; 894 AA.
AC Q8T043; Q9V9B3;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 21-FEB-2006, entry version 24.
DE LD30953p (CG3409-PA)
GN ORFName=CG3409; Dmel_CG3409;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

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RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA Pacieb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [4]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [6]
RN NUCLEOTIDE SEQUENCE.
RX Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacieb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RN NUCLEOTIDE SEQUENCE.
RX FlyBase;
RG FlyBase;
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
CC similarity).
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CC -----
CC EMBL; AY069571; AL39716.1; -; mRNA.
DR EMBL; AE003790; AM70818.2; -; Genomic DNA.
DR FlyBase; FBgn0033095; CG3409.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
DR PROSITE; PS00850; MFS; 1.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 894 AA; 98864 MW; E7515205F19EC998 CRC64;
Query Match 66.7%; Score 6; DB 2; Length 894;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 DDTFFY 8
DB 849 DDTFFY 854
|||||
RESULT 64
Q9VPH1_DROME

ID Q9VPH1_DROME PRELIMINARY; PRT; 900 AA.
AC Q9VPH1;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE CG5528-PA.
DE Names: Toll-9; ORFNames=Dmel CG5528;
GN Drosophila melanogaster [fruit fly].
OS Drosophila melanogaster [fruit fly].
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smet T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Dugan S.P., Frise E., Hodgson A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacieb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective";

Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).

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[4]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kinkler J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RN Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[5]
RN NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirska R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[6]
RN NUCLEOTIDE SEQUENCE.
RG FlyBase;
RN Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AE003591; AAF51581.1; -; Genomic_DNA.
DR HSP; Q15399; 1FYV.
DR FlyBase; FBgn0036978; Toll-9.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003591; LRR typ.
DR InterPro; IPR001571; TIR.
DR Pfam; PF00560; LRR_1; 6.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00369; LRR_TYP; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS0104; TIR; 1.
SQ SEQUENCE 900 AA; 104013 MW; 627062202C192062 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 900;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
DB 304 DTFYV 309

RESULT 65
Q41709 GIBZE
ID Q41709 GIBZE PRELIMINARY; PRT; 1080 AA.
AC Q41709;
DT 16-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN ORFNames=FG06999.1;
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocremycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PH-1 / NRRL 31084; Abouelleil A., Allen N., Anderson S.,
RA Birren B.W., Nusbaum C., Abouelleil A., Bloom T., Boguslavskiy L.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
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RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D.,
RA Galagan J.E., Gardyna S., Gnerre S., Graham L., Grand-Pierre N.,
RA Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W.,
RA Iliev I., Jaffe D., Johnson R., Jones C., Kamal M., Kamat A.,
RA Karatas A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G.,
RA Lui A., Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J.,
RA Manning J., Mihovics C., Mauceli E., McCarthy M., Meldrum J.,
RA Meneus L., Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C.,
RA Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,
RA O'Neil D., Oliver J., Peterson K., Phunkhang P., Pierre N.,
RA Purcell S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C.,
RA Rogov P., Roman J., Schauer S., Schupack R., Seaman S., Severy P.,
RA Smirnov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N.,
RA Stubbs M., Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.S.;
RT "Fusarium graminearum genome sequence.";
RN Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL; AAC01000290; EAA75944.1; -; Genomic_DNA.
DR GO; GO:0000145; C:exocyst; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
DR GO; GO:0006904; P:vesicle docking during exocytosis; IEA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1080 AA; 121264 MW; E8310A2DE90F998B CRC64;

Query Match 66.7%; Score 6; DB 2; Length 1080;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
DB 340 DTFYV 345

RESULT 66
SEC8 NEUCR
ID SEC8 NEUCR STANDARD; PRT; 1111 AA.
AC Q9HE88; O7S707;
DT 25-OCT-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Probable exocyst complex component sec8.
GN Name=sec-8; ORFNames=B13020.150, NCU04190;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=74-OR23-1A / FGSC 987;
EX MEDLINE=22542210; PubMed=12655011; DOI=10.1093/nar/gkg293;
RA Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,
RA Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J.,
RA Schulte U.;
RT "What's in the genome of a filamentous fungus? Analysis of the
RT Neurospora genome sequence.";
RN Neurospora Genome sequence.
RL Nucleic Acids Res. 31:1944-1954(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
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RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
RA Werner-Washburne M., Sellitrennikoff C.P., Kinsey J.A., Braun E.L.,
RA Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamvyselis M.,
RA Mauceli E., Biele C., Rudd S., Frishman D., Kryzsofova S.,
RA Ramussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA Macino G., Catchside D.E.A., Li W., Pratt R.J., Osmari S.A.,
RA DeSouza C.P.C., Glass N.L., Orbach M.J., Berglund J.A., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J.C., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbels D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nuebaum C., Birren B.W.;
RT "The genome sequence of the filamentous fungus *Neurospora crassa*.";
RL Nature 422:859-868(2003).
CC -1- FUNCTION: Component of the exocyst complex involved in the docking
CC of exocystic vesicles with fusions site on the plasma membrane (By
CC similarity).
CC -1- SUBUNIT: The exocyst complex is composed of SEC3, SEC5, SEC6,
CC SEC8, SEC10, SEC15, EXO70 and EXO84 (By similarity).
CC -1- SIMILARITY: Belongs to the SEC8 family.
CC
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CC
CC ENBL; AL451015; CAC18205.1; -; Genomic DNA.
CC EMBL; ABX01000274; EAA31914.1; -; Genomic DNA.
CC BioCyc; NCRA-XX3-01-NCRA-XX3-01-007938-MONOMER; -;
CC InterPro; IPR007191; Sec8 exocyst.
CC Pfam; PF04048; Sec8 exocyst; 1.
CC Exocytosis; Protein transport; Transport.
FT CHAIN 1 llll Probable exocyst complex component sec8.
FT /FTID=PRO_0000118940.
SQ SEQUENCE 1111 AA; 124417 MW; 6AC72D46750E7D0B CRC64;

Query Match 66.7%; Score 6; DB 1; Length 1111;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
Db 338 DTFYV 343

RESULT 67
Q9XVH4 CAEBL PRELIMINARY; PRT; 1256 AA.
AC Q9XVH4
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 32.
DE Hypothetical protein.
GN ORFNames=W02B8.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -1- SIMILARITY: Contains 1 PH domain.
CC
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CC
CC EMBL; Z81136; CAB03458.1; -; Genomic DNA.
CC FIR; T26101; T26101.

DR Ensembl; W02B8.2; Caenorhabditis elegans.
DR WormBase; WBGene00012198; W02B8.2.
DR WormPep; W02B8.2; CE20131.
DR GO; GO:0005083; F:small GTPase regulator activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001180; Citron.
DR InterPro; IPR002219; DAG_P5_bd.
DR InterPro; IPR001849; PH.
DR Pfam; PF00130; Cl_1; 1.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF00169; PH; 1.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00036; CNH; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS50081; ZF_DOM_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1256 AA; 144854 MW; 3036E19DD668CBB2 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 1256;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
Db 1096 DTFYV 1101

RESULT 68
Q61VN1 CAEBR PRELIMINARY; PRT; 1284 AA.
AC Q61VN1;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Hypothetical protein CBG04771.
GN Name=CBG04771;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AF16;
RX PubMed=14624247; DOI=10.1371/journal.pbio.0000045;
RA Stein L.D., Bao Z., Blasiar D., Blumenthal T., Brent M.R., Chen N.,
RA Chinwalla A., Clarke L., Clee C., Coghlan A., Coulson A.,
RA D'Eustachio P., Fitch D.H.A., Fulton L.A., Fulton R.E.,
RA Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R.,
RA Kuwabara P.E., Mardis E.R., Marra M.A., Miner T.L., Minx P.,
RA Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Sohrmann M.,
RA Spieth J., Stajich J.E., Wei C., Willey D., Wilson R.K., Durbin R.,
RA Waterston R.H.;
RT "The genome sequence of *Caenorhabditis briggsae*: a platform for
RT comparative genomics.";
RL PLOS Biol. 1:166-192(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
CC EMBL; CAAC01000021; CAE61028.1; -; Genomic DNA.
DR GO; GO:0005083; F:small GTPase regulator activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001180; Citron.
DR InterPro; IPR002219; DAG_P5_bd.
DR InterPro; IPR011993; PH_Type.
DR Pfam; PF00780; CNH; 1.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00036; CNH; 1.

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DR PROSITE; P550081; ZF DAG PE 2; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1284 AA; 148978 MW; 8C34675D3535D450 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 1284;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVV 9
DB 1123 DTFYVV 1128

RESULT 69
Q21025_CABEL PRELIMINARY; PRT; 1286 AA.
AC Q21025;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 36.
DE Hypothetical protein.
ORFNames=F59A6.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
ON NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=9069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- SIMILARITY: Contains 1 PH domain.
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CC -----
DR EMBL; U01994; AK31526.1; -; Genomic DNA.
DR PIR; T16507; T16507.
DR Ensembl; F59A6.5; Caenorhabditis elegans.
DR WormBase; WBGene00019087; F59A6.5.
DR WormPep; F59A6.5; CE02790.
DR GO; GO:0005083; F.small GTPase regulator activity; IEA.
DR GO; GO:0007242; P.intracellular signaling cascade; IEA.
DR InterPro; IPR002119; DAG_PE_bd.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH_type.
DR Pfam; PF00130; CL_1; 1.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF00169; PH; 1.
DR SMART; SM00109; CL; 1.
DR SMART; SM00036; CNH; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; P550003; PH_DOMAIN; 1.
DR PROSITE; P550081; ZF DAG PE 2; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1286 AA; 148667 MW; 1402C3A80DC12BB4 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 1286;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVV 9
DB 1120 DTFYVV 1125

RESULT 70
Q73C85_BACCC1 PRELIMINARY; PRT; 51 AA.
ID Q73C85_BACCC1

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AC Q73C85;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hypothetical protein.
ORFNames=BCE1181;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
ON NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Raeko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
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CC -----
DR EMBL; AE017194; AAS40111.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 51 AA; 5976 MW; E259DD9994414B92 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFFYVV 9
DB 43 TFFYVV 47

RESULT 71
Q838E6_ENTFA PRELIMINARY; PRT; 56 AA.
ID Q838E6_ENTFA
AC Q838E6;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Hypothetical protein.
ORFNames=EF0621;
GN Enterococcus faecalis (Streptococcus faecalis).
OS Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
ON NCBI_TaxID=1351;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umavam L.A., Brinkac L.M., Beanan M.J.,
RA Dougherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
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CC -----
DR EMBL; AE016830; AAO80448.1; -; Genomic DNA.
DR TIGR; EF0621; -.
DR BioCyc; EF0621:185; EF0621-MONOMER; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 56 AA; 6873 MW; B513B3961EFDB3B CRC64;

Query Match 55.6%; Score 5; DB 2; Length 56;

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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 8
Db 40 DTFY 44

RESULT 72
Q514Y7 ENTHI PRELIMINARY; PRT; 60 AA.
AC Q514Y7;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=72.t00018;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B.J., Anderson I., Davies R., Alemark U.C., Samuelson J.,
RA Anedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoelt U., Bhattacharya A.,
RA Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,
RA Whitehead S., Quail M.A., Rabinowitsch E., Norbertzak H., Price C.,
RA Wang Z., Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S.,
RA Lohia A., Foster P.G., Sacheritz-Ponten T., Weber C., Singh U.,
RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
RA Barrell B.G., Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAFB01000272; EAL48420.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 60 AA; 6772 MW; FDD913B60C39BEB2 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 32 KVDDT 36

RESULT 73
Q81GV6 BACCR PRELIMINARY; PRT; 70 AA.
AC Q81GV6;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Hypothetical protein.
GN OrderedLocusNames=BC1079; ORFNames=BC 1079;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;

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RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kaparal V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Ponstein M., Ehrlich S.D.,
RA Overbeek R., Kyripides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
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CC -----
DR EMBL; AE016877; AAP08066.1; -; Genomic_DNA.
DR BioCyc; BCER226900:BC1079-MONOMER; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 70 AA; 8113 MW; E5E3F6E07AC6AC42 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TFYV 9
Db 44 TFYV 48

RESULT 74
RS27A ASPOF STANDARD; PRT; 78 AA.
AC P31753;
DT 01-JUL-1993, integrated into UniProtKB/Swiss-Prot.
DT 01-JUL-1993, sequence version 1.
DT 07-MAR-2006, entry version 34.
DE 40S ribosomal protein S27a.
OS Asparagaceae; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asparagaceae;
OC Asparagaceae.
OX NCBI_TaxID=4686;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=cv. Limbras 10; TISSUE=Spear;
RA Davies K.M., King G.A.;
RT "Isolation and characterization of Asparagus officinalis L. cDNA
RT clones encoding two forms of ubiquitin mRNA.";
RL N. Z. J. Crop Hortic. Sci. 21:153-159(1993).
CC -1- MISCELLANEOUS: This ribosomal protein is synthesized as a C-
CC terminal extension protein (CEP) of ubiquitin.
CC -1- SIMILARITY: Belongs to the ribosomal protein S27Ae family.
CC -----
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CC -----
DR EMBL; X66875; CAA47346.1; ALT_INIT; mRNA.
DR FIR; S25001; S25001.
DR InterPro; IPR002906; Ribosomal_S27a.
DR Pfam; PF01599; Ribosomal_S27; 1.
KW Metal-binding; Ribonucleoprotein; Ribosomal protein; Zinc;
KW Zinc-finger.
FT CHAIN 1 78 40S ribosomal protein S27a.
FT ZN FING 45 68 C4-type.
FT COMPIAS 1 23 Lys-rich (highly basic).
SQ SEQUENCE 78 AA; 9061 MW; 30D5DB61F5B7A89F CRC64;

Query Match 55.6%; Score 5; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 31 KVDDT 35

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RESULT 75
RS27A_LYCES
ID RS27A_LYCES STANDARD; PRT; 80 AA.
AC P62980; P27083;
DT 31-AUG-2004, integrated into UniProtKB/Swiss-Prot.
DT 31-AUG-2004, sequence version 1.
DT 07-MAR-2006, entry version 11.
DE 40S ribosomal protein S27a.
GN Name=UBI3; Synonyms=RPS27a;
OS Lycopersicon esculentum (tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] (UBI3).
RC MEDLINE=92032784; PubMed=1657246;
RX Hoffman N.E., Ko K., Milkowski D., Pichersky E.;
RT "Isolation and characterization of tomato cDNA and genomic clones
RT encoding the ubiquitin gene ubi3.";
RL Plant Mol. Biol. 17:1189-1201(1991).
CC -!- MISCELLANEOUS: This ribosomal protein is synthesized as a C-
CC terminal extension protein (CEP) of ubiquitin.
CC -!- SIMILARITY: Belongs to the ribosomal protein S27Ae family.
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CC
CC EMBL; X59253; CAA41207.1; ALT_INIT; Genomic_DNA.
DR PIR; S18351; UQO7A.
DR InterPro; IPR002906; Ribosomal_S27a.
DR Pfam; PF01599; Ribosomal_S27; 1.
DR Metal-binding; Ribonucleoprotein; Ribosomal protein; Zinc;
KW Zinc-finger.
FT CHAIN 1 80 40S ribosomal protein S27a.
FT ZN_FING 45 68 C4-type.
FT COMEBIAS 1 23 Lys-rich (highly basic).
FT SEQUENCE 80 AA; 9195 MW; 89FD2C98B1E55B7 CRC64;
SQ
Query Match 55.6%; Score 5; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDT 5
DB 31 KVDDT 35

RESULT 76
RS27A_SOLTU
ID RS27A_SOLTU STANDARD; PRT; 80 AA.
AC P62981; P27083;
DT 31-AUG-2004, integrated into UniProtKB/Swiss-Prot.
DT 31-AUG-2004, sequence version 1.
DT 07-MAR-2006, entry version 11.
DE 40S ribosomal protein S27a.
GN Name=UBI3; Synonyms=RPS27a;
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (UBI3).
RC STRAIN=cv. Lemhi Russet; TISSUE=Tuber;
RX MEDLINE=93004476; PubMed=1327270;
RA Garbarino J.E., Rockhold D.R., Belknap W.R.;
RT "Expression of stress-responsive ubiquitin genes in potato tubers.";
RL Plant Mol. Biol. 20:235-244 (1992).
RN [2]

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RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] (UBI3).
RC STRAIN=cv. Lemhi Russet; TISSUE=Tuber;
RX MEDLINE=94154225; PubMed=8111011;
RA Garbarino J.E., Belknap W.R.;
RT "Isolation of a ubiquitin-ribosomal protein gene (ubi3) from potato
RT and expression of its promoter in transgenic plants.";
RL Plant Mol. Biol. 24:119-127(1994).
CC -!- MISCELLANEOUS: This ribosomal protein is synthesized as a C-
CC terminal extension protein (CEP) of ubiquitin.
CC -!- SIMILARITY: Belongs to the ribosomal protein S27Ae family.
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CC
CC EMBL; Z11659; CAA77735.1; ALT_INIT; mRNA.
DR EMBL; U22576; AAA19247.1; ALT_INIT; Unassigned_DNA.
DR InterPro; IPR002906; Ribosomal_S27a.
DR Pfam; PF01599; Ribosomal_S27; 1.
KW Metal-binding; Ribonucleoprotein; Ribosomal protein; Zinc;
FT CHAIN 1 80 40S ribosomal protein S27a.
FT ZN_FING 45 68 C4-type.
FT COMEBIAS 1 23 Lys-rich (highly basic).
FT SEQUENCE 80 AA; 9195 MW; 89FD2C98B1E55B7 CRC64;
SQ
Query Match 55.6%; Score 5; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDT 5
DB 31 KVDDT 35

RESULT 77
Q3GRU9_9GAMM
ID Q3GRU9_9GAMM PRELIMINARY; PRT; 80 AA.
AC Q3GRU9;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Twin-arginine translocation protein TatA/E.
GN ORFNames=PcrvODRAFT_2424;
OS Psychrobacter cryohalolentis K5.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Psychrobacter.
OX NCBI_TaxID=335284;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K5;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Psychrobacter
RT cryohalolentis K5.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K5;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Psychrobacter
RT cryohalolentis K5.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
CC EMBL; AAJ01000001; EA012126.1; -; Genomic_DNA.

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DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0008565; P:protein transporter activity; IEA.
 DR GO: GO:0015031; P:protein transporter; IEA.
 DR InterPro: IPR003369; MtaA_Hcf106.
 DR InterPro: IPR006312; TATA_E.
 DR Pfam: PF02416; MtaA_Hcf106; 1.
 DR TIGRFAMs: TIGR01411; tataE; 1.
 SQ SEQUENCE 80 AA; 8738 MW; 04992A211384B965 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 73 KVDDT 77

RESULT 78

Q48Q06_STRPM PRELIMINARY; PRT; 81 AA.
 AC Q48Q06;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Phase protein.
 GN OrderedLocNames=M28_Spy1844;
 OS Streptococcus pyogenes serotype M28.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=319700;
 RN [1]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=MGAS6180 / Serotype M28;
 RX PubMed=16088825; DOI=10.1086/430618;
 RA Green N.M., Zhang S., Porcella S.P., Nagiec M.J., Barbian K.D.,
 RA Beres S.B., Lefebvre R.B., Mueser J.M.;
 RT "Genome sequence of a serotype M28 strain of group A Streptococcus:
 RT potential new insights into puerperal sepsis and bacterial disease
 RT specificity.";
 RL J. Infect. Dis. 192:760-770(2005).
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 CC -----
 CC EMBL: CP000056; AAX72954.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 81 AA; 9636 MW; 23DC6107C6B34810 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 81;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 42 KVDDT 46

RESULT 79

Q4F061_PSYAR PRELIMINARY; PRT; 87 AA.
 AC Q4F061;
 DT 30-AUG-2005, integrated into UniProtKB/TrEMBL.
 DT 30-AUG-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Twin-arginine translocation protein Taca/E.
 GN Name=tacA; OrderedLocNames=Psyc_2000;
 OS Psychrobacter arcticum.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Psychrobacter.
 OC NCBI_TaxID=334543;
 RN [1]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=273-4;
 RG NASA Astrobiology Institute;
 RA Ayala-del-Rio H.L., Chain P., Ponder M.A., Di Bartolo G., Ivanova N.,
 RA Bergholz P.W., Hauser L., Land M., Bakermans C., Rodrigues D.,
 RA Klappenbach J.A., Zarka D., Larimer F., Richardson P., Thomashow M.F.,
 RA Tiedje J.M.;
 RT "Complete sequence of Psychrobacter arcticum 273-4.";
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
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 CC EMBL: CP000082; AAZ19847.1; -; Genomic_DNA.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0008565; P:protein transporter activity; IEA.
 DR GO: GO:0015031; P:protein transporter; IEA.
 DR InterPro: IPR006312; TATA_E.
 DR Pfam: PF02416; MtaA_Hcf106; 1.
 DR TIGRFAMs: TIGR01411; tataE; 1.
 KW Complete proteome.
 SQ SEQUENCE 87 AA; 9280 MW; 5240B1E656680D60 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 80 KVDDT 84

RESULT 80

Y3711_CLOAB STANDARD; PRT; 90 AA.
 AC Q4353;
 DT 01-FEB-1994, integrated into UniProtKB/Swiss-Prot.
 DT 29-AUG-2001, sequence version 2.
 DT 07-MAR-2006, entry version 25.
 DE Hypothetical protein CAC3711.
 GN OrderedLocNames=CAC3711;
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OC NCBI_TaxID=1488;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=93273706; PubMed=8501044;
 RA Sauer U., Duerre P.;
 RT "Sequence and molecular characterization of a DNA region encoding a
 RT small heat shock protein of Clostridium acetobutylicum.";
 RL J. Bacteriol. 175:3394-3400(1993).
 RL [2]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RX DOI=10.1128/JB.183.16.4823-4838.2001;
 RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
 RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838(2001).

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 CC -----
 CC EMBL: X65276; CAA46377.1; ALT INIT; Genomic_DNA.
 DR EMBL: A8007866; AAK81631.1; -; Genomic_DNA.
 DR FIR; D97355; D97355.
 DR GenomeReviews; AE001437.GR; CAC3711.
 DR BioCyc; CAC3711-MONOMER; -.

KW Complete proteome; Hypothetical protein.
FT CHAIN 1 90 Hypothetical protein CAC3711.
FT /FTID=PRO 0000207115.
SQ SEQUENCE 90 AA; 10302 MW; DDDSD0F5C2FPD3C3C CRC64;

Query Match 55.6%; Score 5; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDVT 5
|||||
Db 56 KVDVT 60

RESULT 81
Q8JM27_9NUCL PRELIMINARY; PRT; 91 AA.
AC Q8JM27; Integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hypothetical protein.
OS Mamestra configurata NPV-B.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=204440;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22080411; PubMed=12083822; DOI=10.1006/viro.2002.1411;
RA Li L., Donly C., Li Q., Willis L.G., Keddle B.A., Erlandson M.A.,
RA Theilmann D.A.;
RT Identification and genomic analysis of a second species of
RT nucleopolyhedrovirus isolated from Mamestra configurata.";
RL Virology 297:226-244 (2002).

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DR EMBL; AV126275; AAM95113.1; -; Genomic_DNA.
DR InterPro: IPR009317; Chab.
DR Pfam: PF06150; Chab; 1.
KW Hypothetical protein.
SQ SEQUENCE 91 AA; 10720 MW; B34A44F5A99C02FB CRC64;

Query Match 55.6%; Score 5; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 85 DDTFY 89

RESULT 82
Q63CD4_BACCZ PRELIMINARY; PRT; 92 AA.
AC Q63CD4;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DE Hypothetical protein.
DE Hypothetical protein.
GN OrderedLocusNames=BCE3311838;
OS Bacillus cereus (strain ZK / E33L).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL; CP000001; AAU18407.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 92 AA; 10293 MW; AB488CFBD09699D1 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 52 DDTFY 56

RESULT 83
Q81RL2_BACAN PRELIMINARY; PRT; 92 AA.
AC Q81RL2_06H2T8; O6KTS2;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Conserved domain protein.
GN OrderedLocusNames=BA2031, BAS1886, GBAA2031; ORFNames=BA_2031;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=1271629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86 (2003).

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DR EMBL; AE016879; AAP25920.1; -; Genomic_DNA.
DR EMBL; AE017334; AAT31148.1; -; Genomic_DNA.
DR EMBL; AE017225; AAT54201.1; -; Genomic_DNA.
DR MEROPS; M73.001; -.
DR TIGR; BA2031; -.

DW TIGR; GBAA2031; --
 KW Complete proteome.
 SQ SEQUENCE 92 AA; 10279 MW; AB4C57DBDD09699D1 CRC64;

 Query Match 55.6%; Score 5; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 DDTFY 7
 DB 52 DDTFY 56

 RESULT 84
 Q220L6_9ADEN PRELIMINARY; PRT; 92 AA.
 AC Q220L6;
 DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 20-DEC-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Hexon capsid protein (Fragment).
 GN Name=hexon;
 OS Human adenovirus type 38.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=46943;
 RN [1].
 RP NUCLEOTIDE SEQUENCE.
 RA Madisch I., Harste G., Pommer H., Helm A.;
 RT "Phylogenetic Analysis of Main Neutralization (epsilon) and
 RT Hemagglutination(gamma) Determinants of all Human Adenovirus
 RT Prototypes as a Basis for Molecular Classification and Taxonomy.";
 RL J. Virol. 0:0-0(2005).
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 CC -----
 DE EMBL; AJ745893; CAG34210.2; --; Genomic_DNA.
 DR NON_TER 1
 FT NON_TER 92
 FT SEQUENCE 92 AA; 10228 MW; 680705BC73BC3A16 CRC64;

 Query Match 55.6%; Score 5; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KVDVT 5
 DB 71 KVDVT 75

 RESULT 85
 Q2WLY5_CLOBE PRELIMINARY; PRT; 94 AA.
 AC Q2WLY5;
 DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 10-JAN-2006, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Hypothetical protein.
 GN ORFNames=CbeiDRAFT_1625;
 OS Clostridium beijerinckii NCIMB 8052.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=290402;
 RN [1].
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NCIMB 8052;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.;
 RA "Sequencing of the draft genome and assembly of Clostridium
 RT beijerinckii NCIMB 8052.";
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NCIMB 8052;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Clostridium beijerinckii
 RT NCIMB 8052.";
 RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC -----
 DE EMBL; AALQ01000023; EAP59102.1; --; Genomic_DNA.
 DR Hypothetical protein.
 KW SEQUENCE 94 AA; 10807 MW; 65A52A20B248AE6C CRC64;

 Query Match 55.6%; Score 5; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KVDVT 5
 DB 8 KVDVT 12

 RESULT 86
 Q4DFB0_TRYCR PRELIMINARY; PRT; 100 AA.
 ID Q4DFB0_TRYCR
 AC Q4DFB0;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE 10 kDa heat shock protein, putative.
 GN ORFNames=rc00.1047053508209.100, Tc00.1047053508209.90,
 GN Tc00.1047053509505.30, Tc00.1047053509505.70;
 OS Trypanosoma cruzi.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
 OC Schizotrypanum.
 OX NCBI_TaxID=5693;
 RN [1].
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CL Brenner;
 RA El-Sayed N.M.A., Myler P.J., Bartholomeu D.C., Nilsson D.,
 RA Aggarwal G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,
 RA Blandin G., Westenberger S.J., Caler E., Cerqueira G.C., Branche C.,
 RA Haas B., Anapuma A., Arner E., Aslund L., Attipoe P., Bontempi E.,
 RA Bringaud F., Burton P., Cadag E., Campbell D.A., Carrington M.,
 RA Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,
 RA Englund P.T., Fazelina G., Feldblyum T., Ferella M., Frasch A.C.,
 RA Gull K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,
 RA Kluge S., Koo H., Lacerda D., Levin M.J., Lorenzi H., Louie T.,
 RA Machado C.R., McCulloch R., McKenna A., Mizuno Y., Mottram J.C.,
 RA Nelson S., Ochaya S., Osoegawa K., Pai G., Parsons M., Pentony M.,
 RA Pettersson U., Pop M., Ramirez J.L., Rinta J., Robertson L.,
 RA Salzberg S.L., Sanchez D.O., Seyler A., Sharma R., Shetty J.,
 RA Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
 RA Van Aken S., Vogt C., Ward P.N., Wickstead B., Wortman J., White O.,
 RA Fraser C.M., Stuart K.D., Andersson B.;
 RA "The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas'
 RT Disease.";
 RL Science 0:0-0(2005).
 RN [2].
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CL Brenner;
 RA El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J.,
 RA Aggarwal G., Caler E., Renauld H., Worthey E.A., Hertz-Fowler C.,
 RA Ghedin E., Peacock C., Bartholomeu D.C., Haas B.J., Tran A.-N.,
 RA Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Badger J.,
 RA Bringaud F., Cadag E., Carlton J.M., Cerqueira G.C., Creasy T.,
 RA Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivans A.C.,
 RA Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J.,

DE Thioresdoxin.
GN OrderedLocusNames=ABC2772;
OS Bacillus clausii (strain KSM-K16).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=66692;
RN [1]
RA Takaki Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,
RA Kawai S., Ito S., Horikoshi K.;
RT "The complete genome sequence of the alkaliphilic Bacillus clausii
RT KSM-K16";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AP006627; BAD5306.1; -; Genomic DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR012336; Thiorodxin-like_fold.
DR InterPro; IPR006662; Thiorod.
DR InterPro; IPR006663; Thiorodxin_dome2.
DR InterPro; IPR012335; Thiorodxin_fold.
DR Pfam; PF00085; Thiorodxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
KW Complete proteome.
SQ SEQUENCE 108 AA; 12516 MW; 0F5925611B113E56 CRC64;
Query Match 55.6%; Score 5; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 TFYV 9
Db 49 TFYV 53
RESULT 90
Q4XC7 PLACH PRELIMINARY; PRT; 109 AA.
ID Q4XC7 PLACH
AC Q4XC7;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN ORFNames=PC403203.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL; CAJ01007439; CAH85235.1; -; Genomic_DNA.
DR CAAJ01007439;
KW Hypothetical protein.
SQ SEQUENCE 109 AA; 13670 MW; 480F614CD3A2B037 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 TFYV 9
Db 25 TFYV 29
RESULT 91
Q6Y8R4 MYCHO PRELIMINARY; PRT; 116 AA.
ID Q6Y8R4 MYCHO
AC Q6Y8R4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical conserved protein (Fragment).
OS Mycoplasma hominis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2098;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PG21.
RX PubMed=15616325; DOI=10.1128/AAC.49.1.421-424.2005;
RA Raherison S., Gonzalez P., Renaudin H., Charron A., Bebear C.,
RA Bebear C.M.;
RT "Increased Expression of Two Multidrug Transporter-Like Genes Is
RT Associated with Ethidium Bromide and Ciprofloxacin Resistance in
RT Mycoplasma hominis";
RL Antimicrob. Agents Chemother. 49:421-424(2005).
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CC -----
CC EMBL; AY169817; AA039417.1; -; Genomic_DNA.
DR AY169817;
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 116 AA; 13513 MW; ADC7AC6DC5AAB3A7 CRC64;
Query Match 55.6%; Score 5; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 TFYV 9
Db 33 TFYV 37
RESULT 92
Q63BU1 BACCZ PRELIMINARY; PRT; 119 AA.
ID Q63BU1 BACCZ
AC Q63BU1;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Acetyltransferase.
GN OrderedLocusNames=BCE331L2034;
OS Bacillus cereus (strain ZK / E33L).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Hitchcock P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; CP000001; AAU18222.1; -; Genomic_DNA.

DR GO: GO:0008080; F:N-acetyltransferase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR InterPro: IPR000182; GCN5acetyl_trans.
 DR Pfam: PF00583; Acetyltransferase_1; 1.
 KW Complete proteome; Transferase.
 SQ SEQUENCE 119 AA; 13936 MW; B8CCBE34683CF9DAA CRC64;

Query Match 55.6%; Score 5; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 |||||
 Db 34 KVDDT 38

RESULT 93

Q6HJBI_BACHK PRELIMINARY; PRT; 119 AA.
 AC Q6HJBI_1
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Acetyltransferase.
 GN OrderedLocusNames=BT9727.2036;
 OS Bacillus thuringiensis subsp. konkukian.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=180856;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=97-27;
 RA Bretkin T.S.; Bruce D.; Challacombe J.F.; Gilna P.; Han C.; Hill K.;
 RA Hitchcock P.; Jackson P.; Keim P.; Longmire J.; Lucas S.; Okinaka R.;
 RA Richardson P.; Rubin E.; Tice H.;
 RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

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 CC -----
 CC EMBL; AE017355; AAT61224.1; -; Genomic DNA.
 DR GO: GO:0008080; F:N-acetyltransferase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR InterPro: IPR000182; GCN5acetyl_trans.
 DR Pfam: PF00583; Acetyltransferase_1; 1.
 KW Complete proteome; Transferase.
 SQ SEQUENCE 119 AA; 13948 MW; 5989EED70ACF9DAB CRC64;

Query Match 55.6%; Score 5; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 |||||
 Db 34 KVDDT 38

RESULT 94

Q81DZ1_BACCR PRELIMINARY; PRT; 119 AA.
 AC Q81DZ1_1
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE Acetyltransferase (EC 2.3.1.-).
 GN OrderedLocusNames=BC2205; ORFNames=BC 2205;
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=226900;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
 RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
 RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
 RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
 RA Overbeek R., Kyrpides N.C.;
 RT "Genome sequence of Bacillus cereus and comparative analysis with
 RT Bacillus anthracis.";
 RL Nature 423:87-91(2003).
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 CC -----
 CC EMBL; AE016877; AAP09171.1; -; Genomic DNA.
 DR BioCyc; BCR226900; BC2205-MONOMER; -.
 DR LinkHub; Q81DZ1; -.
 DR GO: GO:0008415; F:acetyltransferase activity; IEA.
 DR GO: GO:0008080; F:N-acetyltransferase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR InterPro: IPR000182; GCN5acetyl_trans.
 DR Pfam: PF00583; Acetyltransferase_1; 1.
 KW Acetyltransferase; Complete proteome; Transferase.
 SQ SEQUENCE 119 AA; 14012 MW; BB0A424E269AADBA CRC64;
 Query Match 55.6%; Score 5; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 |||||
 Db 34 KVDDT 38

RESULT 95
 Q81R08_BACAN PRELIMINARY; PRT; 119 AA.
 ID Q81R08_BACAN
 AC Q81R08_1; Q6KT79; Q6KT72;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE Acetyltransferase, GNAT family.
 DE OrderedLocusNames=BA2252, BAS2096, GBAA2252; ORFNames=BA_2252;
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=1392;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Ames / isolate Porton;
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.P.,
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Niernan W.C.,
 RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
 RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
 RT "The genome sequence of Bacillus anthracis Ames and comparison to
 RT closely related bacteria.";
 RL Nature 423:81-86(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Ames ancestor;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RT "Bacillus anthracis comparative genomics.";
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]

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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Sterne;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RL "Complete genome sequence of Bacillus anthracis Sterne.";
RT Submitted (JAN-2004) to the EMBL/GenBank/DBSJ databases.
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CC -----
DR EMBL; AE016879; AAP26128.1; -; Genomic DNA.
DR EMBL; AE017334; AAT31373.1; -; Genomic DNA.
DR EMBL; AE017225; AAT54410.1; -; Genomic DNA.
DR TIGR; BA2252; -.
DR TIGR; GBA2252; -.
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000182; GCN5acetyl_trans.
DR Pfam; PF00583; Acetyltransf_1; I.
DR Complete proteome; transferase.
SQ SEQUENCE 119 AA; 13963 MW; 7A95C8D72145B508 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 34 KVDDT 38

RESULT 96
Q738W2_BAC11
ID Q738W2_BAC11 PRELIMINARY; PRT; 119 AA.
AC Q738W2;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Acetyltransferase, GNAT family.
GN ORFNames=BCE 2281;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OC NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Raiko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
adaptations and a large plasmid related to Bacillus anthracis pXO1."
RL Nucleic Acids Res. 32:977-988(2004).
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CC -----
DR EMBL; AE017194; AAS41200.1; -; Genomic DNA.
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000182; GCN5acetyl_trans.
DR Pfam; PF00583; Acetyltransf_1; I.
DR Complete proteome; transferase.
SQ SEQUENCE 119 AA; 13993 MW; ESAD587D5F1503A3 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 34 KVDDT 38

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RESULT 97
Q8U332_PYRFU
ID Q8U332_PYRFU PRELIMINARY; PRT; 120 AA.
AC Q8U332;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Hypothetical protein PF0643.
GN OrderedLocusNames=PF0643;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OC NCBI_TaxID=2261;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBSJ databases.
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CC -----
DR EMBL; AE010185; AAL80767.1; -; Genomic DNA.
DR BioCyc; PFU186497:PF0643-MONOMER; -.
DR LinkHub; Q8U332; -.
DR Complete proteome.
SQ SEQUENCE 120 AA; 13395 MW; 4B5C2B85C5609085 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
Db 16 VDDTF 20

RESULT 98
Q4MTS5_BACCE
ID Q4MTS5_BACCE PRELIMINARY; PRT; 120 AA.
AC Q4MTS5;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Acetyltransferase.
GN ORFNames=BCE G9241_2217;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OC NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Ralstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
with an illness resembling inhalation anthrax."
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAEK0100006; EAL15572.1; -; Genomic DNA.

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DR GO: GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO: GO:0016740; P:transferase activity; IEA.
KW transferase.
SQ SEQUENCE 120 AA; 14050 MW; 96E8CCE346986E27 CRC64;

Query Match          55.6%; Score 5; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 34 KVDDT 38

RESULT 99
QSDHT7 SCHJA PRELIMINARY; PRT; 126 AA.
AC QSDHT7;
DT 29-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 23-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE SJCCHC02803 protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Han Z.;
RA "The full-length cDNA sequences of Schistosoma japonicum genes.";
RT Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP Liu F., Lu J., Hu W., Wang S.-Y., Cui S.-J., Chi M., Yan Q.,
RA Wang X.-R., Song H.-D., Xu X.-N., Wang J.-J., Zhang X.-L., Wang Z.-Q.,
RA Xue C.-L., Brindley P.J., McManus D.P., Yang P.-Y., Feng Z., Chen Z.,
RA Han Z.-G.;
RT "New Perspectives on Host-parasite Interplay by Comparative
RT Transcriptomic and Proteomic Analyses of the Human Blood Fluke,
RT Schistosoma japonicum.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
[3]
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CC -----
DR EMBL; AY812887; AAW24619.1; -; mRNA.
SQ SEQUENCE 126 AA; 14649 MW; F44CAF4F9495A4DC CRC64;

Query Match          55.6%; Score 5; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 22 KVDDT 26

RESULT 100
Q33XT4 9GAMM PRELIMINARY; PRT; 128 AA.
AC Q33XT4;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Membrane protein, putative precursor.
GN ORFNames=ShewDRAFT_2962;
OS Shewanella sp. PV-1;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=323850;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=PV-4;

```

```

RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Istrani S., Pitluck S., Richardson P., Richardson P.,
RT "Sequencing of the draft genome and assembly of Shewanella sp. PV-4.";
RN Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PV-4;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Shewanella sp. PV-4.";
RA Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AALSO1000003; EAP03875.1; -; Genomic_DNA.
KW Signal.
FT SIGNAL 1 20 Potential.
SQ SEQUENCE 128 AA; 13939 MW; 25FEDA74705A22BB CRC64;

Query Match          55.6%; Score 5; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 78 KVDDT 82

RESULT 101
Q8X3T8 ECOS7 PRELIMINARY; PRT; 128 AA.
AC Q8X3T8;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-FEB-2006, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE No significant matches.
GN OrderedLocustNames=z2511;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
CC -----
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CC -----
DR EMBL; AE005174; AAG56523.1; -; Genomic_DNA.
DR PIR; G85757; G85757.
KW Complete proteome.
SQ SEQUENCE 128 AA; 14229 MW; DA17C71370F86470 CRC64;

Query Match          55.6%; Score 5; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 11 KVDDT 11

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Db      14 KVDDT 18

RESULT 102
Q7NF95 GLOVI
ID Q7NF95 GLOVI PRELIMINARY; PRT; 130 AA.
AC Q9BMK4;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE G113631 protein.
GN OrderedLocustNames=g113631;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Gloeobacteriales; Gloeobacter.
OX NCBI_TaxID=33072;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292; DOI=10.1093/dnares/10.4.137;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Teuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimo S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids.";
RL DNA Res. 10:137-145(2003).
CC -----
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CC -----
CC
CC EMBL; BA000045; BAC91572.1; -; Genomic_DNA.
DR BIOCYG; GVIO251221:G113631-MONOMER; -.
KW Complete proteome.
SQ SEQUENCE 130 AA; 15261 MW; 3BF2C32C8990C7F6A CRC64;

Query Match 55.6%; Score 5; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 11 KVDDT 15

RESULT 103
PA2 APIC
ID PA2 APIC STANDARD; PRT; 134 AA.
AC Q9BMK4;
DT 01-NOV-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2006, sequence version 1.
DT 07-MAR-2006, entry version 31.
DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).
OS Apis cerana cerana (Oriental honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=94128;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC Shen L.R., Zhang C.X., Cheng J.A.;
RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RL
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides (By similarity).
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H2O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC -!- ALLERGEN: Causes an allergic reaction in human (By similarity).
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC -----
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CC -----
CC

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DR EMBL; AF321087; AAK09361.1; -; mRNA.
DR HSSP; P06630; 1POC.
DR SMR; Q9BMK4; 1-134.
DR InterPro; IPR008774; Phospholip_A2.
DR InterPro; IPR013090; Phospholip_A2_AS.
DR InterPro; IPR001211; PhospholipaseA2.
DR PANTHER; PTHR12253; Phospholip_A2; 1.
DR Pfam; PF05826; Phospholip_A2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2_ASP; FALSE_NEG.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Allergen; Calcium; Glycoprotein; Hydrolase; Lipid degradation;
KW Metal-binding.
FT CHAIN 1 134 Phospholipase A2.
FT ACT_SITE 34 34 /FTID=PRO_0000161722.
FT ACT_SITE 64 64 By similarity.
FT METAL 8 8 Calcium (via carbonyl oxygen) (By
FT METAL 10 10 Calcium (via carbonyl oxygen) (By
FT METAL 12 12 Calcium (via carbonyl oxygen) (By
FT METAL 35 35 Calcium (By similarity).
FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).
FT DISULFID 9 31 By similarity.
FT DISULFID 30 70 By similarity.
FT DISULFID 37 63 By similarity.
FT DISULFID 61 95 By similarity.
FT DISULFID 105 113 By similarity.
SQ SEQUENCE 134 AA; 15197 MW; CAC19BF92E4EC849 CRC64;

Query Match 55.6%; Score 5; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7
Db 64 DDTFY 68

RESULT 104
Q8ZI74 YERPE
ID Q8ZI74 YERPE PRELIMINARY; PRT; 134 AA.
AC Q8ZI74;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein YPO0641.
GN OrderedLocustNames=YPO0641;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Tittball R.W., Holden M.T.G.,
RA Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdono-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
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CC -----
CC
CC EMBL; AJ414143; CAC89494.1; -; Genomic_DNA.
DR PIR; AC0079; AC0079.

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RESULT 110
Q4N291_THEPA          PRELIMINARY;   PRT;   141 AA.
AC  Q4N291_1
DT  02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT  02-AUG-2005, sequence version 1.
DT  07-FEB-2006, entry version 3.
DE  Hypothetical protein.
GN  ORFNames-TP04_0466;
OS  Theileria parva.
OC  Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC  Theileria.
OX  NCBI_TaxID=5875;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=Muguga;
RX  PubMed=15994558; DOI=10.1126/science.1110439;
RA  Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA  Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.,
RA  Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA  Jiang L., Lynn J., Weaver B., Shoaibi A., Domingo A.R., Wasawo D.,
RA  Crabtree J., Wortman J.R., Haas B., Anguoli S.V., Creasy T.H., Lu C.,
RA  Suh B., Silva J.C., Uterback T.R., Feldblyum T.V., Pertea M.,
RA  Allen J., Niernan W.C., Taracha E.L., Salzberg S.L., White O.R.,
RA  Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
RT  "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
RL  Lymphocytes.";
RL  Science 309:134-137(2005).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=Muguga;
RA  Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA  Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA  Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA  Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA  Haas B., Anguoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA  Uterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA  Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA  Fraser C.M., Nene V.;
RL  Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC  -!- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
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CC  -----
DR  EMBL; AAGK01000004; EAN31818.1; -; Genomic_DNA.
KW  Hypothetical protein.
SQ  SEQUENCE 141 AA; 17475 MW; 1694DEA5448EFDA CRC64;

Query Match          55.6%; Score 5; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 DDTFY 7
DB  70 DDTFY 74

RESULT 111
ID  Q586G7_9TRYP          PRELIMINARY;   PRT;   147 AA.
AC  Q586G7;
DT  10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT  10-MAY-2005, sequence version 1.
DT  07-FEB-2006, entry version 3.
DE  Mago nashi-like protein, putative.
GN  ORFNames-Tb927_6.4950;
OS  Trypanosoma brucei.
OC  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX  NCBI_TaxID=5691;
RN  [1]

Query Match          55.6%; Score 5; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 DDTFY 7
DB  70 DDTFY 74

RESULT 112
ID  Q60DU6_ORYSA          PRELIMINARY;   PRT;   147 AA.
AC  Q60DU6;
DT  23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT  23-NOV-2004, sequence version 1.
DT  07-FEB-2006, entry version 6.
DE  Hypothetical protein OSUNBa0086E02.8.
GN  Name=OSUNBa0086E02.8;
OS  Oryza sativa (japonica cultivar-group).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP Clade;
OC  Ehrhartoideae; Oryzoae; Oryza.
OX  NCBI_TaxID=39947;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RA  Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA  Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA  Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA  Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA  Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA  Wu H.-P., Shaw J.-P.;
RT  "Oryza sativa BAC OSUNBa0086E02 genomic sequence.";
RL  Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
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CC  -----
DR  EMBL; AC144741; AAV25237.1; -; Genomic_DNA.
DR  Gramene; Q60DU6; -
KW  Hypothetical protein.
SQ  SEQUENCE 147 AA; 16892 MW; D89A9A93DCFLA649 CRC64;

Query Match          55.6%; Score 5; DB 2; Length 147;
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RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=GUTat10.1;
RA  Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
RA  Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
RA  Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
RA  Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
RA  Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=GUTat10.1;
RA  El-Sayed N.M., Khalak H., Adams M.D.;
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=GUTat10.1;
RA  Haas B., Blandin G., El-Sayed N.;
RL  Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC  -----
DR  EMBL; AC008146; AAX80287.1; -; Genomic_DNA.
DR  GO; GO:0005634; C:nucleus; IEA.
DR  GO; GO:0007530; P:sex determination; IEA.
DR  InterPro; IPR004023; Mago_nashi.
DR  PANTHER; PTHR12638; Mago_nashi; 1.
DR  Pfam; PF02792; Mago_nashi; 1.
SQ  SEQUENCE 147 AA; 17147 MW; 1BFEE46A0D3C187 CRC64;

Query Match          55.6%; Score 5; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 DTFY 8
DB  121 DTFY 125

RESULT 113
ID  Q60DU6_ORYSA          PRELIMINARY;   PRT;   147 AA.
AC  Q60DU6;
DT  23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT  23-NOV-2004, sequence version 1.
DT  07-FEB-2006, entry version 6.
DE  Hypothetical protein OSUNBa0086E02.8.
GN  Name=OSUNBa0086E02.8;
OS  Oryza sativa (japonica cultivar-group).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP Clade;
OC  Ehrhartoideae; Oryzoae; Oryza.
OX  NCBI_TaxID=39947;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RA  Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA  Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA  Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA  Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA  Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA  Wu H.-P., Shaw J.-P.;
RT  "Oryza sativa BAC OSUNBa0086E02 genomic sequence.";
RL  Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
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CC  -----
DR  EMBL; AC144741; AAV25237.1; -; Genomic_DNA.
DR  Gramene; Q60DU6; -
KW  Hypothetical protein.
SQ  SEQUENCE 147 AA; 16892 MW; D89A9A93DCFLA649 CRC64;

Query Match          55.6%; Score 5; DB 2; Length 147;
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Best Local Similarity 100.0%; Pred. No. 5.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 KVDDT 5
Db 136 KVDDT 140

RESULT 113
Q8F4Y0 LEPIN PRELIMINARY; PRT; 148 AA.
ID Q72QW4 LEPIC
AC Q72QW4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DE Hypothetical protein.
GN OrderedLocusNames=L1C11994; ORFNames=L1C_11994;
OS Leptospira interrogans serogroup Icterohaemorrhagiae serovar
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=44275;

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Fiocruz LI-130;
RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
RA Ho P.L., Haake D.A., Verjovski-Almeida S., Hartskeerl R.A.,
RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
RA Coutinho L.L., Degraeve W.M., Dellagostin O.A., El-Dorri H.,
RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Giglioli E.A.,
RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo J.L.M., Kimura E.T.,
RA Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Canargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.; reveals
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172(2004).

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EMBL; A016823; AAS70570.1; -; Genomic DNA.
GO; GO:0003824; F: catalytic activity; IEA.
InterPro; IPR003736; PAAI.
InterPro; IPR006683; Thioestr_supf.
Pfam; PF03061; 4HBT; 1.
TIGRFAMs; TIGR00369; unchar dom_1; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 148 AA; 16851 MW; 11B58255C1FC528D CRC64;

Query Match 55.6%; Score 5; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 47 VDDTF 51

RESULT 115
Q5IFZ7 9PROT PRELIMINARY; PRT; 149 AA.
AC Q5IFZ7;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Ammonia monooxygenase subunit A (Fragment).
GN Name=amoA;
OS uncultured ammonia-oxidizing bacterium.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; environmental samples.
OX NCBI_TaxID=152492;

RN NUCLEOTIDE SEQUENCE.
RP PubMed=15691919; DOI=10.1128/AEM.71.2.697-705.2005;
RX O'Mullan G.D., Ward B.B.;
RT "Relationship of Temporal and Spatial Variabilities of Ammonia-
RT Oxidizing Bacteria to Nitrification Rates in Monterey Bay,
RT California";
RL Appl. Environ. Microbiol. 71:697-705(2005).

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EMBL; AV736858; AAV91797.1; -; Genomic DNA.
GO; GO:0016020; C: membrane; IEA.
GO; GO:0004497; F: monooxygenase activity; IEA.
GO; GO:0006807; P: nitrogen compound metabolism; IEA.
DR InterPro; IPR003393; NH3_CH4_mOase_A.
Pfam; PF02461; AMO; 1.
KW Monooxygenase.
FT NON_TER 149
FT NON_TER 149
SQ SEQUENCE 149 AA; 16678 MW; 79D0C6C5190C30B7 CRC64;

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RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).

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EMBL; A010300; AAN49107.1; -; Genomic DNA.
DR GenomeReviews; AE010300 GR; LA1908.
DR BiOCYC; LINT189518:LA1908-MONOMER; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR InterPro; IPR003736; PAAI.
DR InterPro; IPR006683; Thioestr_supf.
DR Pfam; PF03061; 4HBT; 1.
DR TIGRFAMs; TIGR00369; unchar dom_1; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 148 AA; 16851 MW; 11B58255C1FC528D CRC64;

Query Match 55.6%; Score 5; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 47 VDDTF 51

RESULT 115
Q5IFZ7 9PROT PRELIMINARY; PRT; 149 AA.
AC Q5IFZ7;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Ammonia monooxygenase subunit A (Fragment).
GN Name=amoA;
OS uncultured ammonia-oxidizing bacterium.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; environmental samples.
OX NCBI_TaxID=152492;

RN NUCLEOTIDE SEQUENCE.
RP PubMed=15691919; DOI=10.1128/AEM.71.2.697-705.2005;
RX O'Mullan G.D., Ward B.B.;
RT "Relationship of Temporal and Spatial Variabilities of Ammonia-
RT Oxidizing Bacteria to Nitrification Rates in Monterey Bay,
RT California";
RL Appl. Environ. Microbiol. 71:697-705(2005).

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EMBL; AV736858; AAV91797.1; -; Genomic DNA.
GO; GO:0016020; C: membrane; IEA.
GO; GO:0004497; F: monooxygenase activity; IEA.
GO; GO:0006807; P: nitrogen compound metabolism; IEA.
DR InterPro; IPR003393; NH3_CH4_mOase_A.
Pfam; PF02461; AMO; 1.
KW Monooxygenase.
FT NON_TER 149
FT NON_TER 149
SQ SEQUENCE 149 AA; 16678 MW; 79D0C6C5190C30B7 CRC64;

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Query Match 55.6%; Score 5; DB 2; Length 149;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFFYV 9
 |||||
 Db 128 TFFYV 132

RESULT 116

Q9JAM5_9BACT PRELIMINARY; PRT; 150 AA.
 AC Q9JAM5;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE Ammonia monooxygenase (Fragment).
 GN Name=amoA;
 OS uncultured bacterium.
 OC Bacteria; environmental samples.
 OX NCBI_TaxID=77133;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21633822; PubMed=1172633; DOI=10.1128/AEM.68.1.245-253.2002;
 RA Dionisi H.M., Layton A.C., Harms G., Gregory I.R., Robinson K.G.,
 RA Sayler G.S.;
 RT "Quantification of Nitrosomonas oligotropha-like ammonia-oxidizing
 bacteria and Nitrospira spp. from full-scale wastewater treatment
 plants by competitive PCR.";
 RL Appl. Environ. Microbiol. 68:245-253 (2002).
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 CC
 CC EMBL; AF420300; AAL15012.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.
 DR GO; GO:0006807; P:nitrogen compound metabolism; IEA.
 DR InterPro; IPR003393; NH3_CH4_mOase_A.
 DR Pfam; PF02461; AMO; 1.
 KW Monooxygenase.
 FT NON_TER 1
 FT NON_TER 150
 FT NON_TER 150
 SQ SEQUENCE 150 AA; 16801 MW; 11DC7A7630D1E276 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFFYV 9
 |||||
 Db 129 TFFYV 133

RESULT 117

Q9AF59_9PROT PRELIMINARY; PRT; 151 AA.
 AC Q9AF59;
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 13.
 DE Ammonia monooxygenase (Fragment).
 GN Name=amoA;
 OS uncultured bacterium B4-3.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
 OC Nitrosomonadaceae; environmental samples.
 OX NCBI_TaxID=137839;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21141854; PubMed=11229931;
 RX DOI=10.1128/AEM.67.3.1351-1362.2001;
 RA Gieseke A., Furkhold U., Wagner M., Amann R., Schramm A.;

RT "Community structure and activity dynamics of nitrifying bacteria in a
 RT phosphate-removing biofilm.";
 RL Appl. Environ. Microbiol. 67:1351-1362 (2001).
 CC

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CC EMBL; AY007575; AAG22847.1; -; Genomic_DNA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004497; F:monooxygenase activity; IEA.

DR GO; GO:0006807; P:nitrogen compound metabolism; IEA.

DR InterPro; IPR003393; NH3_CH4_mOase_A.

DR Pfam; PF02461; AMO; 1.

KW Monooxygenase.

FT NON_TER 1

FT NON_TER 151

SQ SEQUENCE 151 AA; 16954 MW; 7638BED3BD9236A1 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFFYV 9
 |||||
 Db 130 TFFYV 134

RESULT 118

Q665U0_YERPS PRELIMINARY; PRT; 151 AA.
 AC Q665U0;
 DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Hypothetical protein.
 GN OrderedLocusNames=YPTB3420;
 OS Yersinia pseudotuberculosis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=633;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=IP32953 / Serotype I;
 RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
 RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
 RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
 RA Brubaker R.R., Fowler J., Hinnbusch J., Marceau M., Medigue C.,
 RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
 RA Derbise A., Hauser L.J., Garcia E.;
 RT "Insights into the evolution of Yersinia pestis through whole-genome
 RT comparison with Yersinia pseudotuberculosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831 (2004).
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 CC

CC EMBL; BX936398; CAH23658.1; -; Genomic_DNA.

DR Complete proteome; Hypothetical protein.

SQ SEQUENCE 151 AA; 16976 MW; 7B07E2A6BD70D7C3 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 8
 |||||
 Db 108 DTFYV 112

RESULT 119

Q8CKF9_YERPE PRELIMINARY; PRT; 153 AA.
 ID Q8CKF9_YERPE
 AC Q8CKF9; Q74RR4;

DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Hypothetical.
GN OrderedLocusNames=YF2954, Y3541;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
EX DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.",
RL J. Bacteriol. 184:4601-4611(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=1536893; DOI=10.1093/dnares/11.3.179;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RT avirulent to humans";
RL DNA Res. 11:179-197(2004).
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CC -----
DR EMBL; AE013957; AAM87089.1; --; Genomic DNA.
DR EMBL; AE017138; AAS63134.1; --; Genomic DNA.
DR BiOCyc; YPES187410:Y3541-MONOMER; --
DR BiOCyc; YPES229193:YP2954-MONOMER; --
KW Hypothetical protein.
SQ SEQUENCE 153 AA; 17263 MW; 0FAD7AF02027BB5A CRC64;

Query Match 55.6%; Score 5; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 8
Db 110 DTFY 114

RESULT 120
Q41753 MAIZE
ID Q41753 MAIZE PRELIMINARY; PRT; 155 AA.
AC Q41753;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Ubiquitin fusion protein.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Oh43; TISSUE=Radicle;
RA Liu L., Maillet D.S., Frappier J.H., d'Ailly K., Walden D.B.,
RA Atkinson B.G.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; U29160; AAA70104.1; --; Genomic DNA.
DR HSSP; Q862M4; LAAR.
DR SMR; Q41753; 1-76.
DR Gramene; Q41753;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR002906; Ribosomal_S27a.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF01599; Ribosomal_S27; 1.
DR PRINTS; PR00240; ubiquitin; 1.
DR PRINTS; PR00348; UBIQUITIN.
DR SMART; SM00213; UBO; 1.
DR PROSITE; PS00299; UBIQUITIN_1; 1.
DR PROSITE; PS0053; UBIQUITIN_2; 1.
SQ SEQUENCE 155 AA; 17732 MW; 8AABCBB92F413C3 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDVT 5
Db 107 KVDVT 111

RESULT 121
Q7MXG7 PORGI
ID Q7MXG7 PORGI PRELIMINARY; PRT; 155 AA.
AC Q7MXG7;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE DNA-binding protein, histone-like family.
GN OrderedLocusNames=PQ0222; ORFNames=PQ_0222;
OS Porphyromonas gingivalis (Bacteroides_gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidetes (Class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601(2003).
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CC -----
DR EMBL; AE015924; AAQ65452.1; --; Genomic DNA.
DR TIGR; PG0222;
DR BiOCyc; PGIN242619:PG0222-MONOMER; --
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR005902; HU_DNA_bd_put.
DR TIGRFAMS; TIGR01201; HU_rei; 1.
KW Complete proteome; DNA-binding.
SQ SEQUENCE 155 AA; 17249 MW; F6832CF53F5B4DA7 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5
Db 5

RESULT 122
Q7MXG7 PORGI
ID Q7MXG7 PORGI PRELIMINARY; PRT; 155 AA.
AC Q7MXG7;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE DNA-binding protein, histone-like family.
GN OrderedLocusNames=PQ0222; ORFNames=PQ_0222;
OS Porphyromonas gingivalis (Bacteroides_gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidetes (Class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601(2003).
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QY 1 KVVDT 5
Db 131 KVVDT 135

RESULT 122
ID Q6Q131 RAT PRELIMINARY; PRT; 155 AA.
AC Q6Q131;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 6.
DE LRRGT00177.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Xu C.S., Zhang L., Chang C.F., Han H.P., Wang G.P., Chai L.Q.,
RA Yuan J.Y., Yang K.J., Zhao L.F., Ma H., Wang L., Wang S.F., Xing X.K.,
RA Shen G.M., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY539928; AA66268.1; -; mRNA.
DR Ensembl; ENRN000000033993; Rattus norvegicus.
SQ SEQUENCE 155 AA; 17255 MW; 1188278B491FADEB CRC64;

Query Match 55.68; Score 5; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
Db 147 DTFY 151

RESULT 123
ID Q9VJR2 DROME PRELIMINARY; PRT; 157 AA.
AC Q9VJR2;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 2.
DE 07-FEB-2006, entry version 18.
DE CG15278-PA.
GN ORFNames=CG15278, Dmel CG15278;
OS Drosophila melanogaster (Fruit fly)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers J.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Canter A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Paulis B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

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RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner K., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.W.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AE003645; AAP53417.2; -; Genomic_DNA.
DR FlyBase; FBgn0032554; CG15278.
SQ SEQUENCE 157 AA; 18142 MW; 45259692497BFF19 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.8e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 5 TFFYY 9
Db 33 TFFYY 37

RESULT 124
Q70Z72 CANFA
ID Q70Z72 CANFA PRELIMINARY; PRT; 159 AA.
AC Q70Z72;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 21-FEB-2006, entry version 15.
DE Olfactory receptor (fragment).
GN Name=OR16H06;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Guignon P., Guyon R., Renier C., Cadieu E., Hitte C., Andre C.,
RA Galibert P.;
RT "Comparison of the canine and human olfactory receptor gene
RT repertoire."
RL Genome Biol. 4:R80-R80(2003).
CC -!- FUNCTION: Putative odorant or sperm cell receptor (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
CC similarity).
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CC
EMBL; AJ431547; CAD24257.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0007608; P:sensory perception of smell; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PANTHER; PTHR11398; Olfact_rcpt.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Membrane; Olfaction; Receptor;
KW Sensory transduction; Transducer; Transmembrane.
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 18340 MW; 73CDF660C08026D7 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 5.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 5 TFFYY 9
Db 123 TFFYY 127

RESULT 125
Q4UID3_THEAN
ID Q4UID3 THEAN PRELIMINARY; PRT; 161 AA.
AC Q4UID3;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=TA06515;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RX PubMed=15994597; DOI=10.1258/jrsm.98.7.320;
RA Pain A., Renauld H., Berriman M., Murphy L., Yeats C.A., Weir W.,
RA Kethnou A., Aslett M., Bishop R., Bouchier C., Cochet M.,
RA Coulson R.M.R., Cronin A., de Villiers E.P., Fraser A., Fosker N.,
RA Gardner M., Gobie A., Griffiths-Jones S., Harris D.E., Kozler F.,
RA Larke N., Lord A., Maser P., McKellar S., Mooney P., Morton P.,
RA Nene V., O'Neil S., Price C., Quail M.A., Rabinowitch E.,
RA Rawlings N.D., Rutter S., Saunders D., Seeger K., Shah T., Squares R.,
RA Squares S., Tivey A., Walker A.R., Woodward J., Dobbelaere D.A.E.,
RA Langsley G., Rajandream M.-A., McKeever D., Shiels B., Tait A.,
RA Barrell B., Hall N.;
RT "Genome of the host-cell transforming parasite Theileria annulata
RT compared with T. parva."
RL Science 309:131-133(2005).
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CC
EMBL; CR940347; CAI73156.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005732; C:small nucleolar ribonucleoprotein complex; IEA.
DR GO; GO:0006397; P:RNA processing; IEA.
DR InterPro; IPR006649; Euk_arc_LSM_core.
DR Pfam; PF01423; LSM; 1.
DR PDom; PD020287; snRNP; 1.
DR SMART; SM00651; Sm; 1.
KW Hypothetical protein.
SQ SEQUENCE 161 AA; 18443 MW; 0FB95E14C75ADF5C CRC64;

Query Match 55.6%; Score 5; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 6e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 3 DDTFY 7
Db 31 DDTFY 35

RESULT 126
Q43W25 SOLUS
ID Q43W25 SOLUS PRELIMINARY; PRT; 161 AA.
AC Q43W25;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=AcidDRAFT_3042;
OS Solibacter usitatus Ellin6076.
OC Bacteria; Acidobacteria; Solibacteres; Solibacterales;
OC Solibacteraceae; Solibacter.
OX NCBI_TaxID=234267;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ellin6076;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Solibacter usitatus
RT Ellin6076."

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RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ellin676;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Solibacter usitatus.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAT01000028; EMB56968.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 161 AA; 18142 MW; C897EB62D14A2A07 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFFY 7
DB 83 DDTFFY 87

RESULT 127
Q4N780 THEPA
ID Q4N780 THEPA PRELIMINARY; PRT; 162 AA.
AC Q4N780;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
DE ORFNames=TP01_0940;
GN Theileria parva.
OS Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OC NCBI_TaxID=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RX PubMed=15994558; DOI=10.1126/science.1110439;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoaibi A., Domingo A.R., Wasawo D.,
RA Crabtree J., Wortman J.R., Haas B., Angioli S.V., Creasy T.H., Lu C.,
RA Suh B., Silva J.C., Uterback T.R., Feldblyum T.V., Pertea M.,
RA Allen J., Niernan W.C., Taracha E.L., Salzberg S.L., White O.R.,
RA Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
RT "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
RT Lymphocytes.";
RL Science 309:134-137(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RX Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angioli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Uterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AGK01000001; EAN34178.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005732; C:small nucleolar ribonucleoprotein complex; IEA.
DR GO; GO:0006397; P:mRNA processing; IEA.
DR InterPro; IPR006649; Euk_arc_LSM_core.
DR Pfam; PF01423; LSM; 1.
DR ProDom; PD020287; snRNP; 1.
DR SMART; SM00651; Sm; 1.
KW Hypothetical protein.
SQ SEQUENCE 162 AA; 18708 MW; B5EE7718AE781445 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFFY 7
DB 31 DDTFFY 35

RESULT 128
Q4ZPM6 PSEU2
ID Q4ZPM6 PSEU2 PRELIMINARY; PRT; 163 AA.
AC Q4ZPM6;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical protein precursor.
DE OrderedLocusNames=Peyt_3866;
GN Pseudomonas syringae pv. syringae (strain B728a).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OC NCBI_TaxID=205918;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16043691; DOI=10.1073/pnas.0504930102;
RA Feil H., Fell W.S., Chain P., Larimer F., Dibartolo G., Copeland A.,
RA Lykidis A., Trong S., Nolan M., Goltsman E., Thiel J., Malfatti S.,
RA Loper J.E., Lapidus A., Detter J.C., Land M., Richardson P.M.,
RA Kyriades N.C., Ivanova N., Lindow S.E.;
RT "Comparison of the complete genome sequences of Pseudomonas syringae
RT pv. syringae B728a and pv. tomato DC3000";
RL Proc. Natl. Acad. Sci. U.S.A. 102:11064-11069(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
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CC -----
DR EMBL; CP000075; AAY38896.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein; Signal.
FT SIGNAL 1 32 Potential.
SQ SEQUENCE 163 AA; 18862 MW; E85C44B19B68E332 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
DB 84 VDDTF 88

RESULT 129
Q5SVM6 HUMAN
ID Q5SVM6 HUMAN PRELIMINARY; PRT; 166 AA.
AC Q5SVM6;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Ribosomal protein S6 kinase, 90kDa, polypeptide 1 (Fragment).
GN Names=RP56K1; ORFNames=RP11-492M19.2-007;
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Cactarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Harrison E.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; AL627313; CA114646.1; -; Genomic DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000961; Pkinase.C.
 DR InterPro; IPR000719; Ser_Thr_Kinase.
 DR InterPro; IPR008271; Ser_Thr_Pkin_AS.
 DR InterPro; IPR002290; Ser_Thr_Pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase.C; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS0108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding; Ribosomal protein;
 KW Serine/threonine-protein kinase; Transferase.
 FT NON_TER 1
 FT NON_TER 166
 FT NON_TER 166
 SQ SEQUENCE 166 AA; 18710 MW; D7089EF1616B6134 CRC64;
 Query Match 55.6%; Score 5; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 DDTFY 7
 Db [1]
 4 DDTFY 8
 RESULT 130
 Q51Y06 MONPV
 ID Q51Y06 MONPV PRELIMINARY; PRT; 167 AA.
 AC Q51Y06;
 DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, sequence version 1.
 DE MPKV-WRAIR013 (Hypothetical protein) (MPKV-SL-013) (MPKV-COP- 013).
 GN ORFNames=MPKV-COP-013, MPKV-SL-013, MPKV-WRAIR013,
 GN MPKV_L1B1970_184_018, MPKV_USA2003_039_018, MPKV_USA2003_044_018;
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=MPKV-WRAIR7-61, Sierra Leone, and COP-58;
 RX PubMed=16023693; DOI=10.1016/j.virol.2005.05.030;
 RA Chen N., Li G., Libzewski M.K., Atkinson J.P., Jahrling P.B., Feng Z.,
 RA Schriewer J., Buck C., Wang C., Lefkowitz E.J., Esposito J.J.,
 RA Harms T., Damon I.K., Roper R.L., Upton C., Buller R.M.;
 RT "Virulence differences between monkeypox virus isolates from West
 RT Africa and the Congo basin."
 RL Virology 340:46-63(2005).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=Liberia 1970 184, USA 2003 039, and USA_2003_044;
 RC PubMed=16186219; DOI=10.1099/vir.0.81215-0;
 RX Likos A.M., Sammons S.A., Olson V.A., Frace A.M., Li Y.,
 RA Olsen-Rasmussen M., Davidson W., Galloway R., Khristova M.L.,

RA Reynolds M.G., Zhao H., Carroll D.S., Curns A., Formenty P.,
 RA Esposito J.J., Regnery R.L., Damon I.K.;
 RT "A tale of two clades: monkeypox viruses."
 RL J. Gen. Virol. 86:2661-2672(2005).
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 CC -----
 DR EMBL; AY603973; AAU01223.1; -; Genomic DNA.
 DR EMBL; DQ011156; AAY97415.1; -; Genomic DNA.
 DR EMBL; DQ011157; AAY97613.1; -; Genomic DNA.
 DR EMBL; AY741551; AAW67771.1; -; Genomic DNA.
 DR EMBL; AY753185; AAX09114.1; -; Genomic DNA.
 DR EMBL; DQ011153; AAY96815.1; -; Genomic DNA.
 DR GO; GO:0016032; P:viral life cycle; IEA.
 DR InterPro; IPR004967; Pox_C7_P8A.
 DR Pfam; PF03287; Pox_C7_P8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 167 AA; 19963 MW; 928269D5ADFA1352 CRC64;
 Query Match 55.6%; Score 5; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 TFYV 9
 Db [1]
 95 TFYV 99
 RESULT 131
 Q5C0Z6 SCHJA
 ID Q5C0Z6 SCHJA PRELIMINARY; PRT; 170 AA.
 AC Q5C0Z6;
 DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 08-NOV-2005, sequence version 2.
 DT 07-FEB-2006, entry version 5.
 DE SCHGC08507 protein (Fragment).
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
 OC Schistosomatoidea; Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6182;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP Liu F., Lu J., Hu W., Wang S.-Y., Cui S.-J., Chi M., Yan Q.,
 RA Wang X.-R., Song H.-D., Xu X.-N., Wang J.-J., Zhang X.-L., Wang Z.-Q.,
 RA Xue C.-L., Brindley P.J., McManus D.P., Yang P.-Y., Feng Z., Chen Z.,
 RA Han Z.-G.;
 RT "New Perspectives on Host-parasite Interplay by Comparative
 RT Transcriptomic and Proteomic Analyses of the Human Blood Fluke,
 RT Schistosoma japonicum."
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; AY810790; AAX26679.2; -; mRNA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
 FT NON_TER 1
 FT NON_TER 170
 FT NON_TER 170
 SQ SEQUENCE 170 AA; 18444 MW; EE79561F108B51EC CRC64;
 Query Match 55.6%; Score 5; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVDVT 5


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Db      18 KVDVT 22
|||||
RESULT 132
Q5K255_GUITH PRELIMINARY; PRT; 170 AA.
AC Q5K255;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Putative 29 kDa ribonucleoprotein A (Fragment).
GN Name=riba;
OS Guillardia theta (Cryptomonas phi).
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55529;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gould S.B., Sommer M.S., Hadfi K., Zauner S., Maier U.G.;
RT "Transport of proteins into multimeric plastids."
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; AJ821834; CAH25374.1; -; mRNA.
DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR012677; a_b_plait_nuc_bd.
DR InterPro; IPR000504; RNPI_RNA_Bd.
DR Pfam; PF00076; RRM_1; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR Ribonucleoprotein; Viral nucleoprotein.
FT NON TER 1
SQ SEQUENCE 170 AA; 18877 MW; E62860E70B167E11 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDVT 5
|||||
Db 70 KVDVT 74

RESULT 133
Q6LVZ2_PHOPR PRELIMINARY; PRT; 170 AA.
AC Q6LVZ2;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hypothetical membrane-fusion protein.
GN Name=CBU1094; OrderedLocNames=PBPR0088;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N.,
RA Lauro F.M., Cestaro A., Malacrida G., Simonati B., Cannata N.,
RA Romualdi C., Bartlett D.H., Valle G.;
RT "Life at depth: Photobacterium profundum genome sequence and
RT expression analysis."
RL Science 307:1459-1461 (2005).
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DR EMBL; CR378663; CAG18533.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 170 AA; 18639 MW; 62BC48D6C8E2EB1C CRC64;

Query Match 55.6%; Score 5; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDVT 5
|||||
Db 134 KVDVT 138

RESULT 134
Q7VIT4_HELHP PRELIMINARY; PRT; 171 AA.
AC Q7VIT4;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Hypothetical protein.
GN OrderedLocNames=HH0520; ORFNames=HH_0520;
OS Helicobacter hepaticus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=32025;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 51449 / 3B1;
RX MEDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
RA Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P.,
RA Bell M., Droege M., Partmann B., Fischer H.-P., Ge Z., Hoerster A.,
RA Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
RT "The complete genome sequence of the carcinogenic bacterium
RT Helicobacter hepaticus."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906 (2003).
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CC -----
DR EMBL; AE017125; AAP77117.1; -; Genomic DNA.
DR BioCyc; HHEP235279:HH0520-MONOMER; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 171 AA; 19782 MW; 9EEF2ADEE1B8DC75 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 63 VDDTF 67

RESULT 135
Q6WHR4_BPKV4 PRELIMINARY; PRT; 175 AA.
AC Q6WHR4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical protein.
GN ORFNames=KVP40.0240;
OS Bacteriophage KVP40.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=75320;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22803260; PubMed=12923095;
RX DOI=10.1128/JB.185.17.5220-5233.2003;
RA Miller E., Heidelberg J., Eisen J., Nelson W., Durkin A., Ciecko A.,
```


RA Felblyum T., White O., Paulsen I., Nierman W., Lee J.,
RA Szczybinski B., Fraser C.;
RT "complete genome sequence of the broad-host-range vibriophage KVP40:
RL comparative genomics of a T4-related bacteriophage.";
RL J. Bacteriol. 185:5220-5233(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Miller E., Lee J., Szczybinski B.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AY283928; AAQ64309.1; -: Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 175 AA; 20874 MW; 2D95DAAA8F5E9B39 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 175;
Best Local Similarity 100.0%; Pred.No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
Db 48 VDDTF 52

RESULT 136
Q9DHU6_YLDV PRELIMINARY; PRT; 176 AA.
AC Q9DHU6;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DE 07-FEB-2006, entry version 10.
DR 16L protein precursor.
GN Name=16L;
OS Yaba-like disease virus (YLDV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Yatapoxvirus.
OX NCBI_TaxID=132475;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=21176366; PubMed=11277691; DOI=10.1006/viro.2000.0761;
RA Lee H.-J., Essani K., Smith G.L.;
RT "The genome sequence of Yaba-like disease virus, a yatapoxvirus.";
RL Virology 281:170-192(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lee H.J.;
RL Thesis (2000), Sir William Dunn School of Pathology, University of
RL Oxford, Oxford, UNITED KINGDOM.
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CC -----
DR EMBL: AJ293568; CAC21254.1; -: Genomic_DNA.
KW Signal.
FT SIGNAL 176 176 Potential.
SQ SEQUENCE 176 AA; 20531 MW; 55B33869B12B09DF CRC64;

Query Match 55.6%; Score 5; DB 2; Length 176;
Best Local Similarity 100.0%; Pred.No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 65 KVDDT 69

RESULT 137
Q5GSE5_WOLTR PRELIMINARY; PRT; 179 AA.
ID Q5GSE5_WOLTR
AC Q5GSE5;
DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.

DT 01-MAR-2005, sequence version 1.
DE 07-FEB-2006, entry version 7.
DE Cytochrome oxidase assembly factor.
GN OrderedLocustNames=Wb0491;
OS Wolbachia sp. subsp. Brugia malayi (strain TRS).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachiae; Wolbachia.
OX NCBI_TaxID=292805;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15780005; DOI=10.1371/journal.pbio.0030121;
RA Foster J., Ganatra M., Kamal I., Ware J., Makarova K., Ivanova N.,
RA Bhattacharya A., Kapatal V., Kumar S., Posfal J., Vincze T.,
RA Ingram J., Moran L., Lapidus A., Omelchenko M., Kyrpides N.,
RA Ghedin E., Wang S., Goltzman E., Joukov V., Ostrovskaya O.,
RA Tsukerman K., Mazur M., Comb D., Koonin E., Slatko B.;
RT "The Wolbachia genome of Brugia malayi: endosymbiont evolution within
RT a human pathogenic nematode.";
RL PLoS Biol. 3:599-614(2005).
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CC -----
DR EMBL: AE017321; AAW71079.1; -: Genomic_DNA.
DR GO: GO:0005507; F: copper ion binding; IEA.
DR InterPro: IPR007533; Ctag Cox11.
DR PANTHER: PTHR14053; Ctag Cox11; 1.
DR Pfam: PF04442; Ctag_Cox11; 1.
KW Complete proteome.
SQ SEQUENCE 179 AA; 20337 MW; 07EDC8C372750AC5 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 179;
Best Local Similarity 100.0%; Pred.No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TFFTV 9
Db 96 TFFTV 100

RESULT 138
Q4D000_TRYCR PRELIMINARY; PRT; 180 AA.
AC Q4D000;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DE 07-FEB-2006, entry version 5.
DE 10 kDa heat shock protein, putative.
GN ORFNames=Tc00.1047053509505.50;
OS Trypanosoma cruzi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
OC Schizotrypanum.
OX NCBI_TaxID=5693;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CL Brener;
RA El-Sayed N.M.A., Myler P.J., Bartholomew D.C., Nilsson D.,
RA Agarwal G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,
RA Blandin G., Westenberg S.J., Caler E., Cerqueira G.C., Branche C.,
RA Haas B., Anapuma A., Arner E., Aelund L., Attipoe P., Bontempi E.,
RA Bringsaud F., Burton P., Cadag E., Campbell D.A., Carrington M.,
RA Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,
RA Englund P.T., Fazellina G., Feldblyum T., Ferella M., Frasch A.C.,
RA Gull K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,
RA Kluge S., Koo H., Lacerda D., Levin M.J., Lorenzi H., Louie T.,
RA Machado C.R., McCulloch R., McKenna A., Mizuno Y., Mottram J.C.,
RA Nelson S., Ochaya S., Osogawa K., Pai G., Parsons M., Pentony M.,
RA Pettersson U., Pop M., Ramirez J.L., Rinta J., Robertson L.,
RA Salzman S.L., Sanchez D.O., Seyler A., Sharma R., Shetty J.,
RA Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
RA Van Aken S., Vogt C., Ward P.N., Wickstead B., Wortman J., White O.,
RA Fraser C.M., Stuart K.D., Anderson B.;
RT "The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas'

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RT Disease.";
RL Science 0:0-0(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=CL Brenner;
RC El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J.,
RA Aggarwal G., Caler E., Renaud H., Worthey E.A., Hertz-Powley C.,
RA Ghedin E., Peacock C., Bartholomeu D.C., Haas B.J., Tran A.-N.,
RA Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Badger J.,
RA Brindaud F., Cadag E., Carleton J.M., Cerqueira G.C., Creasy T.,
RA Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivans A.C.,
RA Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J.,
RA Salzberg S.L., Shallow J., Silva J.C., Sundaram J., Westenberg S.,
RA White O., Melville S.E., Donelson J.E., Andersson B., Stuart K.D.,
RA Hall N.;
RT "Comparative Genomics of Trypanosomatid Parasitic Protozoa.";
RL Science 0:0-0(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CL Brenner;
RA El-Sayed N., Bartholomeu D., Haas B.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL; AAKH01001336; EAN85852.1; -; Genomic DNA.
CC DR GO; GO:0005524; F:ATP binding; IEA.
CC DR GO; GO:0051082; F:unfolded protein binding; IEA.
CC DR GO; GO:0006457; P:protein folding; IEA.
CC DR GO; GO:0006986; P:response to unfolded protein; IEA.
CC DR InterPro; IPR001476; Chaprln_Cpn10.
CC DR Pfam; PF00136; Cpn10; 1.
CC DR PRINTS; PR00297; CHAPERONIN10.
CC DR ProDom; PD000566; Chaprln_Cpn10; 1.
KW Chaperone, Heat shock.
SQ SEQUENCE 180 AA; 20098 MW; 031E9A1B5742E90A CRC64;

Query Match 55.6%; Score 5; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 144 KVDDT 148

RESULT 139
Q32EE6_SHIDS PRELIMINARY; PRT; 180 AA.
AC Q32EE6;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Putative transcriptional regulator LYSR-type.
GN Names=yey; OrderedLocusNames=SDY 2224;
OS Shigella dysenteriae serotype 1 (strain Sd197).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=300267;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16275786; DOI=10.1093/nar/gki954;
RA Wang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA Yang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic
RT agents of bacillary dysentery."
RL Nucleic Acids Res. 33:6445-6458(2005).

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CC -----
CC EMBL; CP000034; ABB62309.1; -; Genomic DNA.
CC DR GO; GO:0003700; F:transcription factor activity; IEA.
CC DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
CC KW Complete proteome.
CC SQ SEQUENCE 180 AA; 20000 MW; 30ED00DFFADB95BB CRC64;

Query Match 55.6%; Score 5; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 99 VDDTF 103

RESULT 140
Q5FJR3_LACAC PRELIMINARY; PRT; 182 AA.
AC Q5FJR3;
DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical protein.
GN OrderedLocusNames=LBA1227;
OS Lactobacillus acidophilus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1579;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCFM;
RX PubMed=15671160; DOI=10.1073/pnas.0409188102;
RA Altermann E., Russell W.M., Azcarate-Peril M.A., Barrangou R.,
RA Buck B.L., McAuliffe O., Souther N., Dobson A., Duong T., Callanan M.,
RA Lick S., Hamrick A., Cano R., Klaenhammer T.R.;
RT "Complete genome sequence of the probiotic lactic acid bacterium
RT Lactobacillus acidophilus NCFM."
RL Proc. Natl. Acad. Sci. U.S.A. 102:3906-3912(2005).
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CC -----
CC EMBL; CP000033; AAV43061.1; -; Genomic DNA.
CC KW Complete proteome; Hypothetical protein.
CC SQ SEQUENCE 182 AA; 21096 MW; 2030DA6DBD7F2C05 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
Db 116 DDTFY 120

RESULT 141
Q64LE1_9ADEN PRELIMINARY; PRT; 183 AA.
AC Q64LE1;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hexon (Fragment).
OS Human adenovirus type 38.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=46943;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC VR-988;

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RX PubMed15364976; DOI=10.1128/JCM.42.9.3963-3969.2004;
RA "Sarantis H., Johnson G., Brown M., Petric M., Tellier R.;
RT "Comprehensive detection and serotyping of human adenoviruses by PCR
RL J. Clin. Microbiol. 42:3963-3969(2004).
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CC -----
DR EMBL; AY288124; AAQ24013.1; -; Genomic_DNA.
DR SMR; Q64LE1; 1-182.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000736; Adeno_hexon.
DR Pfam; PF01065; Adeno_hexon; 1.
DR ProDom; PD002815; Adeno_hexon; 1.
FT NON_TER 1
FT NON_TER 183
SQ SEQUENCE 183 AA; 20383 MW; 63F0C725BE3A82C1 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 96 KVDDT 100

RESULT 142
Q5CNC5 CRYHO PRELIMINARY; PRT; 186 AA.
ID Q5CNC5 CRYHO PRELIMINARY; PRT; 186 AA.
AC Q5CNC5;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE NAC domain protein.
GN ORFNames=Chro.60282;
OS Cryptosporidium hominis.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida;
OC Cryptosporididae; Cryptosporidium.
OX NCBI_TaxID=237895;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TU502;
RX PubMed15510150; DOI=10.1038/nature02977;
RA Xu P., Widmer G., Wang Y., Ozaki L.S., Alves J.M., Serrano M.G.,
RA Puiu D., Manque P., Akiyoshi D., Mackey A.J., Pearson W.R., Dear P.H.,
RA Bankier A.T., Peterson D.L., Abrahamsen M.S., Kapur V., Tzipori S.,
RA Buck G.A.;
RT "The genome of Cryptosporidium hominis.";
RL Nature 431:1107-1112(2004).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
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CC -----
DR EMBL; AAEL01000012; EAL38115.1; -; Genomic_DNA.
DR GO; GO:0003779; F:actin binding; IEA.
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; IEA.
DR InterPro; IPR002715; NAC.
DR InterPro; IPR003128; VHP.
DR Pfam; PF01849; NAC; 1.
SQ SEQUENCE 186 AA; 21326 MW; 7AE6C179CBE887B9 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 96 KVDDT 100

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Db 30 KVDDT 34

RESULT 143
Q7YF2 CRYPV PRELIMINARY; PRT; 186 AA.
ID Q7YF2 CRYPV PRELIMINARY; PRT; 186 AA.
AC Q7YF2;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Conserved NAC domain protein (BTF domain, basal transcription factor).
GN ORFNames=IMB.263, csg6_2430;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Bimeriida;
OC Cryptosporididae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Iowa;
RA Bankier A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M.,
RA Vogel C., Teichmann S.A., Ivens A., Dear P.H.;
RT "Integrated mapping, chromosomal sequencing and sequence analysis of
Cryptosporidium parvum.";
RL Genome Res. 0:0-0(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Iowa type II;
RX PubMed15044751; DOI=10.1126/science.1094786;
RA Abrahamsen M.S., Templeton T.J., Enomoto S., Abrahante J.E., Zhu G.,
RA Lantto C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,
RA Bankier A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,
RA Anantharaman V., Aravind L., Kapur V.;
RT "Complete genome sequence of the apicomplexan, Cryptosporidium
parvum.";
RL Science 304:441-445(2004).
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CC -----
DR EMBL; BX538351; CAD98533.1; -; Genomic_DNA.
DR EMBL; AAEE01000002; EAK8988.1; -; Genomic_DNA.
DR GO; GO:0003779; F:actin binding; IEA.
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; IEA.
DR InterPro; IPR002715; NAC.
DR InterPro; IPR003128; VHP.
DR Pfam; PF01849; NAC; 1.
SQ SEQUENCE 186 AA; 21241 MW; 805A07041AFB87A1 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 30 KVDDT 34

RESULT 144
Q47L35 THEFY PRELIMINARY; PRT; 188 AA.
ID Q47L35 THEFY PRELIMINARY; PRT; 188 AA.
AC Q47L35;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Putative ATP/GTP-binding protein.
GN OrderedLocNames=Tfu_2804;
OS Thermobifida fusca (strain YX).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptosporangineae; Nocardiopsaceae; Thermobifida.
OX NCBI_TaxID=269800;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC US DOE Joint Genome Institute;

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RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Di Bartolo G., Chain P., Schmutz J.,
RA Larimer F., Land M., Lykidis A., Richardson P.,
RT "Complete sequence of *Thermobifida fusca* YX.",
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; CP000088; AA256837.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR001806; Ras trnsfrmg.
DR Pfam; PF03029; ATP bind 1; 1.
DR PRINTS; PR00449; RASTNSFRMG.
KW Complete proteome.
SQ SEQUENCE 188 AA; 20464 MW; 9BAC9AEA219FB6F5 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
Db 71 VDDTF 75
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[1]
RESULT 145
Q3Y144_ENTFC
ID Q3Y144_ENTFC PRELIMINARY; PRT; 189 AA.
AC Q3Y144;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Transferase hexapeptide repeat.
GN ORFNames=EfaeDRAFT_1650;
OS Enterococcus faecium DO.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=333849;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DO;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.,
RT "Sequencing of the draft genome and assembly of *Enterococcus faecium*
RT DO.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DO;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.,
RT "Annotation of the draft genome assembly of *Enterococcus faecium* DO.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DO;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.,
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAK03000013; EBN10199.1; -; Genomic_DNA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001451; Hexapep_transf.

DR Pfam; PF00132; Hexapep; 2.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
KW Transferase.
SQ SEQUENCE 189 AA; 20753 MW; AC49EF58AF3D26A8 CRC64;

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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 59 KVDDT 63
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RESULT 146
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AC Q5MJW8;
DT 01-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 01-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Avr9/Cf-9 rapidly elicited protein 36 (Fragment).
GN Name=ACRE36;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15598806; DOI=10.1105/tpc.104.026013;
RA Rowland O., Ludwig A.A., Merrick C.J., Baillieul F., Tracy F.E.,
RA Durrant W.E., Fritz-Laylin L., Nekrasov V., Sjolander K., Yoshioka H.,
RA Jones J.D.;
RT "Functional Analysis of Avr9/Cf-9 Rapidly Elicited Genes Identifies a
RT Protein Kinase, AC1K1, That Is Essential for Full Cf-9-Dependent
RT Disease Resistance in Tomato.";
RL Plant Cell 17:295-310 (2005).
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CC -----
DR EMBL; AY775033; AAV92892.1; -; mRNA.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR009007; Pept_Aspartc_cat.
DR InterPro; IPR001461; Peptidase_A1.
DR PANTHER; PTHR13683; Peptidase_A1; 1.
FT NON TER 1
SQ SEQUENCE 191 AA; 21454 MW; B6CAFD141916CFB1 CRC64;

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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TFYIV 9
Db 31 TFYIV 35
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[1]
RESULT 147
Q6C1O6_YARLI
ID Q6C1O6_YARLI PRELIMINARY; PRT; 192 AA.
AC Q6C1O6;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Similarity.
GN OrderedLocNames=YALI0F142899;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;


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RC STRAIN=DSM 15236;
RG US DOE Joint Genome Institute (JGI-PGP);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israeli S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Rhodofexax
RT ferrireducens DSM 15236.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 15236;
RG US DOE Joint Genome Institute (JGI-ORN);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Rhodofexax ferrireducens
RT DSM 15236.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
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CC preliminary data.
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CC -----
DR EMBL; AAJK01000016; EAO39974.1; -; Genomic_DNA.
DR InterPro; IPR007055; TAD.
DR Pfam; PF04972; BON; 2.
DR PROSITE; PS50914; BON; 2.
KW Signal.
FT SIGNAL 1 27 Potential.
SQ SEQUENCE 196 AA; 20013 MW; BD57C939F69A2CD5 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 126 KVDDT 130

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Search completed: May 17, 2006, 06:27:38
 Job time : 263 secs